

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 18, 2002, 05:20:10 ; Search time 58.31 Seconds

(without alignments)  
1919.809 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICQKFCVVLHWEIVIT.....QTCTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4784.5	76.5	1162	2	PC4184
2	4766.5	76.2	1162	2	S68438
3	3793	60.6	900	2	S68440
4	3785	60.5	892	2	S68439
5	3785	60.5	894	2	S68437
6	3729	59.6	895	2	S74225
7	3340	53.4	805	2	S68441
8	366	5.9	917	2	I49699
9	345.5	5.5	918	2	A36337
10	339.5	5.4	918	2	A44257
11	313	5.0	837	2	A34898
12	294.5	4.7	1097	2	S17308
13	288.5	4.6	863	2	C38252
14	284	4.5	783	2	JH0329
15	281.5	4.5	1092	2	JX0312
16	277	4.4	771	2	B38252
17	251.5	4.0	2302	2	T14328
18	220	3.5	830	2	I50455
19	209.5	3.3	831	2	JQ1655
20	191.5	3.1	6805	2	S20901
21	188	3.0	26926	1	I38344
22	182.5	2.9	1471	2	T19506
23	177	2.8	2481	2	A43908
24	174	2.8	1375	2	T13822
25	172	2.8	1896	2	T08851
26	170	2.7	1232	2	T43027
27	169.5	2.7	1443	2	I50600
28	166.5	2.7	2029	1	TDFFPK
29	166	2.7	3488	2	T34418

30	165	2.6	630	2	I51086
31	165	2.6	1526	2	T13823
32	160	2.6	1197	2	T30581
33	159	2.5	2340	2	I48310
34	158	2.5	1825	2	C88400
35	158	2.5	1825	2	T32828
36	158	2.5	2338	2	I73957
37	156	2.5	1000	2	I46521
38	154.5	2.5	2386	1	FNMU
39	153.5	2.5	440	2	JL0144
40	153.5	2.5	460	2	JL0145
41	153.5	2.5	610	2	A36116
42	150.5	2.4	310	2	A29884
43	150.5	2.4	412	2	A41070
44	150.5	2.4	5005	2	F82884
45	148.5	2.4	610	2	A34631

## ALIGNMENTS

RESULT 1

PC4184

Leptin receptor, Ob-Rb - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 01-Dec-2000

C:Accession: JC4895; JC4896; JC4897; PC4184; JC4797

R: Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta

Biochem. Biophys. Res. Commun. 225, 75-83, 1996

A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi

A:Reference number: JC4895; MUID:96332408

A:Accession: JC4895

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1162 &lt;TA3&gt;

A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAAL2831.1; PID:d1013515; PID:g15

A:Accession: JC4896

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-889, 'RADTL' &lt;TA2&gt;

A:Cross-references: DDBJ:D85557

A:Accession: JC4897

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-796, 'G', 1157-1158, 'TVLLIN' &lt;TA3&gt;

A:Cross-references: DDBJ:D85559

R: Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.

Biochem. Biophys. Res. Commun. 224, 597-604, 1996

A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)

A:Reference number: PC4184; MUID:96295531

A:Accession: PC4184

A:Molecule type: mRNA

A:Residues: 840-1162 &lt;TID&gt;

A:Cross-references: DDBJ:D84550

R: Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.

Biochem. Biophys. Res. Commun. 222, 19-26, 1996

A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f

A:Reference number: JC4797; MUID:96212906

A:Accession: JC4797

A:Molecule type: mRNA

A:Residues: 1-889, 'RADTL' &lt;TID&gt;

A:Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAAL2230.1; PID:g1374708

A:Experimental source: adipose cell

C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa

C:Genetics:

A:Gene: fa

C:Keywords: appetite; transmembrane protein

F:840-860/Domain: transmembrane #status predicted &lt;TM&gt;

F:861-1162/Domain: intracellular #status predicted &lt;IN&gt;

Query Match 76.5%; Score 4784.5; DB 2; Length 1162;  
Best Local Similarity 75.6%; Pred. No. 6.5e-303;

Matches	882;	Conservative	118;	Mismatches	161;	Indels	5;	Gaps	5;
QY	1	MICQKFCVLLHWEFIYVITAFNLSYPITPMRFKLSGCMPPNSFYDYLPAGLSKNTS	NS	60					
Db	1	MTCQKPYVLLHWEFLVITALNLAYPTSPWRFKLCAPSPSTDSDSLSPAGVPNNTSSL	60						
QY	61	NGHYETAPEPKFNSSGTHFSNLSKTTFFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSL	YF	120					
Db	61	KGASEALVEAKFNSTGIYVSELSKTIFFHCCEFGNEQGNCSALTGNTGKTLASVVKPL	YF	120					
QY	121	OQIDANMNIOCMKLGDKLFTCYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLYVQKS	180						
Db	121	ROLGVNWDIECMKGDLTFTICHNEPLLKNPFKNYDSKVHLLYDLPEVIDDLPLPLKDS	180						
QY	181	FOVWHONCSVHECCCECLVPVPYPAKNDLTLLMCLKITSGGVIFQSPDLSMVQPINMKPDP	240						
Db	181	FOYVQCNCYSRE-CECHVPVPRAKVNALLMYLEITSAGVSEFQSPDLSMQPMLVYKPPDP	239						
QY	241	LGTHMEITDDGNLKSWSPPLYPFPLOYQVYKSENSTVIREADKIVATSLSLYDSTLP	300						
Db	240	LGIRMEVTDGDLKISWDSQTKAPFPLOYQVYKLENS-TIVREAIEIVSDTSLVDSTLP	298						
QY	301	GSSYEVQVRGKRDLGPGIWSDMSTPRVFTQDVIYFPKILTSVGSNVSEHCYKKEKNI	360						
Db	299	GSSYEVQVRKRLDGGVWSWDSLPQLFTQDVMYFPKILTSVGSNASFCICIYKKNENQT	358						
QY	361	VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFNLNETKPRGKFTYDAVYCCNEHECHH	420						
Db	359	ISSKQIVMMNLAEKIPETQYNTVSDHISKVTFSNLKATPRGKFTYDAVYCCNEOACHH	418						
QY	421	RYAELVIVDVNINISCEITDGYLTLMTCRWSTSTIQSLAESTIQURHRSLSYCSIDPSIH	480						
Db	419	RYAELVIVDVNINISCEITDGYLTLMTCRWSPSTIQSLVGSYQURHRSLSYCPDNPISIR	478						
QY	481	PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGSDSPTCYLPDSVVKPLPP	540						
Db	479	PTSELKNCYLOTDGFYECVQPIFLLSGYTMIRINHSLSGSDSPTCYLPDSVVKPLPP	538						
QY	541	SSVKAETINIGLKLISWEKVEFPENNLOQOIRYGLSGKEVQWKMEYVDAKSKSVSLPV	600						
Db	539	SNVKAETINTGLKLKSVWEKVEFPENNLOFOIRYGLNGKEIQWKTHEVFDAKSKSASLPV	598						
QY	601	PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV	660						
Db	599	SDLCAYVAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV	658						
QY	661	TLIMKPLMKNDLSLSVQRYVINHTSCNGTWSDEDVGNHTKFEMLTQEAHTVTLAINSI	720						
Db	659	TLIMKPLMKNDLSLSVRRYVVKHRTAHNGTWSQDVGNQNTLFLMAESAHTVTLAINSI	718						
QY	721	GASVANFNLTFSWPMKSVNIYQSLSAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNE	780						
Db	719	GASLVNFNLTFSWPMKSVNAVQSLSAYPLSSCVILSWILSPNDYSLLYVIEWKNLND	778						
QY	781	GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA	840						
Db	779	DGMKWLRIPSNVNKKYIHDNFIPIEKYQFSLYPFMEGVGKPKIINGFTKDDIAKQONDA	838						
QY	841	GLYIVIVPIIISSSILLGLLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQKPEFHEHFT	900						
Db	839	GLYIVIVPIIISSCVLLGLTLLISHQRMKKLFWDDVPNPKNCSSWAQGLNFQKPEFHEHFT	898						
QY	901	KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVSVLSTT-DLEKGSVCISDQF	959						
Db	899	KHAESVIFGPLLEPEPVESEISVDTAMKNKDEMPVAMVSLTTPTDSTRGSICISDQC	958						
QY	960	NSVNFSEAEGETEYVEDESQRPVFKYATLISNSKPSFTEGEEQGLINSSVTKCFSSKNSP	1019						
Db	959	NSANFSGAOSTQGTCEDECSQSPSVKYATLVSNNKYVEIDEEOGAIHSSVSQCIARHSP	1018						
QY	1020	LKDSFSSNSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSYIY	1079						
Db	1019	LKQSFSSNSWEIEAQAFFILSDHPNVIISPOLSES-GLDELELEGNFPEENNHGKESYIY	1077						

[illegible]

QY 421 RYAEYVIDVNNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHYHRSSLYCSDIPSIH 480  
|||||  
Db 419 RYAEYVIDVNNINISCEITDGYLTMTKCRWSPSTIQSLVSTVQLRYHRSSLYCPDSPSIH 478  
QY 481 PISEPKDCYLOSDGFECYICFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPP 540  
|||||  
Db 479 PTSEPKNCVLOSDGFECYICFQPIFLLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPP 538  
QY 541 SSVKAETINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600  
|||||  
Db 539 SNVKAETIVNTGLTKVSWEKPVFPENNLOFQIRYGLSGKEIQWKTHEVFDAKSKSASLLV 598  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRTINDTMMKEKNV 660  
|||||  
Db 599 SDCAVYVQVRCRRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRTINDTMMKEKNV 658  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTSEEDVGNHFKFTFLWTEQAHTFVTLAINSI 720  
|||||  
Db 659 TLLMKPLTKNDLSLCSVQRYVINHTSCNGTSEEDVGNHFKFTFLWTEQAHTFVTLAINSI 718  
QY 721 GASVANENLTFSPMKSRYNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFIEEMKNLND 780  
|||||  
Db 719 GASLVNENLTFSPMKSRYNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFIEEMKNLND 778  
QY 781 GEIKWLRISSSVKRYTHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
|||||  
Db 779 DGMKWLRISSSVKRYTHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 838  
QY 841 GLVYIVPVISSSILLGLTLLISHORMKTLFWDVYVNPKNCSWAQGLNFQKPEFHEHFT 900  
|||||  
Db 839 GLVYIVPVISSSILLGLTLLISHORMKTLFWDVYVNPKNCSWAQGLNFQKPEFHEHFT 898  
QY 901 KHTASVTGPIILLEPITISEDISVDTSMKNKDEMPPTVSVLLSTT-DLEKGSVCISDQF 959  
|||||  
Db 899 KHAESVIFGPIILLEPITISEDISVDTSMKNKDEMPPTVSVLLSTT-DLEKGSVCISDQF 958  
QY 960 NSVNFSEAGTEVTEDESQRPVKYATLISNKSPESETGEEGLINSVYKCFSSKNSP 1019  
|||||  
Db 959 NSANFSGSQSTQVTECECQRPQPSVKYATLISNKSPESETGEEGLINSVYKCFSSKNSP 1018  
QY 1020 LKDSFSSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDDKSIYY 1079  
|||||  
Db 1019 LRQSFSSSSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDDKSIYY 1077  
QY 1080 LGVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLODSCSHFEVENNINLGTSKKTF 1139  
|||||  
Db 1078 LGVTSVNRRESGVLLTGEAGILCTFPAQCLFSDIRIQRGCSHFVENNINLGTSKKTF 1136  
QY 1140 SYMPOFOTCTQTHKIMENKMDLTV 1165  
|||||  
Db 1137 PYMPOFOTCTQTHKIMENKMDLTV 1162

RESULT 3  
S68440  
leptin receptor, splice form Ob-Rd - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Dec-2000  
C:Accession: S68440  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al.  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68440  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-900 <LEE>  
A:Cross-references: EMBL:049109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491  
A:Experimental source: tissue hypothalamus  
C:Comment: The nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Genetics: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68440

A:Gene: Ob-Rd  
C:Keywords: alternative splicing; appetite; transmembrane protein  
F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 60.6%; Score 3793; DB 2; length 900;  
Best Local Similarity 76.8%; Pred. No. 1.4e-238;  
Matches 691; Conservative 83; Mismatches 124; Indels 2; Gaps 2;

QY	1	MICQKFCVLLHMEFIYVITARNLSYPTTPMRFKLSCMPPNSTYDYFLPAGLSKNTSNS	60
Db	1	MMCKEYVVLHMEFLYIAALNLAYPISPWKFLFCGPPTTDUSFLSPAGAPNNASAL	60
QY	61	NGHETAVEPKFNSSGTHFSNISKTPTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	KGASAEIWEAKFNSSGIYVPELSKTFVHCFCFNGEQNCASALTNDTECKTLASVKAASF	120
QY	121	QQIDANWNIQCWLKGDCLKFLICYVESLFKNLFBNYNKVHLLVYLPVLEDSPLVPQKS	180
Db	121	RQLGVNMDIECMKGDLTFLFICHMEPLPKNPFKNYDSKVHLLDYLPVIDDSPLPLKDS	180
QY	181	FQWYHNCNSVHECCCLVPVPAPAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP	240
Db	181	FQYVQCNCSLRG-CECHVPVPRAKLNLYALLMYLEITSAGVSFQSPILMSLQPMLVKPPDP	239
QY	241	LGHMEITDDGNLKSMSSPPLVPPLQYQVKYSENSTVIREADKIVSATSLVDSTLP	300
Db	240	LGHMEVTDGDLKISWDSQIMADPPLQYQVKYLENS-TIVREAEIVSATSLVDSTLP	298
QY	301	GSSYEYQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPFKILTSYGSNVSFHCYKKENKI	360
Db	299	GSSYEYQVRSKRLDGSQWSDWSSPQVFTTQDVIYFPFKILTSYGSNASFHCYKKENQI	358
QY	361	VPSKEIYVMMNLAEKIPQSQDYVYSDHYSKYTFENLNETKPRGKFTYDAVYCCNEHECHH	420
Db	359	ISSKQIYVMMNLAEKIPQIYQSIYSDHYSKYTFENLNETKPRGKFTYDAVYCCNEQACHH	418
QY	421	RYAEIYIDVININISCETDGYLTMTCRMSTSTIQSLAESTLQLRKHYRSSLYCSIDPSIH	480
Db	419	RYAEIYIDVININISCETDGYLTMTCRMSPSTIQSLVSTVQLKHYRSSLYCPDPSIH	478
QY	481	PISPEPDCYLOSDFEYECIFQPIFLISGYTMWIRINHSLSGLSDIPTCVLPDSVVKPLP	540
Db	479	PTSEPRKCVLQRDGEYECVQPIFLISGYTMWIRINHSLSGLSDIPTCVLPDSVVKPLP	538
QY	541	SSVKAETINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWKHYEVYDAKSASVSLP	600
Db	539	SNVKAETIVNTGLLKVSWEKVPFPENNLOQIRYGLSGKEIQWKHYEVYDAKSASASLV	598
QY	601	PDLCAVYAVQVRCKRLDGLGYWMSNNSPAYTVVMDIKVPMRGPEIWRITNGDTMKKEKNV	660
Db	599	SDLCAYVYVQVRCKRLDGLGYWMSNNSPAYTVVMDIKVPMRGPEIWRKMDGDVTKKERNV	658
QY	661	TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSSEDEVGNHTKFTFLTEQAHVTYVLAINSI	720
Db	659	TLLMKPLTKNDLSLCSVRRYVVKHRTAHNGTWSSEDEVGNRTNLTFLTEPAHTVTYVLAIVNSL	718
QY	721	GASVANENLTFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMFYIIEWKNLNED	780
Db	719	GASLVNENLTFSPMSKVSAVESLSAYPLSSSCVILSWTILSPDDYSLLYLVIEWKILNED	778
QY	781	GEIKWLRISSSVKKYIYIHDFIPIEKQFSLYPIFMEGVGPKIINSFTQDDIEKHSDA	840
Db	779	DGMKWLRIPSNVKKFYIHDNFIPIEKQFSLYPVFMEGVGPKIINGFTKDAIDKQONDA	838
QY	841	GLYVIVPVIISSSILLGLTLLISHQMKKLFMEDVPPNPKNCSNAOGLNEOKPETFEHLFI	900
Db	839	GLYVIVPVIISSCVLLGLTLLISHQMKKLFMEDVPPNPKNCSNAOGLNEOKDISLHEVFI	898

RESULT 4  
568439  
leptin receptor, splice form Ob-Rc - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-2000 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68439, S68441  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al.  
Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68439  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 664-892 <LEE1>  
A:Cross-references: EMBL:U49108; NID:g1195488; PIDN:AAC52422.1; PID:g1195489  
A:Experimental source: splice form Rc; tissue hypothalamus  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
A:Accession: S68441  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-796, 'GMCTVLEMD' <LEE2>  
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493  
A:Experimental source: splice form Re; tissue hypothalamus  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
A:Note: this sequence from splice form Re is included to produce a complete sequence  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68441  
C:Genetics:  
A:Gene: Ob-Rc  
C:Keywords: alternative splicing; appetite

Query Match 60.5%; Score 3785; DB 2; Length 892;  
Best Local Similarity 77.3%; Pred. No. 4.5e-238;  
Matches 689; Conservative 81; Mismatches 119; Indels 2; Gaps 2;

QY 1 MIOCKFCVLLHMEFIYVITAFNLSYPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 MIOCKFCVLLHMEFIYVITAFNLSYPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120  
Db 61 KGASEAIVEAKFNSSGTHFSNLSKTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLKFLICVESLFEKNLFRNRYNRYVHLVLPVLEDSPLVPQKS 180  
Db 121 ROLGVNWDIECWMKGLDLEFLICHEMELPKNPKNYDSKVHLLYDLPEVIDDSPPLPKDS 180  
QY 181 FOMVHCNCSVHECCGLVFPVPTAKLNDTLMLCKITSGGVIFQSPIMSVQPINMYKPPDP 240  
Db 181 FQTVQCNCSLRG-CECHVAVPRAKLNALMYLETISAGVSFOSPLMSLOPMLVYKPPDP 239  
QY 241 LGLHMEITDDGNLKSWSPPVLPVLPLOYQVYKSENSTVIYREADKIVSATSLVDSILP 300  
Db 241 LGLHMEVTTDDGNLKSWSPPVLPVLPLOYQVYKSENSTVIYREADKIVSATSLVDSILP 298  
QY 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360  
Db 299 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 358  
QY 361 VPSKEIVMMNLAEKIPQSQDYDVSDHVSQVTFNLETKPRGKFTYDAVYCCNEHCCH 420  
Db 359 ISSKQIVMMNLAEKIPQSQDYDVSDHVSQVTFNLETKPRGKFTYDAVYCCNEHCCH 418  
QY 421 RYAEIYVIDVNNISCEFDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDTPSIH 480  
Db 419 RYAEIYVIDVNNISCEFDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDTPSIH 478  
QY 481 PISEPKDCYLQSDGFYEYFQPIFLLSGYTMMIRINHSLSGLSDSPPTCVLPDPSVYKPLPP 540  
Db 479 PTSEPKNCVLRDGFYEYFQPIFLLSGYTMMIRINHSLSGLSDSPPTCVLPDPSVYKPLPP 538  
QY 541 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQMKMEVYDAKSXSVSLPV 600  
Db 539 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQMKMEVYDAKSXSVSLPV 598  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPWFRIINGDMKKENK 660

Db 599 SDLCAYVAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPWFRIINGDMKKENK 658  
QY 661 TLLMKPLMKNDLSQVRYVINHHSCNGTWSMEDVGNHTKFEFLTQEAHTVTLAINSI 720  
Db 659 TLLMKPLMKNDLSQVRYVINHHSCNGTWSMEDVGNHTKFEFLTQEAHTVTLAINSI 718  
QY 721 GASVANFNLFSPMPSKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKLNED 780  
Db 719 GASVANFNLFSPMPSKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKLNED 778  
QY 781 GEIKMLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKRIINSFTQDDIEKHQSDA 840  
Db 779 DGMKMLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKRIINSFTQDDIEKHQSDA 838  
QY 841 GLYVIVPVIISSSILLLGTLTLLSHQRMKLFMEDVPPNPKNSWAQGLNFQK 891  
Db 839 GLYVIVPVIISSSILLLGTLTLLSHQRMKLFMEDVPPNPKNSWAQGLNFQK 889

RESULT 5

leptin receptor, splice form Ob-Ra - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-2000 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68437  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al.  
Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68437  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-894 <LEE>  
A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485  
A:Experimental source: splice form Ra; tissue hypothalamus  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68441  
C:Genetics:  
A:Gene: Ob-Ra  
C:Keywords: alternative splicing; appetite

Query Match 60.5%; Score 3785; DB 2; Length 894;  
Best Local Similarity 77.3%; Pred. No. 4.6e-238;  
Matches 689; Conservative 81; Mismatches 119; Indels 2; Gaps 2;

QY 1 MIOCKFCVLLHMEFIYVITAFNLSYPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 MIOCKFCVLLHMEFIYVITAFNLSYPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120  
Db 61 KGASEAIVEAKFNSSGTHFSNLSKTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLKFLICVESLFEKNLFRNRYNRYVHLVLPVLEDSPLVPQKS 180  
Db 121 ROLGVNWDIECWMKGLDLEFLICHEMELPKNPKNYDSKVHLLYDLPEVIDDSPPLPKDS 180  
QY 181 FOMVHCNCSVHECCGLVFPVPTAKLNDTLMLCKITSGGVIFQSPIMSVQPINMYKPPDP 240  
Db 181 FQTVQCNCSLRG-CECHVAVPRAKLNALMYLETISAGVSFOSPLMSLOPMLVYKPPDP 239  
QY 241 LGLHMEITDDGNLKSWSPPVLPVLPLOYQVYKSENSTVIYREADKIVSATSLVDSILP 300  
Db 240 LGLHMEVTTDDGNLKSWSPPVLPVLPLOYQVYKSENSTVIYREADKIVSATSLVDSILP 298  
QY 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360  
Db 299 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 358  
QY 361 VPSKEIVMMNLAEKIPQSQDYDVSDHVSQVTFNLETKPRGKFTYDAVYCCNEHCCH 420



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Db 359 ISSKQIWMNRNLAEKIPETQYSIYSDRVSKVTFESNLKATPRGKFTYDAVYCCNEQACH 418
QY 421 RYAEIYIDVININISCEIDGYLTKMTCRSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
Db 419 RYAEIYIDVININISCEIDGYLTKMTCRSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 478
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKNCVLRQDGFECVFPDPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQKMYEVDKSKSVSLPV 600
Db 539 SSVKAEITVNTGLTKVSWKPEPPENNLOFQIRYGLSGKEIQWKTHEVFDKSKSVSLPV 598
QY 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
Db 599 SDCAVYVQVRCRDLGLGYWSNNSPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 658
QY 661 TLLMKPLMKNDLSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 659 TLLMKPLMKNDLSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTVLAINSI 718
QY 721 GASVAFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFTEWKNLND 780
Db 719 GASVAFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFTEWKNLND 778
QY 781 GEIKWLRISSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 779 DGMKWLRIPISNVKKFYIHDNFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 838
QY 841 GLYIVPVITISSILLGLTLLISHQRMKLEWEDVPNPKNCMAQGLNPK 891
Db 839 GLYIVPVITISSILLGLTLLISHQRMKLEWEDVPNPKNCMAQGLNPK 889

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RESULT 6
S74225
leptin receptor, isoform Ob-Rf - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
C:Accession: S74225
R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
FEBS Lett. 392, 87-90, 1996
A:Title: A novel leptin receptor isoform in rat.
A:Reference number: S74225; MUID:96368027
A:Accession: S74225
A:Molecule type: mRNA
A:Residues: 1-895 <MAN>
A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213
A:Experimental source: strain Sprague-Dawley; tissue type brain
C:Genetics:
A:Gene: rob-R
C:Keywords: appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TMM>

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Query Match 59.6%; Score 3729; DB 2; Length 895;
Best Local Similarity 76.5%; Pred. No. 2e-234;
Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;
QY 1 MICQKFCVLLHMEFYITAFNLSYPTIPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MTCQKFEVLLHMEFYITAFNLSYPTIPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFSNLSTKTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
Db 61 KGASEALVEAKFNSTGIYVSELSKTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
QY 121 QQIDANMNIOQWLKGLDKLFCYVESLEFKNLERNYNYKVHLLYVPEVLEDSPLVPQGS 180
Db 121 RQLGVWMDIECWMKGLDLFLICHEMELKPNPKYNSKVVHLLYDPEVIDDLPLPLKDS 180
QY 181 FQWVHCNCSVHECCEGLVFPVFAKINDTLLMCLKITSGVIFQSPMSVQPINMVKPDPP 240

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Db 181 FQVQCNCSVRE-CECHVPVPRAKVNAALIMLEYITSAGVSFQSPMSVQPINMVKPDPP 239
QY 241 LGLHMETDDGNLTKISWSSPLVPPIQYQVKSSENSTVIREADKIVSATSLVDSILP 300
Db 240 LGLHMETDDGNLTKISWSSPLVPPIQYQVKSSENSTVIREADKIVSATSLVDSILP 298
QY 301 GSSYEYQVGRKRLDGPITWSDMSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKENKI 360
Db 299 GSSYEYQVGRKRLDGPITWSDMSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKENKI 358
QY 361 VPSKEIYWMNLAEKIPQSQYDVVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHCCH 420
Db 359 ISSKQIWMNRNLAEKIPETQYNTVSDHISKVTESNLKATPRGKFTYDAVYCCNEQACH 418
QY 421 RYAEIYIDVININISCEIDGYLTKMTCRSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
Db 419 RYAEIYIDVININISCEIDGYLTKMTCRSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 478
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKNCVLRQDGFECVFPDPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQKMYEVDKSKSVSLPV 600
Db 539 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEIQWKTHEVFDKSKSVSLPV 598
QY 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
Db 599 SDCAVYVQVRCRDLGLGYWSNNSPAYTVMDIKVPMRGPEFWRILNGDTMKKEKNV 658
QY 661 TLLMKPLMKNDLSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 659 TLLMKPLMKNDLSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTVLAINSI 718
QY 721 GASVAFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFTEWKNLND 780
Db 719 GASVAFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFTEWKNLND 778
QY 781 GEIKWLRISSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 779 DGMKWLRIPISNVKKFYIHDNFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 838
QY 841 GLYIVPVITISSILLGLTLLISHQRMKLEWEDVPNPKNCMAQGLNPK 891
Db 839 GLYIVPVITISSILLGLTLLISHQRMKLEWEDVPNPKNCMAQGLNPK 889

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RESULT 7
S68441
leptin receptor, splice form Ob-Re - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68441
A:Molecule type: mRNA
A:Status: nucleic acid sequence not shown; translation not shown
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Re; tissue hypothalamus
C:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Re
C:Keywords: alternative splicing; appetite
Query Match 53.4%; Score 3340; DB 2; Length 805;
Best Local Similarity 76.2%; Pred. No. 3.5e-209;

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Matches	608;	Conservative	73;	Mismatches	115;	Indels	2;	Gaps	2;
QY	1	MICQKFCVLLHWEFIYITAENLSYPITPWREKLSMCPNPSTYDYFLPAGLSKNTSNS	60						
Db	1	MMCKQFYVLLHWEFLYIALNLAYPISPWKFKECGPPNTTDDSFSLPAGAPNNASAL	60						
QY	61	NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYE	120						
Db	61	KGASEAIVEAKFNSSGTIYPELSKTVFHCCFGNEQGONCSALTDNTEGKTLASVKAASYE	120						
QY	121	QQIDANNINQCKLKGDLKLFICYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLVPQKS	180						
Db	121	ROLGVNMDIECMKGDLTIFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSPLEPLKDS	180						
QY	181	FQMVHNCNSVHECCELVVPYPTAKLNDTLMLCLKITSQCVIFQSPLMVQPINVAKDDP	240						
Db	181	FQTVQNCNSLRG-CECHVYVPRAKLNYALIMLYLETISAGVSPQSPMLSLQPMLVYKDDP	239						
QY	241	LGHMEITDDGNLKISWSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLVDLSLP	300						
Db	240	LGHMEVTDGNLKISWDSQTMAPFPLQYQVKYLENS-TIVREAEIVSATSLVDLSLP	298						
QY	301	GSSYEVOVRGKRLDGPILMSDWSTPRVFTTQDVIYPPPKILTSVGSNVSFHCITYKENKI	360						
Db	299	GSSYEVOVRSKRLDGSQVSDWSSPQVFTTQDVIYFPFKILLTSVGSNASFHCITYKENQI	358						
QY	361	VPSKEIVWMNLAEKIPQSOQDYVDVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH	420						
Db	359	ISSKQIVWMRNLAEKIPETQYISVSDRVSKVTFSNLKAIRPRGKFTYDAVYCCNEQACHH	418						
QY	421	RYAELVIDVNINISCTEDGYLLTKTCRWSTSTIOSLAESTLQRLRYHRSSLYCSDIPSIIH	480						
Db	419	RYAELVIDVNINISCTEDGYLLTKMTCRWSPSTIOSLYGSTVQLRYHRSLYCPDPSIIH	478						
QY	481	PISEPKDCYLOSDFEECTFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVYKPLPP	540						
Db	479	PTSEPKNCVLORGFEYECFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVYKPLPP	538						
QY	541	SSVKAELITINIGLKISMEKPVFPENNLOQIRYGLSGKEVQWKMEVYDAKSKSYSLPV	600						
Db	539	SNVKAELITVNTGLKVSMEKPVFPENNLOQIRYGLSGKEIQWKTHEVFDAKSKSASLLY	598						
QY	601	PDLCAVYAVQVRCKRLDGLCYWSNWSNPATYTVMDIKVPMRGPEFWRILINGDTMKKEKNV	660						
Db	599	SDLCAYVAVQVRCRRLDGLCYWSNWSNPATYLLMDYKVPMRGPEFWRKMDGDVTKERNV	658						
QY	661	TLMLKPLMKNDLSQSVORYVINHHTSCNGTWSSEDVGNHTKFTELMTQAHVTVLAINSI	720						
Db	659	TLMLKPLTKNDLSQSVRRYVVKHRTAHNGTWSSEDVGNRTNLTFLMTEPAHTVTVLAANSI	718						
QY	721	GASVANENLTFSWPMKSVYNVQSLASAYPLNSSCVIYSWILSPSDYKLMFYIEMKNLNE	780						
Db	719	GASLVNENLTFSWPMKSVAYESLSAYPLSSCVILSWILSPDDYSLLYLVIEKNLNE	778						
QY	781	GEIKMLRISSVKKYIIH 798							
Db	779	DGMKWLRIPSNVKKFYIIH 796							

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RESULT      8
149699      glycoprotein 130 - mouse
C:Species:  Mus musculus (house mouse)
C:Date:      02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: I49699; I48370
R:Salto, M.; Yoshida, K.; Hibl, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title:     Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:92291532
A:Accession: I49699
A:Status:    translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues:  1-917 <RES>

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A;/Cross-references: GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592  
A;/Accession: I48370  
A;/Status: translated from GB/EMBL/DBJ  
A;/Molecule type: mRNA  
A;/Residues: 1-917 <RE2>  
A;/Cross-references: EMBL:X62646; NID:g840816; PIDN:CMA44515.1; PID:g840817  
C;/Genetics:  
A;/Gene: gp130  
C;/Superfamily: cytokine receptor homology  
C;/Keywords: glycoprotein  
F;134-314/Domain: cytokine receptor homology <CRS>

Query Match	5.9%;	Score 366;	DB 2;	Length 917;
Best Local Similarity	20.9%;	Pred. No. 1.2e-15;		
Matches 191;	Conservative 140;	Mismatches 338;	Indels 244;	Gaps 42;

[illegible]

QY 999 GEEGLINSSVTK-CFSSKNSP----LKDSFSSNSWEIEAQAFFILSDQHNPNIISPHLTF 1053  
Db 770 PSVQVFSRSESTGQLDSEBERPDLQLVDSDGDEILPRQPYFKONCSQPE-ACPEISH 828  
QY 1054 SEGDELKLEGN 1066  
Db 829 FERSNOV--LSCN 839

RESULT 9  
A36337  
membrane glycoprotein gp130 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 28-Jul-2000  
C:Accession: A36337  
R:HiBi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.  
Cell 63, 1149-1157, 1990  
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.  
A:Reference number: A36337; MUID:91084844  
A:Accession: A36337  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-918 <HIB>  
A:Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354  
C:Genetics:  
A:Gene: GDB:IL6ST; GP130  
A:Cross-references: GDB:126725; OMIM:600694  
A:Map position: 5q11-5q11  
C:Superfamily: cytokine receptor homology  
C:Keywords: glycoprotein; membrane protein  
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 5.5%; Score 345.5; DB 2; Length 918;  
Best Local Similarity 19.8%; Pred. No. 2.6e-14;  
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;

QY 337 PPKILTSVGSNVSHFCITKK--ENKIVPSKEIYWMNLAEKIPQSQYDVVSDHYSKVTF 393  
Db 33 PESPVVQLHSNFTAVCVLKEKCMDFHVNANYIWKTN-HFTIPKEQYTIINRTASSVTF 91  
QY 394 ENLNETKPRGKFTYDAVYCCNEHECHRYAELVYIDV-----NINISC-ETDGYLTK 444  
Db 92 TDI-----ASLNIQLTLCNLTFLGQLEQNVYGITLISGLPEKPKNLSCIVNEG--KK 141  
QY 445 MTCRMSTSTIQSLAESTLQLRYHRSLSYCSIDPSIHPISEPKDCYLOSDFEGL--FQP 502  
Db 142 MRCEWDG----RETHLETFNFTLKSEWAT-----HKFA---DCKAKRDTPTSGTVDYST 188  
QY 503 IELLGYTMIRINHSLSGLSDSPTCVLPDSVVKLPSPSSVKAETIN---IGLLKISW 558  
Db 189 VYFVN-IEVWVEAENALGKVTSDHINFDPYKAKNPNNLS--VINSEELSLIKLTW 244  
QY 559 EKP-----VFPENNLQFQIRYGLSGKEVQWKMEYVDKAKSKSVSLPVPDL--CAVYAVQV 611  
Db 245 TNPSIKSVIILKYNIOYRTKDAST----WSQIPPEDTASTRSSFTVODLKPTEYVERI 299  
QY 612 RCKRLDGLGYSNMSPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNVTLLMKPLMKND 671  
Db 300 RCMKEDGKGYSDWSEASGITYEDR-PSKAPSFYWKIDPSHTQGYRTVQLVWKTLPPE 358  
QY 672 SLCSVQRYVINHTSCNGTWSSEVDGNH---TKFTFLWTEQAHTVTVLAINSIGASVANF 727  
Db 359 ANGKILDYEV-----LTRMKSHLQNTVNAKTLVNLNDRYLATITVRNLVGSKSDAAV 413  
QY 728 NLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMFYIEWKNLNEDGE--IKW 785  
Db 414 LTIACDFQATHPVMDLKAFF-KDMLMVEWETTPRESVK--KYLEWCVLSDRACPITDW 470  
QY 786 LRISSSVKYYIHDHPIEKYQFSLYPIFMEGVGKPKII----- 825  
Db 471 QOEDGTVHRTYLRGNLAESKCYLLITVTPVYADGPGSPESIKAYLKQAPPSKGPVYRTKKV 530

QY 826 -----NSFTQDDIEKHQSDAGLY- 843  
Db 531 GKNEAVLEMDQLPVQYONGFIRNITYFYRTIGNETAVNVDSHSHTETVLSLSLSDT-LYM 589  
QY 844 -----VIVPVISSSI-LLGLTLISHQR--MKK 869  
Db 590 VRMAAYTDEGKDGPEFTTTPKFAQGEIETAVPVCLAFLLTLGLVLECFNKRDLIKK 649  
QY 870 LEWEDVPNPKNCWAQGLNFQKPEFTEHLEFIKHTASVTCGPLLEPETISEDISVDTSMK 929  
Db 650 HIWPNVPDPKSHIAQWSPHTP-----RH-----NFN 677  
QY 930 NKDEMPPTTVVSLSTLDLEKGSVCISDQFNSVNFSEAGTEVTEDESQROPE---VKY 986  
Db 678 SKDQM-----YSDGNFTDVSVEIEAND--KKPEPEDLKS 710  
QY 987 ATLISNSKPSSETGEEGLINSSVTKCFSSKNSPLKDSFNS 1028  
Db 711 LDLFKKEKINTEGHSSGIGGSS---CMSSSRPSISSSDENES 749

RESULT 10  
A44257  
interleukin-6 signal transducing molecule gp130 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Jul-2000  
C:Accession: A44257  
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.  
Genomics 14, 666-672, 1992  
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc  
A:Reference number: A44257; MUID:93052397  
A:Accession: A44257  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-918 <WAN>  
A:Experimental source: liver  
A>Note: sequence extracted from NCBI backbone (NCBIP:118488)  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 5.4%; Score 339.5; DB 2; Length 918;  
Best Local Similarity 20.8%; Pred. No. 6.3e-14;  
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

QY 327 VFTQDVI-----YPPKILTSVGSNVSHFCITKKENKIYPSKE--IYWMNLAE 374  
Db 14 IFLTTEISIGLVEPCGYIYEPFPVQSGSNFTATCVLKEKCLQVYSVNATYIWKTNHV- 72  
QY 375 KIPQSQYDVVSDHVSQYTFENLNETKPRGKFTYDAVY-----CCNEHECHRYAELVYI- 428  
Db 73 AVPKQVTVINRTASSVTF-----TDVVFQNVQLTLCNLSFGQIEQNVYGIT 119  
QY 429 -----DVNINISC-ETDGYLTKMTCRMSTSTIQSLAESTLQLRYHRSLSYCSIDPSIH 480  
Db 120 IISGYPPDIPNLSCIVNEG--KNMLCQ-----LDGRETYLETNYTLKSEWATE----- 167  
QY 481 PISEPKDCYLOSDFEGL--FQPIFLLSGYTMIRINHSLSGLSDSPTCVLPDSVVKPL 538  
Db 168 ---KFPDCRTK-HGTSSCMGYTPIYFVN-IEVWVEAENALGNVSEPIINFDPYDKVPS 222  
QY 539 PSSSVKAEITINI-GLLKISW-----EKPVPENNLOFQIRYGLSGKEVQWKMEYVDK 592  
Db 223 PPHNLVSTNSEELSLIKLAWNSGLDSILRLKSDIQYRTKDAST----WIQVPLEDTV 277  
QY 593 SKSVSLPVPDL--CAVYAVQVRCKRLDGLGYSNMSPAYTVVMDIKVPMRGPEFWRIN 650  
Db 278 SPRTSETVQDLKPFTEYVERIRISIKENGKGYSDWSEASGITYEDR-PSKAPSFYWKVN 336  
QY 651 GDTMKKEKNVTLLMKPLMKNDLSQVQRY--VINHTSCNGTWSSEVDGNHTKFTFLWTEQ 708  
Db 337 ANHPQEYRSARLIWKIPLSEANGKILDIYEVVLTQSKSVSQTYTV--NGTELIVNLINN 393

[illegible]

RESULT 11  
A34898  
granulocyte colony-stimulating factor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 05-Nov-1999  
C:Accession: A34898  
R:Fukunaga, R.; Ishizaka-Ikeda, E.; Seto, Y.; Nagata, S.  
Cell 61, 341-350, 1990  
A:Title: Expression cloning of a receptor for murine granulocyte colony-stimulating factor  
A:Reference number: A34898; MUID:90235283  
A:Accession: A34898  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-837 <FUK>  
A:Cross-references: GB:M58268; NID:g193454; PIDN:AAA37673.1; PID:g193455; GB:M32699  
C:Keywords: transmembrane protein

```

Query Match          5.0%; Score 313; DB 2; Length 837;
Best Local Similarity 20.0%; Pred. No. 2.9e-12;
Matches 183; Conservative 125; Mismatches 311; Indels 298; Gaps 40;

QY 337 PPKILTSVGSNVSEHC-IYKKENKIVPSKEIYVMMNLAEKIQSQDYVSD--HVKVTF 393
      || : : | | | : : : : : : : : : : : : : : : : :
Db 33 Pp--VVRIGDPVLASCTISPNKSLDQQAKITMRLQDEPIQEPGRQHLLPDGTQESLITL 90

QY 394 ENLNETKPRGKFTY-----DAVYCCNEHECHHRYAELIYVDVININIS CETDGYLT KMT C 447
      : || | : | : : : : : : : : : : : : : : : : :
Db 91 PHLNYTQ--AFLECLVPWEDSVQLLDQAELHAGYPPA---SPSNLSCLMHLTNSLVC 143

QY 448 RWTSTSTQSLAESTLQLRHRSLSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQP----- 502
      : | | | | : : : : : : : : : : : : : : : : : :
Db 144 QWEPGPETHLPTSTI-LKSFRR-----ADCOYQGDITIPDCAVAKKRQNNC 187

QY 503 -----IFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKLPDPSSVKA EITINI----- 551
      : | : : : : : : : : : : : : : : : : :
Db 188 $IPRKNLLLYQYMAIWQAENMLGSSSESPKLCCLDPMQVYKLEPPMLQALDIDGPDVYSHQP 247

QY 552 GLLKISWEKVPFEPENNL--QFOIRYGLSGKEVQWKMVEYVDAKSKSVSLPVPDLCA--- 605

```

[illegible]

RESULT 12  
S17308  
Leukemia Inhibitory factor receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S17308  
R:Gearling, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; PR  
EMBO J. 10, 2839-2848, 1991  
A:Title: Leukemia Inhibitory factor receptor is structurally related to the IL-6 sign  
A:Accession: S17308  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1097 <GEA>  
A:Cross-references: GB:X61615; NID:q34365; PIDN:CAA43805.1; PID:q34366

```

Query Match          4.7%; Score 294.5; DB 2; Length 1097;
Best Local Similarity 19.2%; Pred. No. 7e-11;
Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;

QY   161 LLYLVPEVLDSPLVPQKGSFOWHC-----NCS-----VHECC----- 194
      |||:::~!         ::||:       ~!||        :~!~!
Db    35 LLYLMNQVNSQ-----KKGAPHDKCVTNLQVWNCMSWKAPSGTGRGCTDYEVCIENRSRS 89
```



```

QY 195 -----ECLVPVPTAKINDTLMLCKITSGVIFQSPMLMSVQPINMVKPPDPLGLHMEIT- 248
Db 90 CYQLEKTSIKIPALSHGDEYITINSIHDFGSSSTKFTLNEQNSLI-PDTEILNLSDAF 148
QY 249 DDGNLKISWSSPLVPPLQYQVYKSENSTVIR-----EADKIVSATSL----- 294
Db 149 STSTLYLKWDRGSV-FPHRSNVIW---ELKVLKRESMELVKLVTHNTTLNGKDTLHHS 204
QY 295 --VDSILPGSSYEQVR---GKRLDGPGLMSDSTPRVFT---TQDVIFPPKILTSVG 345
Db 205 WASDMPLECAIHFEVETRCYIDNLHPSGLEWSDWSPVKNISWIPDSQTKVPQDKVILVG 264
QY 346 SNVSFHCYKKENKIIVPSKEIWMNMNLAEKIPQSQYDV---SDHVSQVTFEENETKPR 402
Db 265 SDITFCV-----SQEKV---LSALIGHNCPPLHLDGENVA-IKIRNISVSASS 310
QY 403 GKFTYDAVYCCNEHECHHRYAELVIDVINISCEPDGYLTMTCRMSTSTIOSLA---E 459
Db 311 GT---NVFTTEDNIFGTVIFAGYPPDTPQOLNCEIHD-LKEIICSMNPGRAVAVGPRA 366
QY 460 STLQRYHRSLSYCSIDPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHS 519
Db 367 TSYTLVESFSKGYVRLKRAEAPTNES-----YQLFQMLPNOETIYNFTLANHPL 416
QY 520 GSLDSPPTCVLPDSVAKLPPSSVKAETINTGLKISWEKP-----VFPEN 566
Db 417 GRSQSTILVNITEKVY-PHTPTSEKVK-DINSTAVKLSWHLPGNFAKINFLCEIETIKSN 474
QY 567 NLOFQIRYGLSGKEVOMKMEVYDAKSKSVSLPVPDCAVYAVQVRCKRLDGLGYSNWS 626
Db 475 SVQFORNVTIKVE-----NSSYLVALDKLNPYLTYPFRIRCS-TETEMWSKWS 523
QY 627 NPATYVMDIKVPMRGPEFWRIINGDTMKKEKNVTLKPLMKNDSLCSVQRYVINHTS 686
Db 524 NKKOHLTTEAS-PSKGPDTWREWSSD---GKNLITYKPLPINEA---NGKILSYNWS 574
QY 687 CNG-----TWSEDVGNHTKFTFLMTEQAHVTVLAINSIGASVANFNLFSPWPMKYNIV 741
Db 575 CSSDEETQSLSEIPDPQKAEIRLDKNDYIISVAKNSYVSSPPSKIASMEIPNDLKE 634
QY 742 QSLAYPLNSSCVIWSILSPS---DYKLMYFIEMKN--LNEDGEIKWLRI-SSSVKYY 795
Db 635 QVYGM---GKGLLTWHYDPMTCDY---VTKWCSRSRSEPCMLMDWRKVPNSIETV 685
QY 796 YIHDHFIPIEKYQFSLYPTFMEG-----VG-----KPKIINSFTODD----- 832
Db 686 IESDEFPRGIRYNEFTLYGCRNQGYQLRSMIGYIEELAPIVAPNFTVEDTSADSLVKE 745
QY 833 -----IEKHQSD----- 839
Db 746 DIPVELRGFLRGYLFYFGKERDTSKMRVLESGRSDIKYKNITDISOKTLRIADLOKT 805
QY 840 -----AGLYVI-----VPYIISSSILLGLTLISHOR--M 867
Db 806 SYHLVLRATYTDGVPKESMVTYTKENSVGLIATLPYAVAVIVGVTSILCYRKREWI 865
QY 868 KKLWEDVNPKNCSMAQGLNFQK-----PETFEHLFIKHTASVTCGPLL 912
Db 866 KETFEYDPIDNPENC---KALQFQKSVCEGSSALKLTLEMNCTPNNVLEVLETRSAF-PKI 920
QY 913 LEPEITISEDIVDTSMKNDEMPTTVVSLSTLDEKGSVC---ISDQNSVNFSEADG 969
Db 921 EDTETIIS---PVAERPEDSDAEPENHVV-----SYCPPIIEEIIPNPADEAGG 968
QY 970 T-EVITYED-ESQROPFVKYATLLISNKPSETGEEOGL-----INSSVTKGFS- 1014
Db 969 TAQVIYIDVQSMYOP-----QAKPEEQENDPYGAGYKPMHLPINSTVEDIAAE 1019
QY 1015 ---SKNSPLKDSFSNSSWEIQAQAFILSDQHPNIIISP 1049
Db 1020 EDLDKTAGYRPAQANVTM-----NLVSP 1042

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RESULT 13
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence, revision 30-Jan-1993 #text, change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A:Note: clones pHG1 and pHG5
A:Accession: A38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680, 708-863 <FUK>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHQ3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680, 708-863 <LAR>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A:Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20650.1; PID:g240884
A:Experimental source: granulocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Hanlu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: 1p35-1p34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F:25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TM>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred
Query Match 4.6%; Score 288.5; DB 2; Length 863;
Best Local Similarity 20.0%; Pred. No. 1.2e-10;
Matches 156; Conservative 125; Mismatches 280; Indels 219; Gaps 38;
QY 341 LTVSGSNVSFHCYKKE-NKIYPSKEIWMNMNLAEKIPQSQYDVSD--HVSQVTFEENLN 397
Db 35 IVHLGDPITASCIRKQNSHLDPEPQLMRLG-AELQPGGRQORLSDGTQESITLPHLN 93
QY 398 ETKPRGKFTYDAVYCCNEHECHHRYAELVID-----VNINISCEPDGYLTGMT 446

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Db 94 HTQ-----AFISC-----CLNMGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLI 141
QY 447 CRWSTSTIOSLAES-TLQRLYHRSSLYCSDIPSIHIPSEPKDCYLQSDGFYECI----- 499
Db 142 CQWEPGPEETHLPTSFLLKSFKSRG-----NCQTQGDSTLDCVPKDGOS 184
QY 500 -----FQPIPLISGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLLYQNMGIWQAENALGTSMPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP 243
QY 549 INIGLKISWEKVPFP--ENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPVP----- 601
Db 244 PQAGCLQLCWE-PWQPLHINQKCELRHKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVRCKRLDGLGYSNMSNPATVMDIKVPMRGP-----EFWRIIN 650
Db 292 YELCGLPATAYTLQIRCIKRWPLPGHSDWS-PS---LELRTTERAFTVRLDTWVR--- 343
QY 651 GDTMKKEKNVTLLMKPLMKNDLSQVQRYVINHTS-----CNGTWSQEDVGNHTKF 701
Db 344 -QRLDPRYVQLFWKVPVPLEEDSGRIQGYVSWRPSGQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHTVTVLAINSIGASVANFNLFSPMSKVNIVQSLAVPLNSSCVIVSWILS 761
Db 396 TFLPSEAOEVALVAYNSAGTSRPT-PVYFS--ESRGPALTRLHMAARDPHSLWGW--E 450
QY 762 PSDYKLMYFIEM-----KNLNEDEIKW-LRISSVKKYIYHDHFIPIEKYQFSLYP 813
Db 451 PPNPWPQGYVIEWGLGPPSASNSNK---TWMEQNGRATGFLKENIRPFQLEYEITVP 506
QY 814 IFMEGVGKPKTIINSFTODDIEKHQSDAGL-----YVIVPVIISSILLGLTLLI 862
Db 507 LYQDTMGPSQOHVAYASQEMAPSHAPLHLKHIGKTWAQLEWVPEPELGKSPLTHTY--- 563
QY 863 SHQRMKLFWEDEVNPNKNCSWAQLNFQ-----KPETFEHLFIK-----HTASVT 907
Db 564 -----IFW---TNAQNSFSAILNASSRGFVLHGLEPASLYHILMAASQAGATNSTV 613
QY 908 CGPLLEPETISEDIV-----DTSW-----KNKDEMPPT----- 937
Db 614 LTLMTLPBGSELHIILGLFGLLLLTCLCGTAWLCCSPNKNPLMPSPVDPDAHSSLSGSW 673
QY 938 --TVVSL-----STLDLEKGSV---CISQFNSVNFSEAGTEVYEDESQROP 982
Db 674 VPTIMEELPGRPGOWLGQTSSEMSRALTRPHCVQDAFQLPGLGTPPTTKLTVLEDEKKP 733

RESULT 14
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: Placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <A
F:25-627/Domain: extracellular #status predicted <EX>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
```

Query Match

4.5%; Score 284; DB 2; Length 783;

```
Best Local Similarity 20.3%; Pred. No. 2e-10;
Matches 153; Conservative 121; Mismatches 287; Indels 192; Gaps 35;

QY 341 LTVSGSNVSFHCITYKKE-NKIVPSKEIYVMMNLAEKIPQSQYDVVSD--HVKVTFEFLN 397
Db 35 IVHLGDPITASCIKONCSHLDPEPILMRIG-AELQPGGRQQRISDGTQESIITLPHLN 93
QY 398 ETKPRGKFTYDAVCCNEHECHRAELVID-----VINISCEYDGLTKMT 446
Db 94 HTQ-----AFISC-----CLNMGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLI 141
QY 447 CRWSTSTIOSLAES-TLQRLYHRSSLYCSDIPSIHIPSEPKDCYLQSDGFYECI----- 499
Db 142 CQWEPGPEETHLPTSFLLKSFKSRG-----NCQTQGDSTLDCVPKDGOS 184
QY 500 -----FQPIPLISGYTMWIRINHSLSGSDPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLLYQNMGIWQAENALGTSMPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP 243
QY 549 INIGLKISWEKVPFP--ENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPVP----- 601
Db 244 PQAGCLQLCWE-PWQPLHINQKCELRHKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVRCKRLDGLGYSNMSNPATVMDIKVPMRGP-----EFWRIIN 650
Db 292 YELCGLPATAYTLQIRCIKRWPLPGHSDWS-PS---LELRTTERAFTVRLDTWVR--- 343
QY 651 GDTMKKEKNVTLLMKPLMKNDLSQVQRYVINHTS-----CNGTWSQEDVGNHTKF 701
Db 344 -QRLDPRYVQLFWKVPVPLEEDSGRIQGYVSWRPSGQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHTVTVLAINSIGASVANFNLFSPMSKVNIVQSLAVPLNSSCVIVSWILS 761
Db 396 TFLPSEAOEVALVAYNSAGTSRPT-PVYFS--ESRGPALTRLHMAARDPHSLWGW--E 450
QY 762 PSDYKLMYFIEM-----KNLNEDEIKW-LRISSVKKYIYHDHFIPIEKYQFSLYP 813
Db 451 PPNPWPQGYVIEWGLGPPSASNSNK---TWMEQNGRATGFLKENIRPFQLEYEITVP 506
QY 814 IFMEGVGKPKTIINSFTODDIEKHQSDAGL-----YVIVPVIISSILLGLTLLI 862
Db 507 LYQDTMGPSQOHVAYASQEMAPSHAPLHLKHIGKTWAQLEWVPEPELGKSPLTHTY--- 563
QY 863 SHQRMKLFWEDEVNPNKNCSWAQLNFQ-----KPETFEHLFIK-----HTASVT 907
Db 564 -----IFW---TNAQNSFSAILNASSRGFVLHGLEPASLYHILMAASQAGATNSTV 613
QY 908 CGPLLEPETISEDIV-----DTSW-----KNKDEMPPTTVVSLSTLDLE 949
Db 614 LTLMTLPBGSELHIILGLFGLLLLTCLCGTAWLCCSPNKNPLMPSPVDPDAHSSLSGSW 673
QY 950 KGSVCISDQFNSVNFSEAGTEVYEDESQROP 982
Db 674 VPTIMEEDAFQLPGLGTPPTTKLTVLEDEKKP 706

RESULT 15
JX0312
differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor -
C:Species: Mus musculus (house mouse)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JX0312; JC2181; S38942
R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
J. Biochem. 115, 557-562, 1994
A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
A:Reference number: JX0312; MUID:94334302
A:Accession: JX0312
A:Molecule type: mRNA
A:Residues: 1-1092 <TOM>
A:Cross-references: DDBJ:D26177; NID:g473718; PIDN:BAA05165.1; PID:d1005707; PID:g825
A:Accession: JC2181
A:Molecule type: mRNA
A:Residues: 1-717, 'EA' <TOM1>
```



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:54:01 ; Search time 39.61 Seconds

(without alignments)  
1138.810 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICKKPCVVLHMEFIYIT.....QTCSTQTHKIMENKCDLTV 1165

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6246	99.9	1165	1	LEPR_HUMAN
2	4784.5	76.5	1162	1	LEPR_RAT
3	4766.5	76.2	1162	1	LEPR_MOUSE
4	366	5.9	917	1	IL6B_MOUSE
5	345.5	5.5	918	1	IL6B_HUMAN
6	339.5	5.4	918	1	IL6B_RAT
7	313	5.0	837	1	GCSR_MOUSE
8	294.5	4.7	1097	1	GCSR_HUMAN
9	284	4.5	836	1	GCSR_HUMAN
10	281.5	4.5	1092	1	LIFR_MOUSE
11	220.5	3.5	862	1	IL12S_HUMAN
12	220	3.5	830	1	PRLR_COLLI
13	220	3.5	874	1	IL12S_MOUSE
14	209.5	3.3	831	1	PRLR_CHICK
15	190	3.0	831	1	PRLR_MEIGA
16	184	2.9	2481	1	PINC_XENLA
17	173.5	2.8	1493	1	NEOL_MOUSE
18	172	2.8	2012	1	DSCA_HUMAN
19	170.5	2.7	1461	1	NEOL_HUMAN
20	169.5	2.7	1443	1	NEOL_CHICK
21	166.5	2.7	2029	1	LAR_DROME
22	165	2.6	630	1	PRLR_ORENI
23	162	2.6	1447	1	DCC_MOUSE
24	158.5	2.5	462	1	IL6A_RAT
25	154.5	2.5	2386	1	PINC_HUMAN
26	153.5	2.5	460	1	IL6A_MOUSE
27	151	2.4	1377	1	NEOL_RAT
28	150.5	2.4	610	1	PRLR_RAT
29	147.5	2.4	638	1	GHR_MACMU
30	146	2.3	3063	1	CA1C_HUMAN
31	145.5	2.3	2477	1	PINC_RAT
32	144.5	2.3	1302	1	NRG_DROME
33	144	2.3	581	1	PRLR_CEREL

34	143.5	2.3	1447	1	DCC_HUMAN	P43146 homo sapien
35	143	2.3	638	1	GHR_HUMAN	P10912 homo sapien
36	142.5	2.3	3135	1	S230_PLAFO	Q08372 plasmodium
37	141	2.3	581	1	PRLR_BOVIN	Q28172 bos taurus
38	141	2.3	878	1	IL3B_MOUSE	P26954 mus musculus
39	140.5	2.2	638	1	GHR_PIG	P19756 sus scrofa
40	140.5	2.2	638	1	GHR_RABIT	P19941 oryctolagus
41	139	2.2	635	1	TPOR_HUMAN	P40238 homo sapien
42	138	2.2	1897	1	PTPE_HUMAN	P10586 homo sapien
43	138	2.2	2265	1	PINC_BOVIN	P07589 bos taurus
44	136	2.2	928	1	PMP9_CHLPPN	Q92398 chlamydia p
45	135.5	2.2	1013	1	EPA5_CHICK	P54755 gallus gall

#### ALIGNMENTS

RESULT	ID	LEPR_HUMAN	STANDARD	PRT	1165 AA.
AC	P48357;				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).				
GN	LEPR OR OBR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=96128129; PubMed=8548812;				
RA	Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,				
RA	Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,				
RA	Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,				
RA	Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;				
RT	"Identification and expression cloning of a leptin receptor, OB-R.;"				
RL	Cell 83:1263-1271(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Thompson D.B., Ossowski V., Sutherland J., Apel W.,				
RA	Riesterfeldt J.;				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	VARIANT ARG-223.				
RX	MEDLINE=96270489; PubMed=8666155;				
RA	Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;				
RT	"The hypothalamic leptin receptor in humans: identification of				
RT	identical sequence polymorphisms and absence of the db/db mouse and				
RT	fa/fa rat mutations.;"				
RL	Diabetes 45:992-994(1996).				
RN	[4]				
RP	VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.				
RX	MEDLINE=97289527; PubMed=9144432;				
RA	Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,				
RA	Andersen T., Chung W.K., Leibel R.L., Pedersen O.;				
RT	"Amino acid variants in the human leptin receptor: lack of association				
RT	to juvenile onset obesity.;"				
RL	Biochem. Biophys. Res. Commun. 233:248-252(1997).				
RN	[5]				
RP	VARIANTS ARG-109; ARG-223 AND ASN-656.				
RX	MEDLINE=97431549; PubMed=9287054;				
RA	Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,				
RA	Sothern M., Udall J.N., Kahle B., Leibel R.L.;				
RV	"Exonic and intronic sequence variation in the human leptin receptor				
RT	gene (LEPR).;"				
RL	Diabetes 46:1509-1511(1997).				
RN	[6]				
RP	VARIANTS ARG-109 AND ARG-223.				
RX	MEDLINE=97301763; PubMed=9158141;				
RA	Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;				

RT "Structure and sequence variation at the human leptin receptor gene in  
RT lean and obese Pima Indians."  
RL Hum. Mol. Genet. 6:675-679(1997).  
RN [7]  
RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.  
RX MEDLINE=99075638; PubMed=9860295;  
RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,  
RT Slegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.,  
RT "Transmission disequilibrium and sequence variants at the leptin  
RT receptor gene in extremely obese German children and adolescents."  
RL Hum. Genet. 103:540-546(1998).  
RN [8]  
RP VARIANTS ARG-109; ARG-223 AND ASN-656.  
RX MEDLINE=97318795; PubMed=9175732;  
RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,  
RT Strosberg A.D., Mckeligue P.M., Scott J., Altman T.J.,  
RT "Leptin receptor gene variation and obesity: lack of association in a  
RT white British male population."  
RL Hum. Mol. Genet. 6:869-876(1997).  
CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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CC -----  
DR EMBL; U43168; AAA93015.1; -  
DR EMBL; U59263; AAB09673.1; -  
DR EMBL; U59248; AAB09673.1; JOINED.  
DR EMBL; U59249; AAB09673.1; JOINED.  
DR EMBL; U59250; AAB09673.1; JOINED.  
DR EMBL; U59252; AAB09673.1; JOINED.  
DR EMBL; U59253; AAB09673.1; JOINED.  
DR EMBL; U59254; AAB09673.1; JOINED.  
DR EMBL; U59255; AAB09673.1; JOINED.  
DR EMBL; U59256; AAB09673.1; JOINED.  
DR EMBL; U59257; AAB09673.1; JOINED.  
DR EMBL; U59258; AAB09673.1; JOINED.  
DR EMBL; U59259; AAB09673.1; JOINED.  
DR EMBL; U59260; AAB09673.1; JOINED.  
DR EMBL; U59261; AAB09673.1; JOINED.  
DR EMBL; U59262; AAB09673.1; JOINED.  
DR HSSP; P40189; IBOU.  
DR MIM; 601007; -  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Polymorphism.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 1165 LEPTIN RECEPTOR.  
FT DOMAIN 22 841 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 842 862 POTENTIAL.  
FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 537 623 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 738 823 FIBRONECTIN TYPE-III 3.  
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 688 688 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 728 728 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 109 109 K -> R.  
FT VARIANT 204 204 /FTID-VAR\_002703.  
FT VARIANT 223 223 K -> R.  
FT VARIANT 223 223 /FTID-VAR\_002704.  
FT VARIANT 656 656 K -> N.  
FT VARIANT 675 675 /FTID-VAR\_002706.  
FT VARIANT 675 675 S -> T.  
SQ SEQUENCE 1165 AA; 132449 MW; 8FF21D9AF5125808 CRC64;  
Query Match 99.9%; Score 6246; DB 1; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MICQFCVLLHWEFIYVITAFNLSTYPTWRFKLSGMPNSTYDYLPLAGLSKNTSNS 60  
DB 1 MICQFCVLLHWEFIYVITAFNLSTYPTWRFKLSGMPNSTYDYLPLAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTEFHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAVERPKFNSSGTHFSNLSKTEFHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANWNIQCWLKGLKFLICYVESLFKNLFRNRYKYVHLVLPVLEDSPLVPQGS 180  
DB 121 QQIDANWNIQCWLKGLKFLICYVESLFKNLFRNRYKYVHLVLPVLEDSPLVPQGS 180  
QY 181 PQMVHCNCSVHECCCLVPPVPTAKLNDTLMLCKITSGGVIFQSPLSVQPINMYKDDPP 240  
DB 181 PQMVHCNCSVHECCCLVPPVPTAKLNDTLMLCKITSGGVIFQSPLSVQPINMYKDDPP 240  
QY 241 LGLHMEITDDGNLKIWSVSPPLVPFLOQVYKSENSTVIYREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKIWSVSPPLVPFLOQVYKSENSTVIYREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPGLMSDSTPRVFTTQDVYIFPKILTSVGSNVSFHCYKKNKI 360  
DB 301 GSSYEYQVRGKRLDGPGLMSDSTPRVFTTQDVYIFPKILTSVGSNVSFHCYKKNKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOQDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHCCH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOQDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHCCH 420  
QY 421 RYAEIYVIDVININISCEITDGLTKMTCRWSTSTIOSLAESTLQLRHYRSSLYCSIDPSIH 480  
DB 421 RYAEIYVIDVININISCEITDGLTKMTCRWSTSTIOSLAESTLQLRHYRSSLYCSIDPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINSLGSLDSPPTCVLPDSYKPLPP 540  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINSLGSLDSPPTCVLPDSYKPLPP 540  
QY 541 SSYKAEITINIGLKIWEKVEPENNLQFOIRYGLSGKEVQWKMYEYDAKSKVSLPV 600  
DB 541 SSYKAEITINIGLKIWEKVEPENNLQFOIRYGLSGKEVQWKMYEYDAKSKVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYTVMDIKYPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYTVMDIKYPMRGPEFWRIINGDTMKKEKNV 660

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QY 661 TLLMKPLMKNDISLCVQRYVINHTSCNGTSEEDVGNHTKFTFLMTQAHVTVLAINSI 720
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Db 661 TLLMKPLMKNDISLCVQRYVINHTSCNGTSEEDVGNHTKFTFLMTQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPWMSKVNIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780
    |||||||
Db 721 GASVANFNLTFSPWMSKVNIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKRYTHDHFIPTEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
    |||||||
Db 781 GEIKWLRISSSVKRYTHDHFIPTEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNSWAQGLNFQKPEFHEHLEI 900
    |||||||
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNSWAQGLNFQKPEFHEHLEI 900
QY 901 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPPTVSLSTDLKSGVCISDQFN 960
    |||||||
Db 901 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPPTVSLSTDLKSGVCISDQFN 960
QY 961 SVNFSEAGTEVYEDSQRQPFVKYATLISNSKPSETGEEGLINSSVTKCFSSKNSPL 1020
    |||||||
Db 961 SVNFSEAGTEVYEDSQRQPFVKYATLISNSKPSETGEEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSWIEAQAFFILSDQHPNIIISPHLTFSEGIDELKLEGNFPEENNDKRSIYLL 1080
    |||||||
Db 1021 KDSFNSSWIEAQAFFILSDQHPNIIISPHLTFSEGIDELKLEGNFPEENNDKRSIYLL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFEVNNINLGTSKKTFA 1140
    |||||||
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFEVNNINLGTSKKTFA 1140
QY 1141 YMPQFOTCSTQTHIKIMENKMDLTV 1165
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Db 1141 YMPQFOTCSTQTHIKIMENKMDLTV 1165

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## RESULT 2

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LEPR_RAT STANDARD; PRT: 1162 AA.
AC 062959; Q63007; P70493; P70494; P70495; Q63385; Q63386; Q54805;
AC P97589; Q35772;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEPR OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
RX MEDLINE=96295531; Pubmed=8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (glutamine --> proline) of the leptin
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
RT (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96332408; Pubmed=8769097;

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RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
RA Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
RT DNA -- identification of a missense mutation in Zucker fatty (fa/fa)
RT rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
RA Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96212906; Pubmed=8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
RT Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
RT "Analysis of rat leptin receptor gene.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 694-878 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Pancreas;
RA Ma Z.;
RT "Identification of a leptin receptor in islet.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
RC STRAIN-SPRAGUE-DAWLEY;
RA Chien E.K., Hara M., Rouvard M., Yano H., Philippe N., Polonsky K.S.,
RA Bell G.I.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RP VARIANT FA PRO-269.
RX MEDLINE=96314329; Pubmed=8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
RA Leibel R.L.;
RT "Phenotype of fatty due to Glu269Pro mutation in the leptin receptor
RT (Lepr).";
RL Diabetes 45:1141-1143(1996).
CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
CC WHICH COULD BE SECRETED.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
CC TISSUE.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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DR EMBL: U52966; AAC52587.1; -
DR EMBL: D84550; BAA12697.1; -
DR EMBL: D84551; BAA12698.1; -
DR EMBL: D85557; BAA12830.1; -

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DR EMBL; D85558; BAA12831.1; -  
DR EMBL; D85559; BAA12832.1; -  
DR EMBL; U60151; AAB06616.1; -  
DR EMBL; D84125; BAA12230.1; -  
DR EMBL; D84126; BAA12231.1; -  
DR EMBL; AB011006; BAA24899.1; -  
DR EMBL; U67207; AAB40654.1; -  
DR EMBL; AF007818; AAB63201.1; -  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam; PF00041; fn3; 2.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Polymorphism; Alternative splicing.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 1162 LEPTIN RECEPTOR.  
FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 840 860 POTENTIAL.  
FT DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 236 318 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 535 621 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 736 821 FIBRONECTIN TYPE-III 3.  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 890 894 PETFE -> RADTL (IN ISOFORM A).  
FT VARSPLIC 895 1162 MISSING (IN ISOFORM A).  
FT VARSPLIC 890 892 PET -> VTV (IN ISOFORM C).  
FT VARSPLIC 893 1162 MISSING (IN ISOFORM C).  
FT VARSPLIC 797 805 DNFIPIEKY -> GNCVLLLN (IN ISOFORM E).  
FT VARSPLIC 806 1162 MISSING (IN ISOFORM E).  
FT VARIANT 269 269 Q -> P (IN FA).  
FT CONFLICT 2 2 T -> M (IN REF. 4).  
FT CONFLICT 12 12 H -> P (IN REF. 6).  
FT CONFLICT 34 34 K -> R (IN REF. 6).  
FT CONFLICT 751 752 CV -> SL (IN REF. 7).  
FT CONFLICT 846 846 I -> V (IN REF. 8).  
SQ SEQUENCE 1162 AA; 130832 MW; BA7AC2CA2D2E62AF CRC64;

Query Match 76.5%; Score 4784.5; DB 1; Length 1162;  
Best Local Similarity 75.6%; Pred. No. 4.6e-316;  
Matches 882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;

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DB 1 MTCQKFYVLLHMEFLVITAFNLAYPTSPWRFKLFCAPSTTDDSLSPAGVANNISSL 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSIVNSLVF 120  
DB 61 KGASEALVEAKFNSTGIYSELSKTIHCCFGNCGQNCALTGNTGKTLASVVKPLVF 120  
QY 121 QOIDANMNIOGWLKGLKLFICVYESLFKNLFERNYKVVHLLVLPVLEDSPLVPQKGS 180  
DB 121 RQGVNWDIEGWMKGLTLFICHMEPLLNPKFNYSKVHLLYDLPEVIDDLPLPKDS 180  
QY 181 RQVHNCNVHCECECLVFPVPTAKLNDTLMLCKLITSGGVIFQSPLMVQPINNVKPPDP 240

DB 181 FQTVQNCNSVRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSLMSLQPMLVKPPDP 239  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQKYSSENSTTVIREADKIVSATSLVDSILP 300  
DB 240 LGLHMEVTDGNNLKISWDSQTKAPFPLOQYQKYLENS-TIVREAEIVSDTSLVDSILP 298  
QY 301 GGSIEVQVRGKRLDGPGISDMSSTPRVFTTQDVYFPPKILTSVGSNVSFHCITYKREKI 360  
DB 299 GGSIEVQVRKRLDGSVGSWDSMLPQLFTTQDVYFPPKILTSVGSNASFCICIKMENQOT 358  
QY 361 VPSKEIWMNNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCH 420  
DB 359 ISSKQIVMMNNLAEKIPETQYNTVSDHISKVTFSLNKAIRPRGKFTYDAVYCCNEHCH 418  
QY 421 RYAEIVIDVININISCEPDGYLTMTQRMSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
DB 419 RYAEIVIDVININISCEPDGYLTMTQRMSPSTIQSLVSTVQLRHRSLYCPDPSIR 478  
QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLP 540  
DB 479 PISELKNVLOTDFEYECVQPIFLLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLP 538  
QY 541 SSVKAEITINIGLKISWEKVPENNLOQIRYGLSGNEVQMKYEVYDAKSYSILPV 600  
DB 539 SSVKAEITINIGLKISWEKVPENNLOQIRYGLNGEIKQWKTHEVDAKSYSILPV 598  
QY 601 PDLCAYVAVOVRCKRLDGLGWSMNSPAYTVVMDIKVPMRGPEFWRIINGDTMKERNV 660  
DB 599 SDLCAYVAVOVRCKRLDGLGWSMNSPAYTVVMDIKVPMRGPEFWRIINGDTMKERNV 658  
QY 661 TLLMKPLKNDLSQVRYVNHHTSCNGTSEVDGNTKFTFLNTIOAHTVTLAINSI 720  
DB 659 TLLMKPLKNDLSQVRYVNHHTSCNGTSEVDGNTKFTFLNTIOAHTVTLAINSI 718  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIYVWILSPDOKLMYFIEMKNLND 780  
DB 719 GASLVNENLTFSPMSKVNIVQSLAYPLNSSCVIYVWILSPDOKLMYFIEMKNLND 778  
QY 781 GEIKWLRISSVKKYVTHHFPIEIKYQPSLYPIFMEGVGKPKIINSFTODDIEKHSDA 840  
DB 779 DGKMKWLRISSVKKYVTHHFPIEIKYQPSLYPIFMEGVGKPKIINSFTODDIEKHSDA 838  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVDPNPKNSWAQGLNFQKPEFHELF 900  
DB 839 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVDPNPKNSWAQGLNFQKPEFHELF 898  
QY 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTVVSLLSTT-DLEKGSVCISDOF 959  
DB 899 KHAESVTFGPLLEPEPVSSEISVDTAWKNKDEMPVAMVSLLTTPDSTRGSLCISDOC 958  
QY 960 NSVNFSEAEGETEVTYEDESQRPVFKYATLISNSKPSPEGEQGLINSSVTKCFSSKNSP 1019  
DB 959 NSANFSGAOSTQGTCEDECOQSPVKYATLISNSKPSPEGEQGLINSSVTKCFSSKNSP 1018  
QY 1020 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYY 1079  
DB 1019 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYY 1077  
QY 1080 LGVTSIKKRESGVLTDRKSRVSCPFPAPCLFTDIRVQDSCSHFVENNINLGTSKRTFA 1139  
DB 1078 LGVSSGNKRENDMLTDEAGVLCPPPAHCLFSDIRILQESCSHFVENNINLGTSK-KNFV 1136  
QY 1140 SYMPOFQTCSTQTHKIMENKCDLTV 1165  
DB 1137 PYMPOFQSCSTHSHKIENKCDLTV 1162  
RESULT 3  
LEPR\_MOUSE STANDARD; PRT; 1162 AA.  
ID LEPR\_MOUSE P48356; Q61215; Q64309; O54986;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)



01-MAR-2002 (Rel. 41, last annotation update)  
 DE Leptin receptor precursor (lep-r) (OB receptor) (OB-R) (B219  
 DE receptor).  
 GN LEPR OR OBR OR DB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (VARIANT A).  
 RC TISSUE=Choroid plexus;  
 RX MEDLINE=96128129; PubMed=8548812;  
 RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,  
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,  
 RA Muir C., Sanker S., Moriarty A., Moore R.J., Smutko J.S.,  
 RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;  
 RT Identification and expression cloning of a leptin receptor, OB-R.;  
 RL Cell 83:1263-1271(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (VARIANT B).  
 RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;  
 RX MEDLINE=96190816; PubMed=8608603;  
 RA Chen H., Charlat O., Tartaglia L.A., Wolf E.A., Weng X.,  
 RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,  
 RA Dwyer G.M., Tepper R.I., Morgenstern J.P.;  
 RT Evidence that the diabetes gene encodes the leptin receptor;  
 RT Identification of a mutation in the leptin receptor gene in db/db  
 RT mice.;  
 RL Cell 84:491-495(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (VARIANTS A TO E).  
 RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;  
 RX MEDLINE=96231997; PubMed=8628397;  
 RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,  
 RA Lee J.I., Friedman J.M.;  
 RT Abnormal splicing of the leptin receptor in diabetic mice.;  
 RL Nature 379:632-635(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (VARIANT C).  
 RC STRAIN=BA1B/C; TISSUE=Liver;  
 RX MEDLINE=96206286; PubMed=8616721;  
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,  
 RA Mikhail A., Platika D., Snodgrass H.R.;  
 RT Novel B219/OB receptor isoforms: possible role of leptin in  
 RT hematopoiesis and reproduction.;  
 RL Nat. Med. 2:585-589(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A. (VARIANT B).  
 RC STRAIN=NEW ZEALAND OBESSE / NZO; TISSUE=Hypothalamus;  
 RX MEDLINE=97462708; PubMed=9322935;  
 RA Igel M., Becker W., Herberg L., Joost H.G.;  
 RT Hyperleptinemia, leptin resistance, and polymorphic leptin receptor  
 RT in the New Zealand obese mouse.;  
 RL Endocrinology 138:4234-4239(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (VARIANTS A AND B).  
 RC STRAIN=FVB/N; TISSUE=Spleen;  
 RX MEDLINE=96270520; PubMed=8692797;  
 RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,  
 RA Skoda R.C.;  
 RT Defective STAT signaling by the leptin receptor in diabetic mice.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).  
 RN [7]  
 RP SEQUENCE FROM N.A. (VARIANT E).  
 RC STRAIN=129/J;  
 RX MEDLINE=98008913; PubMed=9344648;  
 RA Chua S.C., Kouttras I.K., Han L., Liu S.M., Kay J., Young S.J.,  
 RA Chung W.K., Leibel R.L.;  
 RT Fine structure of the murine leptin receptor gene: splice site  
 RT transcripts.;  
 RL Genomics 45:264-270(1997).  
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN  
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT  
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E  
 CC WHICH COULD BE SECRETED.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN  
 CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.  
 CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND  
 CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:  
 CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.  
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U42467; AAA93014.1; -  
 CC EMBL: U46135; AAC52408.1; -  
 CC EMBL: U49106; AAC52420.1; -  
 CC EMBL: U49107; AAC52421.1; -  
 CC EMBL: U49108; AAC52422.1; -  
 CC EMBL: U49109; AAC52423.1; -  
 CC EMBL: U49110; AAC52424.1; -  
 CC EMBL: U52915; AAC52599.1; -  
 CC EMBL: Y10298; CAA71343.1; -  
 CC EMBL: U58861; AAC52705.1; -  
 CC EMBL: U58862; AAC52706.1; -  
 CC EMBL: U58863; AAC52707.1; -  
 CC EMBL: AF039456; AAB95334.1; -  
 CC EMBL: AF039443; AAB95334.1; JOINED.  
 CC EMBL: AF039444; AAB95334.1; JOINED.  
 CC EMBL: AF039445; AAB95334.1; JOINED.  
 CC EMBL: AF039446; AAB95334.1; JOINED.  
 CC EMBL: AF039447; AAB95334.1; JOINED.  
 CC EMBL: AF039448; AAB95334.1; JOINED.  
 CC EMBL: AF039449; AAB95334.1; JOINED.  
 CC EMBL: AF039450; AAB95334.1; JOINED.  
 CC EMBL: AF039451; AAB95334.1; JOINED.  
 CC EMBL: AF039452; AAB95334.1; JOINED.  
 CC EMBL: AF039453; AAB95334.1; JOINED.  
 CC EMBL: AF039454; AAB95334.1; JOINED.  
 CC EMBL: AF039455; AAB95334.1; JOINED.  
 CC HSSP: P40189; 1BQU.  
 CC MGD: MGI:104993; Lepr.  
 CC InterPro: IPR002996; CRIA.  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
 CC Pfam: PF00041; fn3; 3.  
 CC SMART: SM00060; FN3; 3.  
 CC PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 CC Polymorphism; Alternative splicing.  
 CC SIGNAL 1 21 POTENTIAL.  
 CC CHAIN 22 1162 LEPTIN RECEPTOR.  
 CC DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 840 860 POTENTIAL.  
 CC DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 236 318 FIBRONECTIN TYPE-III 1.  
 CC DOMAIN 535 621 FIBRONECTIN TYPE-III 2.  
 CC DOMAIN 736 821 FIBRONECTIN TYPE-III 3.  
 CC CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 890 894 PETEE -> RTDL (IN ISOFORM A).
FT VARSPLIC 895 1162 MISSING (IN ISOFORM A).
FT VARSPLIC 890 1162 PET -> VTV (IN ISOFORM C).
FT VARSPLIC 893 1162 MISSING (IN ISOFORM C).
FT VARSPLIC 890 900 PETEHLFTKH -> DISFEVEFIER (IN ISOFORM D).
FT VARSPLIC 901 1162 MISSING (IN THE ISOFORM D).
FT VARSPLIC 797 805 DNEPIEKEY -> GMCTVLEMD (IN ISOFORM E).
FT VARSPLIC 806 1162 MISSING (IN ISOFORM E).
FT VARSPLIC 541 541 V -> I (IN STRAIN NOZ).
FT VARSPLIC 651 651 V -> I (IN STRAIN NOZ).
FT VARSPLIC 1044 1044 T -> I (IN STRAIN NOZ).
FT CONFLICT 140 140 F -> I (IN REF. 6).
FT CONFLICT 720 720 A -> T (IN REF. 5).
SQ SEQUENCE 1162 AA; 130788 MW; 0E1E75B076BA60A2 CRC64;
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Query Match 76.2%; Score 4766.5; DB 1; length 1162;  
Best Local Similarity 75.4%; Pred. No. 7.7e-315;  
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

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QY 1 MICQKFCVLLHMEFIYVITAPNLSTPTWRFKLSQMPNSTYDYFLLPAGLSKNTS 60
DB 1 MNCQKRYVLLHMEFLYVIALNLAVPISPKFKLFCGPPNTDSDFLSPAGAPNNASAL 60
QY 61 NGHYTAVPEPKFNSSGTHFSNLSTKTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLV 120
DB 61 KGASEAIYEAKFNSSGIVPELSKTYVHCFCFNGOGONCSALTDNTEGKTLASVAKASVF 120
QY 121 QQIDAMNNIOQWLGDKLFLICYVESLFKNLFERNYNYKHLLYVLPVLEDSPLVPQKS 180
DB 121 RQIGVNMWDIECMWKGDLTLFICHMPLPKNPFKNYDSKVHLLYDLPEVIDSDPLPLKDS 180
QY 181 FQWVHCNCSVHECCCLVPVPFPAKNDTLMLCKITSGVIFQSPMLSVQPINMKPDP 240
DB 181 FQTVQCNCSLRG-CECHVPVPRAKNLVALLMYLEITSAGVSQSPMLSLQPMVVKPDP 239
QY 241 LGLHMETDDGDKLISWSSPLVPEFLQYQVXSENSTVIREADKIVSATSLVDSILP 300
DB 240 LGLHMETDDGDKLISWSSQTMARFPLQYQVYLENS-TIVREAEIVSATSLVDSVLP 298
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
DB 299 GSSYEVOVRSKRLDGGSGVMSDWSPOVFTTQDVITYFPFKILTSVGSNASFHCITYKENQI 358
QY 361 VPSKEIVMMNLAEKIPQSQYDVYSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420
DB 359 ISSKOIVMMNLAEKIPQSQYDVYSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEQACHH 418
QY 421 RYAEIVYDVNININISCEITDGYLTKMTCRWSTSTQSLAESTQLRYHRSLSYCSIDPSIH 480
DB 419 RYAEIVYDVNININISCEITDGYLTKMTCRWSTSTQSLAESTQLRYHRSLSYCSIDPSIH 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPCTCVLPDSVVKPLPP 540
DB 479 PISEPKNCVLRQDGFYECVFPFLLSGYTMWIRINHSLSGLSDSPCTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPPVPPENNLQFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
DB 539 SSVKAEITVNTGLKVSWEKPPVPPENNLQFQIRYGLSGKEIQWKTHEVDAKSKSVSLPV 598
QY 601 PDLCAVYAVOVRCRRLDGLGYWSNMSNPATTVMDIKVPMRGPEFWRIINGDTMKKERNY 660
DB 598 PDLCAVYAVOVRCRRLDGLGYWSNMSNPATTVMDIKVPMRGPEFWRIINGDTMKKERNY 660
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DB 599 SDLCAYVYQVRCRRLDGLGYWSNMSNPATTVMDIKVPMRGPEFWKKMDGVTKKERNY 658
QY 661 TLLMKPLKNDLSQVQRYVINHTSCNGTWSQWSDVGNHTKFTFLMTLOAHVTVLAINSI 720
DB 659 TLLMKPLKNDLSQVQRYVINHTSCNGTWSQWSDVGNHTKFTFLMTLOAHVTVLAINSI 718
QY 721 GASVANENLTFESWPMKSVNIVOSIAYPLNSSCVIYVSWILSPSDYKIMYFIEMKNLNE 780
DB 719 GASVANENLTFESWPMKSVNIVOSIAYPLNSSCVIYVSWILSPSDYKIMYFIEMKNLNE 778
QY 781 GEIKMLNIISSVKKYIHOHFPIEKKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 779 DGMKRLIPSNNKKFYIHDNFIPIEKKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 838
QY 841 GLYIVYVYIISSSILLGLTLLISHQRMKKLFMEDVDPNPKNCSNAQGLNFQKPEFHEHFI 900
DB 839 GLYIVYVYIISSSILLGLTLLISHQRMKKLFMEDVDPNPKNCSNAQGLNFQKPEFHEHFI 898
QY 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPITVYVSLSTT-DLEKGSVCISDQF 959
DB 899 KHAESVIEGPLLLEPEPISEISVDTAMKKNKDEMPVPAAMVSLTLTPDPRESSICISDOC 958
QY 960 NSVNSEAEGETEVTYEDESQROPVRYATLISNSKPSFEGEGLINSSVTKCFSSKNSP 1019
DB 959 NSANFSGSQSTQVTCEDCEQROPVRYATLISNSKPSFEGEGLINSSVTKCFSSKNSP 1018
QY 1020 LKDSFNSSSWEIEAOAFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKSIY 1079
DB 1019 LKDSFNSSSWEIEAOAFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKSIY 1077
QY 1080 LGVTSIKKRESGVLLTDKRSVSCBPAPCLFTDIRVLQDSCSHFVENNINIGTSKKTFA 1139
DB 1078 LGVTSVNRRESGVLLTGAGILCTFPACQLFSDIRILOERCSHFVENNINIGTSKKTFA 1136
QY 1140 SYMPOFQTCSTQTHKIMENKMDLTV 1165
DB 1137 PYMPOFQTCSTQTHKIMENKMDLTV 1162
RESULT 4
IL6_MOUSE STANDARD; PRT; 917 AA.
AC Q00560;
DT 01-FEB-1995 (Rel. 31, Created).
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibl M., Taya T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
RT transducer, gp130, and its regulated expression in vivo.";
RL J. Immunol. 148:4066-4071(1992).
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT.
CC - SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CC CELLS.
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CC      -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC      6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC      DURING THE REST OF EMBRYOGENESIS.
CC      -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC      -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -----
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CC -----  
DR EMBL; X62646; CAA44515.1; -  
DR EMBL; M83336; AAA37723.1; -  
DR HSSP; P40189; 1BCU  
DR MGD; MGI:96560; IL6st.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003962; FnIII\_repeat.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam; PF00041; fn3; 4.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.

FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	917	INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT	DOMAIN	23	617	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	618	639	POTENTIAL.
FT	DOMAIN	640	917	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	26	120	IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	124	220	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	221	322	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	323	420	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	422	515	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	516	611	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	723	741	SER-RICH.
FT	DISULFID	28	54	BY SIMILARITY.
FT	DISULFID	48	103	BY SIMILARITY.
FT	DISULFID	134	144	BY SIMILARITY.
FT	DISULFID	172	180	BY SIMILARITY.
FT	DISULFID	456	464	BY SIMILARITY.
FT	CARBOHYD	43	43	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	131	131	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	225	225	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	476	476	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	551	551	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	917 AA;	102452 MW;	FCEFD220BC2466F4 CRC64;

Query Match	5.9%;	Score 366;	DB 1;	Length 917;
Best Local Similarity	20.9%;	Pred. No. 5.9e-17;		
Matches 191;	Conservative 140;	Mismatches 338;	Indels 244;	Gaps 42;

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QY      323 STPRVETTQDVIYF-----PPKILTSVGSNVSFHCIIYK---ENKIYV 362
      | | | : | : : |      : | | : | : : |
Db      2  SAPRIWLAQALLFELLTTESIGOLLEPGYIYPEFPVQRGSNFTAICTLKEACIQHYVN 61

QY      363 SKETVMMNLAEKIPQSOYDVVSDHVSKEYFENLNETKPRGKFTYDAVYCCNEHECHIRY 422
      : | | | | : | : | : | : | : | : | : |
Db      62 ASLYIWKTNHA-AVPREQVYINRTSSYTFDQV--VLPSVQLT-----CNLSFGQIE 112

QY      423 AELIYI-----DVNINISC-ETDGYLTKMTCRWSTSTIOSLAESTLOLRHYRSSLYC 473
      : | : | | | : | : | : | : | : | : | : |
Db      113 QNYVGYTMLSGFPPDPKPTNLTCIVNEG--KNMLCQWDPG---RETYLETNTYLUKSEWA 165

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QY 474 SDIPSIHIPISPEPKDCYQSDGFYECI--FOPIFLLSGYTMWIRIHSLGSLDSEPTCVLP 531
Db 166 TE-----KEPDC--QSKHGTSCMVSYPMTYYVN-IEVWEAEINALGVKSSSEINEDP 214
QY 532 DSVVKPLPPSSVKAETINI-GLLKISWEKVPFPENNIOFOIRKGLSG---KEYO-- 582
Db 215 VDKVKPTPPYNLSVTNSEBLSILKLSW-----VSSGLGILLDKSDIQYRT 261
QY 583 -----WKMEYEVYDAKSKSVSLPVPDL--CAVAYAOVRCRRLDGLGYWSNMSNPAYTVMD 635
Db 262 KDASTWIOVPLEDTMSPRSTFTVQDLKPFTEYVFRIRSIKDSGKGYSWDSWEASGTTYE 321
QY 636 IKVPMRGPEFWRILINGDTMKKEKNVTLMLKPLMKNDLSLSQORY--VINHTSCNGTWSE 693
Db 322 DR-PSRPPSFWMKYKTNPSHGOEYRSVRLIMKALPLSEANGKILDYEVILTQSKSVSQTYV 380
QY 694 DVGNIHTKFTFLMTEQAHVTVLAINSIGASVANENLTFSPW-MSKVNIYQSLSAVPLNSS 752
Db 381 ---TGTELTVNLTNDRIYASLARNKVGSAAAV-LTIPSPHVTAAYSVVNLKAFP-KDN 435
QY 753 CVIVSWILSPSDYKIMYFIEMKNLNEDEI--KWLRISSVKKYIHDHFPIPIEYQFS 810
Db 436 LIMVEW--TPPKPVSKYIIEWCVLSENAPCEDWQODATVNRTHLRGRLLSEKCYQIT 493
QY 811 LYPFMEG----- 818
Db 494 VTPEVATGPGGSESLKAYVLKQAPARGPTVRTKRVKNEAVLAWDQIPVDDQNGFITRYS 553
QY 819 -----VGKPKII--NSFTQDDIEKHQSDAGLY----- 843
Db 554 ISYRTSVGKEMVHVHSDSHTEYTLSSLSST-LYMWVMAAYTDEGKGDPETFTTPKEA 612
QY 844 -----VIVPVISSSI-LLGLTLLISHOR--MKKLFWEDVYPNPKNCWSAOGLNQKPE 894
Db 613 QGEIEAIVPVCIAFLTTLGLVLCFCFNKRDLIKHNPNVDPDESKSHIAQWSPHTPE-- 670
QY 895 FEHLFIKHTASVTCGPLLEPETISEDISVDISWKNKDEMPITVVSLLSTTDLEK---- 950
Db 671 -RHNFNSKDQMYSDGNF-----TDVSVEIEANNNKPCPDD---LKSVDLEKKEV 717
QY 951 -----GSVCISDQFNSVNFSEAGTEVYTEDESQRO--PVEKYATLISNKRSET 998
Db 718 STEGHSSGIGGSSCMSSSRPSSISNE-----ENESAQSTASVETVSVHSGYRHQV 769
QY 999 GEEQGLINSSVTK-CFSSKNSP---LKDSFSNSSWEIEAQAFELISDQHPNIIISPHLTF 1053
Db 770 PSYQVFSRSESTQPLLDSEEREDLQLVDSVDGDEILDRQPYFKQNCQPE-ACPELISH 828
QY 1054 SEGDELLEKLEGN 1066
Db 829 FERSNQV--LSGN 839

RESULT 5
IL6B_HUMAN STANDARD: PRT; 918 AA.
AC P40189; Q9UQ41;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130) (Oncostatin M
DE receptor) (CDw130) (CD130 antigen).
GN IL6ST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
MEDLINE=91084844; PubMed=2261637;

```

RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;  
RT "Molecular cloning and expression of an IL-6 signal transducer,  
gp130.";  
RL Cell 63:1149-1157(1990).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE-Synovium;  
RX MEDLINE-20341529; PubMed-10880057;  
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,  
RA Murakami M., Nakao K.;  
RT "Cloning of novel soluble gp130 and detection of its neutralizing  
autoantibodies in rheumatoid arthritis.";  
RL J. Clin. Invest. 106:137-144(2000).  
RN [3]  
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE-21269388; PubMed-11098061;  
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;  
RT "Determination of the disulfide structure and N-glycosylation sites of  
the extracellular domain of the human signal transducer gp130.";  
RL J. Biol. Chem. 276:8244-8253(2001).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.  
RX MEDLINE-98169383; PubMed-9501088;  
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;  
RT "Crystal structure of a cytokine-binding region of gp130.";  
RL EMBL J. 17:1665-1674(1998).  
CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for  
IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for  
initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)  
complex, resulting in the formation of high-affinity IL-6 binding  
sites, and transduces the signal. Does not bind IL-6. May have a  
role in embryonic development (By similarity).  
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and  
secreted (isoform 2).  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/gp130-  
RAPS; are produced by alternative splicing.  
CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines  
examined. Expression not restricted to IL-6 responsive cells.  
CC -1- DISEASE: gp130-RAPS is an autoantigen found in rheumatoid  
arthritis (RA) but it is not specific to patients with RA.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;  
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".  
CC -----  
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or send an email to license@sib-sib.ch).  
CC -----  
DR EMBL; M57230; AAA59155.1; -  
DR EMBL; AB015706; BAA78112.1; -  
DR PIR; A36337; A36337.  
DR PDB; 1BOU; 26-AUG-98.  
DR MIM; 600694; -  
DR InterPro; IPR002996; CRLA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003962; FNIII\_repeat.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam; PF00041; fn3; 3.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 3.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
FT Repeat; 3D-structure; Alternative splicing.  
FT SIGNAL 1 22  
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.  
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 620 641  
FT DOMAIN 642 918  
FT DOMAIN 26 120  
FT DOMAIN 124 222  
FT DOMAIN 223 324  
FT DOMAIN 325 423  
FT DOMAIN 424 517  
FT DOMAIN 518 613  
FT DOMAIN 725 755  
FT DISULFID 28 54  
FT DISULFID 48 103  
FT DISULFID 134 144  
FT DISULFID 172 182  
FT DISULFID 458 466  
FT CARBOHYD 43 43  
FT CARBOHYD 83 83  
FT CARBOHYD 131 131  
FT CARBOHYD 157 157  
FT CARBOHYD 227 227  
FT CARBOHYD 379 379  
FT CARBOHYD 383 383  
FT CARBOHYD 553 553  
FT CARBOHYD 564 564  
FT VARSPLIC 325 329  
FT VARSPLIC 330 918  
SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;  
  
POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
IG-LIKE C2-TYPE DOMAIN.  
FIBRONECTIN TYPE-III 1.  
FIBRONECTIN TYPE-III 2.  
FIBRONECTIN TYPE-III 3.  
FIBRONECTIN TYPE-III 4.  
FIBRONECTIN TYPE-III 5.  
SER-RICH.

Query Match 5.5%; Score 345.5; DB 1; Length 918;  
Best Local Similarity 19.8%; Pred. No. 1.4e-15;  
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;  
  
QY 337 PPKILTSVGSNVSEHCYKK--ENKIYPSKEIWMWMLAEKIPQSYDVSDHVSQVTF 393  
DB 33 PESPVQLHSNFTAVCVLKEKCMDFHVNANYIVWKTN-HFTIPKEQYTIINRTASSVTF 91  
QY 394 FNLNETKPRGFTYDAVCCNEHECHHRYAELVIDV-----NINISC-ETDGYLTK 444  
DB 92 TDI-----ASLNQLTCNLTFTGQLQNNGYGITIISGLPPEKPNLSQIVNEG--KK 141  
QY 445 MTCRWSTSTIQLAESTLQLRYHRSLSYCSDDIPSIHPISEPKDCYLSDFEYECI--FQP 502  
DB 142 MRCEWDG-----RETHLETNFTLKSEWAT-----HKFA--DCNAKRDPSTCTVDYST 188  
QY 503 IFLSGYTMIRINHSLSGSDSPPTCYLPDSVVKPLPPSSVKAETITN----IGLKLISW 558  
DB 189 VYFVN-IEVWEAENALGKVTSDHINDPVYKVPNPNNLS--VINSELSILKLTW 244  
QY 559 EKP----VPPENLQFOIRYGLSGEYQWKMEVYDAKSKSVSLPVDL--CAVAYQV 611  
DB 245 TNPSTKSVITLKYNITQYRTKDAST-----WSQIPPEDASTRSSITVQDLKPFTEYVFI 299  
QY 612 RCKRLDGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLMLKPLMKND 671  
DB 300 RCMKEDGKGYWSDMSEASGITIEDR-PSKAPSFWYKIDPSHTQGYKTVQLVWKTLPPE 358  
QY 672 SLCSVQRYVINHTSCNGTWSDEVGNH---TKFTFLWTEQAHVTYVLAINSIGASVANF 727  
DB 359 ANGKILDEYV-----LTRWKSHLQNTVYNAKTLVNTLNDRLATLTVRNLVGKSDAAV 413  
QY 728 NLTFSPMSKVNIVQSLAYPLNSCVIVSWILSPSDYKLMFTIEWKNLNEDGE--IKW 785  
DB 414 LTIACDFQATHPVMDLKAFP-KDNMLVWEWTTPRESVK--KYLEWCYLSKAPCITDW 470  
QY 786 LRISSVKKYIYIDHFIPIEKYQSLPIFMEGVGKPKII----- 825  
DB 471 QOEDGTVHRTYLRGNLAESKCYLITVTVYADGPGSPESIKAYLKQAPSPSGPTVTRTKV 530  
QY 826 -----NSFTODDIEKHOSDAGLY- 843  
DB 531 GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSHTEYTLSSLTSDT-LYM 589  
QY 844 -----VIVPVITISSST-LLGLTLLISHOR--MKR 869



Db 590 VRMAATDEGKDGPEFTTTPKFAQGEIAIVPCLAFLLTTLGLVLCFNKRDILIK 649  
OY 870 LEWEDVPNPKNSWAGLNFQKPEFELHFIKHTASVTCGPLLEPETISEDIVDTSWK 929  
Db 650 HIMPVNPDPKSHIAQWSDHTPP-----RH-----NFN 677  
OY 930 NKDEMPPTTVSLSTPLEKGSVCISDOFNSVNSEAGTEVYEDESQROPF---VKY 986  
Db 678 SKDQM-----YSDGNFTDVSVVEIEAND---KKEPFDLKS 710  
OY 987 ATLISNSKPSSETGEGLINSSVTKCFSSKNSPLKDSFSNSS 1028  
Db 711 LDLFKKEKINTEGHSSGIGGSS---CMSSSRPSISSDENES 749  
RESULT 6  
IL6B\_RAT STANDARD; PRT; 918 AA.  
AC P40190;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin  
6 signal transducer) (Membrane glycoprotein 130) (GP130).  
GN IL6ST.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93052397; PubMed=1427893;  
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;  
RT "Molecular cloning and characterization of the rat liver IL-6 signal  
transducing molecule, gp130.";  
RT Genomics 14:666-672(1992).  
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR  
IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING  
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,  
RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,  
AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN  
EMBRYONIC DEVELOPMENT (BY SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS  
AND ENDOTHELIAL CELLS.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M92340; -, NOT\_ANNOTATED\_CDS.  
DR PIR: A44257; A44257.  
DR HSSP: P40189; 1B0U.  
DR InterPro: IPR002996; CR1A.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam: PF00041; fn3; 3.  
DR SMART: SM00060; FN3; 3.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
Repeat.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.

FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 619 640 POTENTIAL.  
FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.  
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.  
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.  
FT DOMAIN 724 754 SER-RICH.  
FT DISULFID 28 54 BY SIMILARITY.  
FT DISULFID 48 103 BY SIMILARITY.  
FT DISULFID 134 144 BY SIMILARITY.  
FT DISULFID 172 181 BY SIMILARITY.  
FT DISULFID 457 465 BY SIMILARITY.  
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECEFR087F7 CRC64;  
Query Match 5.4%; Score 339.5; DB 1; Length 918;  
Best Local Similarity 20.8%; Pred. No. 3,7e-15;  
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;  
OY 327 VFTTQDVI-----YPPKILTSVGSNVSEHCYKKNKIYDSKE---IYWMNLAE 374  
Db 14 IFLWTESIGQLVEPCGYLYPEPPVQGSNFTATCLKRCLOVSVNATYIWMKMHV- 72  
OY 375 KIPQSQYDVVSDHVSQVTFNNEKTRPKGFTYDAVY-----CNEHECHRYAELVYI- 428  
Db 73 AVPEQGVTVINRTASSVTF-----TDVVFQNVQLTCNLSFGQIEQNVGILT 119  
OY 429 -----DVNINISC-ETDGYLTKMTCRWSTSTIQSLAESTYLQRYHRSSLYCSDIPSIH 480  
Db 120 ILGSPDPDIPNLSCIVNEG--KNMLCQ-----LDPGRETYLETNYTLKSEWATE----- 167  
OY 481 PISEKDCYLQSDGFYECT--FQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPL 538  
Db 168 ---KPPDCRTK-HGTSSCMAGTPIYFVN-IEVWEAEALGNVSSHPINFDPVDKVRPS 222  
OY 539 PPSSVKAETITNI-GLLKISW-----EKVPPENNLOFQIRYGLSGKEVQWKMEYVDAR 592  
Db 223 PPHNLSVTNSEELSSILKLAWNSGLDSILRLKSDIQRTKDAST-----WIQVPLEDTV 277  
OY 593 SKSVSLPVPDL--CAVYAVQVRCRLDGLGYMSNPNAYTVVMIDIKVPMRGPEFWRIIN 650  
Db 278 SPRTSEFTVQDLKPTEYEVFRIRSIKENGKGYMSDWEASGTYIEDR-PSKAPSFMYKVN 336  
OY 651 GPTMKKEKNVTLLMKPLMKNDSLCSVQRY--VINHTSCNGTMSHDVGNHTKFTFLMTQEQ 708  
Db 337 ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTV---NGTELIYVNLFTNN 393  
OY 709 AHGVYVLAINSIGASVANFNLFSPWMSKV-NIVQSLASAVPLNSCYIVSWILSPSDYKL 767  
Db 394 RYVASLAAARNVVGKSPATV-LTIGSHFKASHPVDLKAFP-KDNLMLWEW--TPPSKPV 449  
OY 768 MYFIEMKNLNEDEI--KWLRISSSVKYYIHDFIPIEKYQFSLYPIFMEGVGKPP--- 822  
Db 450 NKYLEWCYLSNSPCIPDWQEDGTIVNRTHLRGLSLESKCYLITVTVPFPGGPGSPESM 509  
OY 823 -----KI 824  
Db 510 KAYLQAPPSKGPVTVRTKKVGKNEAVLEWDHLPVDVQNGFIKNYSISYRTSVGKEMVVRV 569



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Db 463 -----LIEWESSPSYNSYKSWMEIPNGNITGILKDNINPQLYRITVAPLPGIYGP 517
QY 822 PRINSFT----- 829
Db 518 PVNVYTFAGERAPHPAPALHLKHVGTWAOLEWVPEAPRLGMIPLTHYIIFWADAGHSF 577
QY 830 -----QDDIEKHQSDAGLY-----VIVPV 848
Db 578 SVTLNLSLHDFVLKHLERASLYHYLMATSRAGSTNSTGLRLTLDPSDLNIFLGICLV 637
QY 849 IISSSILLGLTLLSHQMKKLEWEDVPNPKNCMAQGLNFOKPEFELFKHTASVTC 908
Db 638 LITTCVV--TWLCCRRKRTSFWSDVDPDAHSSLSWL----- 674
QY 909 GPLLEPETISEDISVTSKMKDEMPVTVSLSTDLKGSVCIS-DQFNSVNES-- 965
Db 675 -PTMTEET---FQLPSFW-----DSSVPSITKITELEEDKKPTHWDESSSGNSLP 722
QY 966 -----EAGTEVTEDESOQOPFVKYATLISNSKPSGTGEE-----Q 1002
Db 723 ALVOAYVLQDPREIS---NQSQP-----PSRTGQVLGYQVLESPTSPGV 766
QY 1003 GLINSSVTKCFSSKNSPLKDSFSSSWEIEAQAFTLSDQHPN-----IISPHLTFS--- 1054
Db 767 QYIRSDSTQPLGPTSPKSYENIMWFHSRQETFW--PQBPNDQDCVFGPFDPLRQ 824
QY 1055 ----EGLDELLKLEGNF 1067
Db 825 GLOVHGVEE---QCGF 837

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RESULT 8
LIFR_HUMAN
ID LIFR_HUMAN STANDARD; PRT; 1097 AA.
AC P42702;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukemia inhibitory factor receptor precursor (LIF-R).
GN LIFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92007727; PubMed=1915266;
RA Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,
RA King J., Price V., Cosman D., Beckmann M.P.;
RT "Leukemia inhibitory factor receptor is structurally related to the
RT IL-6 signal transducer, gp130.";
RL EMBO J. 10:2839-2848(1991).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC WITH GPI30. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC -!- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GPI30.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC MEMBRANE-BOUND AND A SECRETED FORM.
CC -!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
CC MAY ARISE BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; X61615; CAA43805.1; -
DR MIM; 151443; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SMO0060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Alternative splicing; Repeat.
FT SIGNAL 1 44
FT CHAIN 45 1097 LEUKEMIA INHIBITORY FACTOR RECEPTOR.
FT DOMAIN 45 833 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 834 858 POTENTIAL.
FT DOMAIN 859 1097 CYTOPLASMIC (POTENTIAL).
FT DISULFID 55 65 BY SIMILARITY.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 787 787 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1097 AA; 123742 MW; C8602897E359FCES CRC64;

```

Query Match 4.7%; Score 294.5; DB 1; length 1097;  
 Best Local Similarity 19.2%; Pred. No. 5.3e-12;  
 Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;

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QY 161 LLYVLEPEVLEDSPLVPQKGSFGVHVC-----NCS-----VHECC----- 194
Db 35 LLYLMNQVNSQ-----KKGAPHDLKCVTNLQVWNCWKAPSGIGRGTDYEVCIENRSRS 89
QY 195 -----ECLVVPPTAKLNDTLMLCKITSGVIFQSPIMSVQPIWVKPDPPLGLHMEIT- 248
Db 90 CYOLEKTSIKIPALSHGDEYETITNSLHDFGSSSTKFTLNEQNSLI-PDTPEILNLSADF 148
QY 249 DDGNLKISWSSPPLVPFPLOYQVKSSENSTVIR---EADKIVASVSL----- 294
Db 149 STSTLYLKWNDRGSV-FPHRSNVILW---EIKVLKRESMELVYLVTHNTTLNGKDTLHMS 204
QY 295 --VDSILPGSSYEVOVR---GKRLDGPGLWSDWSTPRVFT---TQDVIFPPKILTSVG 345
Db 205 WASDMPLECAIHFEVEIRCYIDNLHFSGLEWSDWSPVKNISWITPDSQTKVFPPQKVILVG 264
QY 346 SNVSPHCITYKKENKIYPSKEIWMNMLAEKIPQSQDYV---SDVSKVTFPFLNETKPR 402
Db 265 SDITFCVV-----SQEKV-----LSALIGHTNCPLIHLDGENVA-IKIRNISVSASS 310
QY 403 GKFTDAVYCCNEHECHHRYAELVIDVINISCEITDGLYTKMKCRGSTSTIOSLA---E 459
Db 311 GT---NVVFTTEDNIFGTIVFAGYPPDTPQOLNCEITHD-LKEIICSANPGRTALVGPRA 366
QY 460 STLQRLYHRSSLYCSDIPSIHPISSEPKDCYLQSDGFYEFCFOPITPLSGYTMIRINSL 519
Db 367 TSYTLVESFSGKYVRLKRAEAPTNES-----YQLLFQMLPNQEIYNTFLNAHNP 416
QY 520 GSLDSPPTCVLPDSVVKPLPPSSVKAETITINIGLKISWERP-----VPEEN 566

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Db 417 GRSOSTILVNITEKV-PHTPTSFKVK-DINSTAVKLSWHLPGNFAKINFLCEIEIKSN 474  
QY 567 NLQFOIRYGLSGKEVQMKMEYVDAKSKSVSLPEVPLCAVYAVQVRCRRLDGLGYWSNMS 626  
Db 475 SVQEOBNVTIKGVE-----NSSYLVALDKLNIPYTLTYFRIRCS-TEFTFWKWSKMS 523  
QY 627 NPATYVMDIKVPMGPEEFWRINGDTMKKEKNVTLMKPLMKNDLSGVQRYVINHTS 686  
Db 524 NKKOHLTEAS-PSKGPDPDWREMSD---GNLIIYWKPLPINEA---NGKILSYNVS 574  
QY 687 CNG-----TWSEDEVNHTKFTFLWTEQAHVTVAINSIGASVANFNLTFSWPMKSVNIV 741  
Db 575 CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISYVAKNSVSGSSPPSKIASMEIPNDLKIT 634  
QY 742 QSLAYPLNSSCVIVSWILSPS---DYKLMFIEWMKN--LNEDGEIKWRL-SSSVKKY 795  
Db 635 QVYGM---GKGILLTWHDYDPNMTCDY---VIKWCNSSRSEPCIMDWKRPVPSNSTETV 685  
QY 796 YIHDHFIPIEKYQSLYPIEMEG-----VG-----KPKIINSFTQDD----- 832  
Db 686 IESDEFPGIRNFFLYGCRNOGYOLRSMIGYIEELAPIVAPNFTVEDISADSLVKE 745  
QY 833 -----IEKHQSD----- 839  
Db 746 DIPVEELRGFLKGLFYFGKERDTSKMRVLESGRSKDIKVNITDISQTLRIADLOGKT 805  
QY 840 -----AGLYVI-----VPVISSSILLGTLILSHQR--M 867  
Db 806 SYHLVLRAYTDGVGPEKSMYVTKENSVGLIAILIPVAVAVIGVYTSILCYRKREWI 865  
QY 868 KKLFWEDVPNPKNGSWAQLNFOK-----PETFEHLFIKHTASVTCGPLL 912  
Db 866 KETFYDPDIPNENC---KALQFKSVCEGSSALKLEMNPCPTPNNEVELETRSAF--PKI 920  
QY 913 LEPETISEDIVDTSMKNKDEMPPTVVSLLSTTDLKGSVC---ISDPNSVNFSEAG 969  
Db 921 EDTEIIS---PVAERPEDRSDAEPENHYV-----SYCPPIEEELIPNPADEAGG 968  
QY 970 T-EVITYED-ESQRPFEKVATLISNSKPSFEGEGL-----INSSVTKCFPS- 1014  
Db 969 TAQVIYIDVQSMQP-----QAKPEEGENDPVGAGYKPPQMLPINSTVEDIAAE 1019  
QY 1015 ---SKNSPLKDSFSSNSWEIEQAFFILSDQHPNIISP 1049  
Db 1020 EDLDKTAGYRPOANVNTW-----NLVSP 1042

RESULT 9  
GCSR\_HUMAN STANDARD: PRT: 836 AA.  
AC Q99062;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)  
DE (CD114 antigen).  
GN CSF3R OR GCSFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=91079757; PubMed=2147944;  
RA Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman D.,  
RA Park L., Sorensen E., March C.J., Smith C.A.;  
RT "Expression cloning of a human granulocyte colony-stimulating factor  
RT receptor: a structural mosaic of hematopoietin receptor,  
RT immunoglobulin, and fibronectin domains.";  
RL J. Exp. Med. 172:1559-1570(1990).  
RN [2]  
RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;  
RX MEDLINE=91062348; PubMed=1701053;  
RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;  
RT "Three different mRNAs encoding human granulocyte colony-stimulating  
RT factor receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92091782; PubMed=1530796;  
RA Seto Y., Fukunaga R., Nagata S.;  
RT "Chromosomal gene organization of the human granulocyte colony-  
RT stimulating factor receptor.";  
RL J. Immunol. 148:259-266(1992).  
RN [4]  
RP DOMAINS STRUCTURE.  
RX MEDLINE=92007729; PubMed=1717255;  
RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;  
RT "Functional domains of the granulocyte colony-stimulating factor  
RT receptor.";  
RL EMBO J. 10:2855-2865(1991).  
RN [5]  
RP STRUCTURE BY NMR OF 227-334.  
RX MEDLINE=97331327; PubMed=9187659;  
RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;  
RT "Solution structure of an extracellular domain containing the WSxWS  
RT motif of the granulocyte colony-stimulating factor receptor and its  
RT interaction with ligand.";  
RL Nat. Struct. Biol. 4:498-503(1997).  
RN [6]  
RP 3D-STRUCTURE MODELING OF 125-331.  
RX MEDLINE=98037802; PubMed=9368043;  
RA Layton J.E., Taria J., Smith D.K., Treutlein H.R.;  
RT "Identification of a ligand-binding site on the granulocyte colony-  
RT stimulating factor receptor by molecular modeling and mutagenesis.";  
RL J. Biol. Chem. 272:29735-29741(1997).  
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-  
CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION  
CC EVENTS AT THE CELL SURFACE.  
CC -1- SUBUNIT: DIMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,  
CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM  
CC OF THE RECEPTOR.  
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; GCSFR-1 (SHOWN HERE),  
CC GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY  
CC ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN  
CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN  
CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.  
CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE  
CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.  
CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;  
CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD114 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X55721; CAA39253.1; -  
DR EMBL; X55720; CAA39252.1; -  
DR EMBL; S71484; AAB20660.1; -  
DR EMBL; M59818; AAA63176.1; -  
DR EMBL; M59819; AAA63177.1; -  
DR EMBL; M59820; AAA63178.1; -  
DR PIR; JH0329; JH0329.





Accession	Source	Protein	Function	Location	Structure	Properties	Notes
RT	Three different cDNAs encoding mouse D-factor/LIF receptor.						
RL	J. Biochem. 115:557-562(1994).						
CC	-1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY WITH GPI30. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.						
CC	-1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GPI30.						
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.						
CC	-1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS MAY ARISE BY ALTERNATIVE SPLICING.						
CC	-1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN, AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF THE SECRETED FORM.						
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.						
CC	-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.						
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or-send-an-email-to-licence@isb-sib.ch">http://www.isb-sib.ch/announce/or-send-an-email-to-licence@isb-sib.ch</a> ).						
CC	-----						
DR	EMBL; S73496; AAC60698.1; -						
DR	EMBL; S73495; AAC60697.1; -						
DR	EMBL; D26177; BAA05165.1; -						
DR	EMBL; D17444; BAA04258.1; -						
DR	MGD; MGI:96788; L1fr.						
DR	InterPro: IPR002996; CRIA.						
DR	InterPro: IPR003961; FN_III.						
DR	InterPro: IPR003529; Hematopo_receptor_L_F2.						
DR	pfam; PF00041; fn3; 4.						
DR	SMART; SM00060; FN3; 3.						
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.						
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Alternative splicing; Repeat.						
FT	SIGNAL	1	43	POTENTIAL.			
FT	CHAIN	44	1092	LEUKEMIA INHIBITORY FACTOR RECEPTOR.			
FT	DOMAIN	44	828	EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM	829	853	POTENTIAL.			
FT	DOMAIN	854	1092	CYTOPLASMIC (POTENTIAL).			
FT	DISULFID	53	63	BY SIMILARITY.			
FT	CARBOHYD	164	164	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	238	238	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	261	261	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	385	385	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	421	421	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	440	440	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	453	453	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	476	476	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	567	567	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	647	647	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	658	658	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	675	675	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	724	724	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	782	782	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	718	719	AP -> EA (IN SECRETED ISOFORM).			
FT	VARSPPLIC	720	1092	MISSING (IN SECRETED ISOFORM).			
FT	VARSPPLIC	1092	122573	MM; 6F02BBC8E154DE70 CRC64;			
SEQUENCE							

Query Match	4.5%;	Score 281.5;	DB 1;	Length 1092;
Best Local Similarity	18.8%;	Pred. No. 4e-11;		
Matches 217;	Conservative 177;	Mismatches 392;	Indels 371;	Gaps 577;

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Qy      178 KGSFQWVHCNSVHECCCECLVPVP-----TAK--LNDTLTMC--LKITSGGVIFOSP- 225
      . | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      45  KRGVQDLKCTTNNMRVWDCWTAPAPLGVSPGTVKDICIKNDRFHSCHPLETTNVKIPALSPG 104

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[illegible]

Db 1043 ---TDSNNEVSEFGSPC 1056

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RESULT 11
112S_HUMAN STANDARD; PRT; 862 AA.
AC Q99665;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-
2) (IL-12R-beta2).
GN IL12RB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
beta-type cytokine receptor subunits."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
LOW AFFINITY.
CC -1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH
AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
IL12RB2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-----
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CC
DR EMBL: U64198; AAB36675.1; -
DR HSSP: P40189; 1BQU.
DR MIM: 601642; -
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 862 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
FT DOMAIN 22 624 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 625 641 POTENTIAL.
FT DOMAIN 642 862 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 224 306 FIBRONECTIN TYPE-III 1.
FT DOMAIN 421 508 FIBRONECTIN TYPE-III 2.
FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 862 AA; 97134 MW; 67C0E0D94688DD58 CRC64;

```

Query Match 3.5%; Score 220.5; DB 1; Length 862;

Best Local Similarity 19.8%; Pred. No. 3.8e-07; Matches 182; Conservative 129; Mismatches 322; Indels 285; Gaps 49;

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QY 332 DVIYFPKILTSVGSNVSFHCI-----YKKENKIVPSKEIYVWMMNLAEKIQSOYD 382
Db 32 DVTVKPSHVIL-LGFTVNTICSLKPRGCGFHYSRMKLILYK-----FD 74
QY 383 -VVS DH-----VSKVTFEENETKPRGKFTYDAVYCCNEHECHRYAEIYV---IDVIN 433
Db 75 RINFHHGHSLSQVTLGLTTLFVCKIA-----CINSDEIQIGAEIFVGADEQPQN 129
QY 434 ISCEDGYLTKMTCRNSTIQLS-ABSTIQLRYHRSLSY---CSD1PSIHPISEPKDC- 488
Db 130 LSCIQKGEGTVACTWNERGRDTHLYTEYTIQLSGPKNLTWOKCKDI-----YCD 179
QY 489 YIQSDGFYECIFQPIFLLSGYTMWIRINSLGSLDSPPTCVLPDSVVKPLPSSVKAEL- 547
Db 180 YLD---FGINLTPESPESNFTAKVTAVNSLSSSSSLPSTFTPLDIVRPLPMDIRIKFQ 235
QY 548 TINIGLLKISWEKVPFENNLOFQIRYGLSGKEVOMKEYEYDAKSKSVSLPVDLCAYV 607
Db 236 KASVSRCTLYWRDEGLVLLN---RLRYRPSNSRL-WNVVNTKAKGRHLLDLKPF-TEY 290
QY 608 AVQVRCKRLDGLGYWSNWSNPAVTVMDIKVPMRGP---EFWRITNGDTMKK-----EK 658
Db 291 EQQISSKHLHYKGSWSDMSGS-----LRAQTPDEEPTGMDVW-----YMKRHIDYSRQ 339
QY 659 NYTLMLKPLMKNDLSQVQRYVINHTSCNG-TWSEDEVNHTKFTFLWTEQAH-TYTYLA 716
Db 340 QISLFWKNLSVSEARGKILHYQVTLQELTGKAMQNTGHTSWTIVIPRTGNMAYVSA 399
QY 717 INSIGASVANENLTFSPMKVNIV-----QSLSAVPLNSSCVIVSWILSPSD-Y 765
Db 400 ANSKGSSLP-----TRINIMNLCEAGLAPROYSANSEGMDNLTWOPPRKDPDS 449
QY 766 KIMYFIEMKNLNEGE---IKWL-----ISSVKKYIYHD----- 799
Db 450 AVOEYVEWRELHPGGDIQVPLMWLRSRPNYSALISENIKSYICYEIRYALSGDGGC 509
QY 800 -----HPIPEKYQFSL--YPIF--MEGVKGP 822
Db 510 SSIIGNSKHKAPLGSPHINATEEKGSIISWSNIPVQMGCLHYRIYWKERDSNSQP 569
QY 823 KI-----INS-----FTQDDIEKH-----QSDAGLYVIVPV 848
Db 570 QICEIPYRVSONSHPINSLQPRVTVYVLMTALTAAEGSSHGENRPFQLOGKANMAYAP 629
QY 849 IISSSILLGLTLLISHQRMKLF-----W--EDVNPKNCSWAQGLNFQKPEP--- 894
Db 630 SICIAITMGV-IFSTHYFQGVVLLAALRPQWCSRELPDANSYCAKKYPIAEKTYLP 688
QY 895 FEHFIKHTASVTGPLLLEPETISEDISVDT-----SWKNKDEMPTTVVSLIST 945
Db 689 LDRLLIDWPT-----PEDPEPLVISEVLHOVTPVFRHPPCSNMPQREK----- 731
QY 946 TDLKGSVCISDOFNSVNFs-----EAEGETEVT--YE-----DESORQFVKYATLI 990
Db 732 -GIGQHQAASEKMDMHASAPPRALQAESRQLVDLYKYLESGSDPKPENPACPTVLP 790
QY 991 SNKRPSSETGEEQGLINSVTRCFSSSKNSPLKDSFSNSMEIEAQ---AFFILSDQHNI 1046
Db 791 AGDIPT-----HDGYLPSNIDD-LPSHEAPLADSL-----ELFPQHSLSVFPSSSLRP-- 839
QY 1047 ISPHLTFSEG---LDEL 1060
Db 840 -----LTFSCGDKLTLDOL 853

```

```

RESULT 12
PRLR_COLL1 STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)

```

DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 15-JUL-1998 (Rel. 36, last annotation update)  
DE Prolactin receptor precursor (PRL-R).  
GN PRLR.  
OS Columba livia (Domestic pigeon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauaria; Aves; Neognathae; Columbiformes; Columbidae; Columba.  
OX NCBI\_TaxID=8932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cropsac;  
RX MEDLINE=94283267; PubMed=7516866;  
RA Chen X., Horseman N.D.;  
RT "Cloning, expression, and mutational analysis of the pigeon prolactin  
RT receptor";  
RL Endocrinology 135:269-276(1994).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U07694; AAA20646.1; .  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SM00060; FN3; 4.  
DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 23  
FT CHAIN 24 830  
FT DOMAIN 24 439  
FT TRANSMEM 440 460  
FT DOMAIN 461 830  
FT DOMAIN 25 122  
FT DOMAIN 123 226  
FT DOMAIN 229 326  
FT DOMAIN 327 429  
FT DISULFID 36 46  
FT DISULFID 75 86  
FT CARBOHYD 59 59  
FT CARBOHYD 91 91  
FT CARBOHYD 100 100  
FT CARBOHYD 112 112  
FT CARBOHYD 132 132  
FT CARBOHYD 263 263  
FT CARBOHYD 304 304  
FT CARBOHYD 316 316  
FT CARBOHYD 336 336  
SQ SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFP CRC64;  
  
Query Match 3.5%; Score 220; DB 1; Length 830;  
Best local Similarity 20.8%; Pred. No. 3.9e-07;  
Matches 165; Conservative 126; Mismatches 308; Indels 194; Gaps 37;  
  
QY 476 IPSIHPISEPKDCYLQSDGFYECIFQPIFLSG-----YTMWIRINHSL 519  
DB 56 LPTNVTLEFYSKD---SEKIYEC---PDYGMGPNSCYFDKNTNTPWTTYNITVMAMNEI 109  
QY 520 GSLDSPPTCYLPSDVVKPLPP--SSVKAETITINIGLKISWEKPVFPE-----NNLQFOI 572  
DB 110 GSNSSDPQYVDVTIVQPDAPVNLSETKTSASTTYLLAKMSPPPLADVTSNSHVRYREL 169

QY 573 RYGLSGKEVQWKMEYVDKSKSVSLPYDLCAY-----VAQVRCRLDGLGYWSN 624  
DB 170 RLKPEEKE-EM-----ETVSAGVQIQYKVNRLQAGVKYVQVRCV-LD-IGEWSE 216  
QY 625 WSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLWKPLKKNDSLCSVQRYVINNH 684  
DB 217 WSSERHIHPINGESP---PEKPTTIKCRSPEKE-TFTCWMPK----- 254  
QY 685 TSCNGTWSSEVGNHTKFTFLWTEQA-----HT-----VTV 714  
DB 255 -----GSDGHPNTNYTLTYSKEGERVEYECPDYKTAGPNSCYFDKHTSEWTYNITV 307  
QY 715 LAINSIGAVAN--FNLTFSWPMG-KVINVOSLSAYPLNSSCVIVSWILSP-SDYKLMY 769  
DB 308 KATNEIGSNVSDPLYVDVTYIVQTPDPVNVTLLEKKTYNRKPYLVLTWSPPLADVRSWG 367  
QY 770 FIIEWK-NLNEDGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIEMEGVGPKIINSF 828  
DB 368 LTLDYELRLKPEAEEMETIFVGOQTHYKMFSLNPGKKYVQIH-----CKPDHGSW 420  
QY 829 TODDIEKHQ-----SDAGLYIVPVIISSSILLG-TLLISHQMKKLLFWEDVPNPK 879  
DB 421 SEMSLEKYLQIPTDFRIKDMVWIIYGLVSSLICLVMSWTWLVKGYRMIAFILPPVGPBK 480  
QY 880 NCSWAQGLNFQKPETFE-----HLFIKHTASVTCGPLLEPETI--SEDISVDT 927  
DB 481 ----IKGIDTHLLETGKSEELLSALGCHGF---PPTSDEELLILEVEDESDQOLMPS 533  
QY 928 WKNKDEMPPTVVSLLSTDLKGSVCISDQFNSVNFSEAGTEVTEDESQROPFVKYA 987  
DB 534 HDNGHPSKNAKMIAKETSDSGRGS-CDSPSLSEKCREKRAILSTLOTQDIR----- 585  
QY 988 TLISNKPSETGEEGLINSVTCFSSKNSPLKDSFSNSSWELEAQAFFILSDQHPNI 1047  
DB 586 -----DVQENNGRRHWE-TQCIASEQKIL--LENNESTKSPIMPAAQLPDNQPPMF 633  
QY 1048 SPHLTFSEGLDELKLEGNFPE--ENNDKSIYLLGVTSI-----KKRESGVLL-TDK 1097  
DB 634 AYHSTVDVHKITLCTIDVNIAPVLENEQHOPOYPITETVHDNMEKHREVENLYSKTDQ 693  
QY 1098 SRV-----SCPAPCLFTDI---RVLQDS-CSHEVENNINLTSSKKTFASYMPO 1144  
DB 694 TTVQVQNRPNNDKSPFSKPKLMDYEVHKKVRODEVAVALLKHKEMSKIEKYTVPGTSKE 753  
QY 1145 FQTCSTQT-HKIM 1156  
DB 754 YTKVSTVVDHNIL 766  
  
RESULT 13  
ID 112S\_MOUSE STANDARD; PRT; 874 AA.  
AC P97378;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-  
DE 2) (IL-12R-beta2).  
GN IL12RB2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97098510; PubMed=8943050;  
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,  
RA Gately M.K., Gubler U.;  
RT "A functional interleukin 12 receptor complex is composed of two  
RT beta-type cytokine receptor subunits";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).  
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A

```
CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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-----
DR EMBL; U64199; AAB36676.1; -.
DR HSSP; P40189; 1BQU.
DR MGD; MGI:1270861; Il12rb2.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 4.
DR PRINTS; PR00014; FNTPPEIII.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 20
FT CHAIN 1 874
FT DOMAIN 21 639
FT TRANSMEM 640 656
FT DOMAIN 657 874
FT DOMAIN 137 230
FT DOMAIN 240 322
FT DOMAIN 436 523
FT DOMAIN 534 622
FT CARBOHYD 48 48
FT CARBOHYD 101 101
FT CARBOHYD 114 114
FT CARBOHYD 142 142
FT CARBOHYD 151 151
FT CARBOHYD 169 169
FT CARBOHYD 179 179
FT CARBOHYD 224 224
FT CARBOHYD 252 252
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 323 323
FT CARBOHYD 391 391
FT CARBOHYD 495 495
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 3.5%; Score 220; DB 1; Length 874;
Best Local Similarity 20.3%; Pred. No. 4.2e-07;
Matches 166; Conservative 95; Mismatches 286; Indels 270; Gaps 42;

QY 433 NISCETDGYLTMTGCRWSTSTIOSLAES-TIQLRVHRSSLYCSDIPSIRHISEPKDCYLQ 491
Db 142 NISCVOEGENGTVACSNMNGKVTYLTNTYTLQLS-GPNNLTCQ-----KOCF-- 187
QY 492 SDGFYEC-----IFQPIFLLSGYTMIRINHSGLSDSEPTCVLPDSVVKPLPPSSVK 544
Db 188 SDNRQNCNRLDLGLINSLPDLAESRFIVRTAINDLGNSSSLPHTFTFLDIVITPLPPWDIR 247
QY 545 AEITINIGLKIS-----WE-KVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSV 596
Db 248 -----INFLNAGSGRGLQWEDQGVNLQRLRYQPLNSTS-----WMVNATNAGK-- 294
QY 597 SLFVPDL--CAVAYVOYCK-RLDGLGYWSNWSNPATVVMIDIKVPMRGP---EEWRIT 649
Db 295 -YDLRDLRPFTEYEFQISSKHLHSG-GSWSNWSESLRT-----RTPEEPVGILDIM-YM 346
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QY 650 NGDTMKKEKNVTLKPLMKNDLSCVQRYVINHHFSCNGTWSIEDVGNHTKFTPLMTE-- 707
Db 347 KQDIDYDRQOISLFWKSNPSEARGKILHYQVTLQEVTKTKTTLQNTTRHTS---WTRVI 402
QY 708 ---QAHTVTLAINSIGASVANENLTFSPMSKVNIY-----QSLAYPLNSSCV 754
Db 403 PRGAWTASVASANSKGSAP-----THINIVDLCTGLLAIPHQVSAKSENMDNI 452
QY 755 IVSWILSP---SDYKLMYFIEMKNLNDEGEI-----KMLR-----ISSYKKYYI 797
Db 453 LVTW--QPPKKADSAVREIVEMRAL-QPGSITKFPFWLRIPPDNMSALISENIKPYIC 509
QY 798 HD-----HFIP-----EKYQ----- 808
Db 510 YEIRVHALSESQGCSSIRGDSKHKAPVSGPHITAITEKKELEFISWTHIPPEQRCIL 569
QY 809 -ESLYPIFMEGVGKPKII-----NSFTQDDIEKH----- 836
Db 570 HRYTWKERDSTAQPELCEIQYRRSONSHPISSLOPRVTVLNMVAVTAGESQGNERE 629
QY 837 ---QSDAGLYVIVPVIISSILLGLTLLSHQRMK-----K)FW--EDVPNPKNCW 883
Db 630 FCPQGANWKAFVISSICIAITVGTFSIRYFQKAPFTLLSTLK)QWYSRTIPDANSTW 689
QY 884 AQGLNFQKPEFHEHFIKHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTYVSL 943
Db 690 VK-----KY-----PILEEKIQLPID-NLLMANPTPEEPEPLIHEVL 726
QY 944 -----STTDLEKGSVCISDQFNSVNFSEAECTEVTYDEDSQROP 982
Db 727 YHMIPVVRQPYEYKRGQCGYISTSKQDAMYIANPQATCTLTAEIQLVNLKYLESRD 786
QY 983 FVKYATLIS-----NSRPSETGEEQGLINSVYKCPSSKNSPLKDSFNSGWEIEAQ- 1034
Db 787 DSKLANLTSPLTVPVNYLPS---HEGYLPSNIEDISPHEADP-----TDSFDEHQH 836
QY 1035 ---AFFILSDQHPNII-SPHLTFSE--GLDELKLE 1064
Db 837 ISLSIFASSSLRPLIFGGERLTLDRLKMGYDSIMSNE 873

RESULT 14
PRLR_CHICK STANDARD; PRT; 831 AA.
AC 004594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-Kidney;
RX MEDLINE-93075121; PubMed-1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
-----
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DR EMBL: D13154; BAA02439.1; -  
DR PIR: J01655; J01655.  
DR HSSP: P14787; IAN3.  
DR InterPro: IPR002996; CRI1.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SM00060; FN3; 3.  
DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 831 PROLACTIN RECEPTOR.  
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 439 459 POTENTIAL.  
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 75 86 BY SIMILARITY.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADB9 CRC64;

Query Match 3.3%; Score 209.5; DB 1; Length 831;  
Best Local Similarity 20.4%; Pred. No. 2e-06;  
Matches 174; Conservative 127; Mismatches 291; Indels 263; Gaps 46;

QY 476 IPSIHPISEPKDCYLOSDFEYECIFQPIFLSG-----YTMWIRINHS 519  
DB 56 LPTNYTLFYSKD--SEEIYEC--PDYRTSGPNSCYFNKNHTSPWTFNITVATFNEI 109  
QY 520 GSLDPTCVLPDSVVKPLPPSSVKAET--TINIGLKISWEKPEPE--NNL-QFOIR 573  
DB 110 GSNSSDPQYVDVTSIVQSPVNLLETKRANINMYIMAKWSPPLADASSNHLHYELR 169  
QY 574 YGLSGKEVQWKMYEVYDAKSKSVLPVPLCAV-----YAVQVRCKRLDGLGYSWN 625  
DB 170 IKPEKE-EW-----ETISGVQTOCKINRLNAGMRYVQVRC-TLDP-GEWSEN 216  
QY 626 SNPATYVMDIKVPMRGPEFWRIINDTMKKEKNVTLWKPLMKNDSLCSVQRYVINHT 685  
DB 217 SSERHILIPSGQSP--PEKPTIKCRSPEKE-TFTCMWKPLDGC-----GHPT 261  
QY 686 SCNGTWSED-----VGNHT----KFTFLWTEQAHTVTLAINSIGASVAN- 726  
DB 262 NYTLYSKEGEEQVECPDYRTAGPNSCYFDKHTSFT--IYNITVRATNEMGSNSSDP 319  
QY 727 --FNLTPE-SWPMKSVNIQVSLAYPLN-SSCVIVSWILSP-SDYKLMFYIEM--KNLNE 779  
DB 320 HYVDVYIVQDPDPVNVTLLEKK-PINRKPYLVLTWSPPLADYRSGWLTLLEYELRLKPE 378  
QY 780 DGEIKMLRISSSVKYIYHDFPLEKYQFSLYPIFMGEVGPKEIINSFTODDIEKH--- 836  
DB 379 EGE-EMETIFVGOOTOYKMFSLNKGKYYIIQIH-----CKPDHGSWSSESENYYQI 430  
QY 837 -----QSDAGLYIVIVPITSSSILLG-TLLISHQRMKLEWEDVYPNPKNSWAQGLNQ 890  
DB 431 PNDFRYKDMIVWIVLGLVLSLILCLINSWTAVLKGYRMITFMLPPVPGPK---IKGIDTH 486

QY 891 KPET-----FEHLFIKH-----TASYT- 907  
DB 487 LLETGKSEELLSALGCHGLPTSDCEELLIEYLEVEDSEDOQLMPSHDNGHPSKNAKTR 546  
QY 908 -----C-GPLL-----EPETISEDISVDTSMKNKDEMMPTT 938  
DB 547 KETDSDSGRGSCDSPSLSEKRETCALPYLOTQEVRYDQEKAAKRSWET--QYVASE 604  
QY 939 VVSLSTTDLEKGSVCISDOF-NS-----VNFSEAGTEVTEYEDSOR 980  
DB 605 RKALLSNSESAASSSTWPAVQLPNSQPPMFAHSHVDAHKITLNTINVAAYLVEDEEH 664  
QY 981 QPFVKYATLISNSKPSSETGEEQGL-----INSSVTKCFSSKNSPLKDSFSNSWEIEAQ 1034  
DB 665 QSQSLTETIPGEMEKQ-GEMENLHSKTEQTAAQVKQNRSNRKLPELDAALMDYEVHK- 722  
QY 1035 AFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNDKSTY-----YLGVTIRK 1086  
DB 723 --VIRQDEPAVLKH-----KENGKIEKYTISGASKEYTKVSTVM 762  
QY 1087 KRESGVLLTDKSRVSCFPA---PCLFTDIRVLQDSCHFEVENIN-----LG 1131  
DB 763 DHNITVLMPD-SRVP-HTPASQEPRAKETSQSLQGG---VEKNISYCLTAPSDCKRETG 816  
QY 1132 TSSKKTFASTMPQFO 1146  
DB 817 GSEYMDPSSFMPSFK 831

RESULT 15  
PRLR\_MELGA STANDARD; PRT; 831 AA.  
ID PRLR\_MELGA Q91094; Q91092;  
AC Q91094; Q91091; Q91092;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Prolactin receptor precursor (PRL-R) (TPRLR).  
GN PRLR.  
OS Meleagris gallopavo (Common turkey).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
OX NCBI\_Taxid=9103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97057891; Pubmed=8902221;  
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlehn U.;  
RT "Molecular cloning, tissue distribution, and expression of the  
RT prolactin receptor during various reproductive states in Meleagris  
RT gallopavo.";  
RL Biol. Reprod. 55:1081-1090(1996).  
RN [2]  
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.  
RC TISSUE=Ovary;  
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;  
RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U76587; AAB01544.1; -  
DR EMBL: U22947; AAA75038.1; -







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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:52:56 ; Search time 96.26 Seconds  
(without alignments)  
2093.695 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 6254  
Sequence: 1 MICQKFCVVLHWEFIYVIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvivirus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6254	100.0	1165	4	Q92921	Q92921 homo sapien
2	5967	95.4	1163	6	Q9MYL2	Q9MYL2 macaca mula
3	5941.5	95.0	1194	6	Q9MYL0	Q9MYL0 macaca mula
4	5269	84.3	1165	6	Q02671	Q02671 sus scrofa
5	4831.5	77.3	958	4	Q92920	Q92920 homo sapien
6	4826	77.2	896	4	Q92919	Q92919 homo sapien
7	4819.5	77.1	958	4	Q13592	Q13592 homo sapien
8	4816	77.0	906	4	Q13593	Q13593 homo sapien
9	4814	77.0	896	4	Q13594	Q13594 homo sapien
10	4761.5	76.1	1162	11	Q9QMG3	Q9QMG3 mus musculus
11	4591	73.4	925	6	Q9MYK9	Q9MYK9 macaca mula
12	4590	73.4	894	6	Q9MYL1	Q9MYL1 macaca mula
13	3970.5	63.5	848	6	Q9MZS2	Q9MZS2 sus scrofa
14	3729	59.6	895	11	Q62960	Q62960 rattus norv
15	2790.5	44.6	1147	13	Q9DDK1	Q9DDK1 meleagris g
16	2775	44.4	1148	13	Q9IBA7	Q9IBA7 gallus galli

17	2693	43.1	1146	13	Q918V6	Q918V6 gallus galli
18	1074	17.2	246	11	Q35773	Q35773 rattus norv
19	981.5	15.7	273	11	Q9QWV5	Q9QWV5 mus musculus
20	801	12.8	203	6	Q28604	Q28604 ovis aries
21	683	10.9	161	6	Q28606	Q28606 ovis aries
22	660.5	10.6	173	6	Q9XSN9	Q9XSN9 sus scrofa
23	616	9.8	147	6	Q95257	Q95257 sus scrofa
24	588	9.4	152	6	P79115	P79115 bos taurus
25	497	7.9	123	6	Q9N1P9	Q9N1P9 sus scrofa
26	477	7.6	121	6	O18980	O18980 bos taurus
27	456	7.3	145	13	Q91A32	Q91A32 gallus galli
28	444	7.1	881	13	Q57519	Q57519 xenopus lae
29	409.5	6.5	918	13	Q9W6U9	Q9W6U9 gallus galli
30	366	5.9	102	6	Q9XSH3	Q9XSH3 equus caball
31	354	5.7	710	13	Q57520	Q57520 xenopus lae
32	325	5.2	74	11	Q9ER14	Q9ER14 rattus norv
33	312.5	5.0	1093	11	Q70535	Q70535 rattus norv
34	299	4.8	57	6	Q97778	Q97778 elephas max
35	299	4.8	57	6	Q99650	Q99650 loxodonta a
36	267	4.3	979	4	Q99650	Q99650 homo sapien
37	251.5	4.0	2302	11	O88488	O88488 rattus norv
38	232.5	3.7	970	11	O88821	O88821 mus musculus
39	228	3.6	971	11	O70458	O70458 mus musculus
40	213	3.4	57	13	Q90WY8	Q90WY8 gallus galli
41	197	3.1	861	6	Q9BEG2	Q9BEG2 bos taurus
42	195	3.1	1598	4	Q9P214	Q9P214 homo sapien
43	191.5	3.1	6875	6	Q28733	Q28733 oryctolagus
44	189.5	3.0	1114	5	Q9VSG6	Q9VSG6 drosophila
45	188	3.0	26926	4	Q10466	Q10466 homo sapien

## ALIGNMENTS

RESULT 1  
ID Q92921 PRELIMINARY; PRT; 1165 AA.  
AC Q92921;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96398968; PubMed=8805376;  
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,  
RA Mathews W.;  
RT "A role for leptin and its cognate receptor in hematopoiesis.";  
RL Curr. Biol. 6:1170-1180(1996).  
DR EMBL: U66497; AAB07497.1; -.  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CR1A.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam: PF00041; fn3; 2.  
DR SMART: SM00060; FN3; 1.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602DGA CKC64;

Query Match 100.0%; Score 6254; DB 4; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MICQKFCVVLHWEFIYVITAFNLSYPTTPWRFKLSMPNSTRYDFLLPAGLSKNTSNS 60  
|||||

Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDIFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPENSSTHFSNLSKTTFHCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPENSSTHFSNLSKTTFHCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANWNICWLGDKLFLICYVESLFRNLYKVLHLLVLPVLEDSPLVPKGS 180  
Db 121 QOIDANWNICWLGDKLFLICYVESLFRNLYKVLHLLVLPVLEDSPLVPKGS 180  
QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
Db 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPPLVPFLOQYKYSNSTTVIREADKIVSATSLVDILP 300  
Db 241 LGLHMETDDGNLKLISWSSPPLVPFLOQYKYSNSTTVIREADKIVSATSLVDILP 300  
QY 301 GSSYEVOVRGKRLDGPGLMSDWPSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPGLMSDWPSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCESTDGYLTMTCRWSTSTQSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVNNISCESTDGYLTMTCRWSTSTQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
Db 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISMEKVPFPENNLOEQIRYGLSGKEVQWKMEYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISMEKVPFPENNLOEQIRYGLSGKEVQWKMEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQYRCKRLDGLGYSWNSNPAITYVMDIKVPMRGPEFIRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQYRCKRLDGLGYSWNSNPAITYVMDIKVPMRGPEFIRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLFSPMSKVNIVQSLASAPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLFSPMSKVNIVQSLASAPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
Db 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTTVVSLSTIDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTTVVSLSTIDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETVYEDESOROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETVYEDESOROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSWETEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
Db 1021 KDSFNSSWETEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
RESULT 2  
ID Q9MYL2 PRELIMINARY; PRT: 1163 AA.  
AC Q9MYL2;  
DT 01-OCT-2000 (TRENBLREL. 15, Created)  
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
DE LEPTIN RECEPTOR LONG FORM.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_Taxid=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98408931; PubMed=9738551;  
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA  
RT expression in the adipose tissue of normal, hyperinsulinemic, and type  
RT 2 diabetic rhesus monkeys."  
RL Obes. Res. 6:353-360(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF222960; AAF34683.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;  
Query Match 95.4%; Score 5967; DB 6; Length 1163;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 1114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;  
QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDIFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNSTYDIFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPENSSTHFSNLSKTTFHCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPENSSTHFSNLSKTTFHCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANWNICWLGDKLFLICYVESLFRNLYKVLHLLVLPVLEDSPLVPKGS 180  
Db 121 QOIDANWNICWLGDKLFLICYVESLFRNLYKVLHLLVLPVLEDSPLVPKGS 180  
QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
Db 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPPLVPFLOQYKYSNSTTVIREADKIVSATSLVDILP 300  
Db 241 LGLHMETDDGNLKLISWSSPPLVPFLOQYKYSNSTTVIREADKIVSATSLVDILP 300  
QY 301 GSSYEVOVRGKRLDGPGLMSDWPSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPGLMSDWPSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCESTDGYLTMTCRWSTSTQSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVNNISCESTDGYLTMTCRWSTSTQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
Db 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISMEKVPFPENNLOEQIRYGLSGKEVQWKMEYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISMEKVPFPENNLOEQIRYGLSGKEVQWKMEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQYRCKRLDGLGYSWNSNPAITYVMDIKVPMRGPEFIRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQYRCKRLDGLGYSWNSNPAITYVMDIKVPMRGPEFIRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLFSPMSKVNIVQSLASAPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLFSPMSKVNIVQSLASAPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
Db 841 GLYIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTTVVSLSTIDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTTVVSLSTIDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETVYEDESOROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETVYEDESOROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSWETEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
Db 1021 KDSFNSSWETEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140

QY 361 VPSKEIWMNLAEKIPQSYDVSDHVKVTFENLNKPRGKFTYDAVYCCNEHECH 420  
| : : : : :  
Db 359 VSSKRIWMNLAEKIPQSYDVSDHVKVTFENLNKPRGKFTYDAVYCCNEHECH 418  
QY 421 RYAEIYIDVININISCEIDGVLTKMTCRWSSTSTIOSLAESTIOLRYHRSSLYCSDIPSIH 480  
| : : : : :  
Db 419 RYAEIYIDVININISCEIDGHLTKMTCRWSSTNTIOSLAGSTIOLRYHRSSLYCFDIPSIH 478  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPICVLPDSVVKPLPP 540  
| : : : : :  
Db 479 PISKPKDCYLOSDFEYECVFPPIFLLSGYTMWIRINHPGLSLDSPICVLPDSVVKPLPP 538  
QY 541 SSVKAEITINIGLLKISWEKPVPEPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
| : : : : :  
Db 539 SSVKAEITINIGLLKISWEKPVPEPENNLOFOIRYGLSGKEIOWKMYDVYDAKSKSVSLPV 598  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
| : : : : :  
Db 599 PDFCAVYAVQVRCKRSDGLGLMSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658  
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTLAINSI 720  
| : : : : :  
Db 659 TLLMKPLMKNESLQVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTLAINSI 718  
QY 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
| : : : : :  
Db 719 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVILSWILSPSDYKLMYFIIEWKNLNED 778  
QY 781 GEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840  
| : : : : :  
Db 779 GEIKMLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFAQDNTKEHQNDA 838  
QY 841 GLYVIVPVITSSSILLGLTLLISHQMKKLFMEDVNPKNCSWAQGLNEOKPETFEHLFI 900  
| : : : : :  
Db 839 GLYVIVPVITSSSILLGLTLLISHQMKKLFMEDVNPKNCSWAQGLNEOKPETFEHLFI 898  
QY 901 KHTASVTCGPLLEPETISEDIVTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960  
| : : : : :  
Db 899 KHTASVTCGPLLEPETISEDIVTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 958  
QY 961 SVNFSEAEGETEYTEDSQRQPFYKATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
| : : : : :  
Db 959 SVNFSEAEGETEYTEDSQRQPFYKATLISNSKPSSETDEEOGLINSSVTKCFSSKNSPL 1018  
QY 1021 KDSFNSWSWEIEAOAFILSDQHPNIIISPHLTFSEGLDELLEKGNPEENNDDKSIYYL 1080  
| : : : : :  
Db 1019 KDSFNSWSWEIEAOAFILSDQHPNIIISPHLTFSEGLDELLEKGNPEENNDEKSIYYL 1078  
QY 1081 GVTSIKKRESGVLTLTKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
| : : : : :  
Db 1079 GVTSIKKRESGVLTLTKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1138  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
| : : : : :  
Db 1139 YMPQFQTCSTQTHKIMENKMDLTV 1163

RESULT 3  
Q9MYLO PRELIMINARY; PRT: 1194 AA.  
AC Q9MYLO: 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR LONG INSERT ISOFORM.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_Taxid-9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-ADIPOSE TISSUE;

RX MEDLINE-98408931; PubMed-9738551;  
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;  
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA  
RT expression in the adipose tissue of normal, hyperinsulinemic, and type  
RT 2 diabetic rhesus monkeys."  
RL Obes. Res. 6:353-360(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-ADIPOSE TISSUE;  
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF225874; AAF35388.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
RW Receptor.  
SO SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;

Query Match 95.0%; Score 5941.5; DB 6; Length 1194;  
Best local similarity 93.1%; Pred. No. 0;  
Matches 1114; Conservative 18; Mismatches 31; Indels 33; Gaps 2;

QY 1 MICQKFCVLLHWEFIVITAFNLSTPTPWKRLSCMPNSTYDYELLPAGLSKNTS 60  
| : : : : :  
Db 1 MICQKFCVLLHWEFIVITAFNLSTPTPWKRLSCMPNSTYDYELLPAGLSKNTS 60  
QY 61 NGHYETAPEKFNSSGTHESNLSTKTFHCCFRSEQDRNCSLCADNEGKTFVSTVNSLVF 120  
| : : : : :  
Db 61 NGHYETAPEKFNSSGTHESNLSTKTFHCCFRSEQDRNCSLCADNEGKTFVSTVNSLVF 118  
QY 121 QOIDANMNIOQWLKGLDLKFLICYVESLEKLNFRNRYKVVHLLVYLPVLEDSPLVPQGS 180  
| : : : : :  
Db 119 QOIDANMNIOQWLKGLDLKFLICYVESLEKLNFRNRYKVVHLLVYLPVLEDSPLVPQGS 178  
QY 181 FQMVHNCVSHECECLVPVPTAKLNDTLLMCLKITSQVIEQSPIMSVQPINMKPDP 240  
| : : : : :  
Db 179 FQMVHNCVSHECECLVPVPTAKLNDTLLMCLKITSQVIEQSPIMSVQPINMKPDP 238  
QY 241 LGLHMEITDDGNLAKISWSSPPLVPFPLOYQVYKSENSTVIREAKIVSATSLVDSILP 300  
| : : : : :  
Db 239 LGLHMEITDDGNLAKISWSSPPLVPFPLOYQVYKSENSTVIREAKIVSATSLVDSILP 298  
QY 301 GSSYEVOVRGKRDLGPGIWSDWSTPRAVTTQDVIYFPFKILTSVGSNVSFHCITYKENKI 360  
| : : : : :  
Db 299 GSSYEVOVRGKRDLGPGIWSDWSTPRAVTTQDVIYFPFKILTSVGSNVSFHCITYKENKI 358  
QY 361 VPSKEIWMNLAEKIPQSYDVSDHVKVTFENLNKPRGKFTYDAVYCCNEHECH 420  
| : : : : :  
Db 359 VSSKRIWMNLAEKIPQSYDVSDHVKVTFENLNKPRGKFTYDAVYCCNEHECH 418  
QY 421 RYAEIYIDVININISCEIDGVLTKMTCRWSSTSTIOSLAESTIOLRYHRSSLYCSDIPSIH 480  
| : : : : :  
Db 419 RYAEIYIDVININISCEIDGHLTKMTCRWSSTNTIOSLAGSTIOLRYHRSSLYCFDIPSIH 478  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPICVLPDSVVKPLPP 540  
| : : : : :  
Db 479 PISKPKDCYLOSDFEYECVFPPIFLLSGYTMWIRINHPGLSLDSPICVLPDSVVKPLPP 538  
QY 541 SSVKAEITINIGLLKISWEKPVPEPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
| : : : : :  
Db 539 SSVKAEITINIGLLKISWEKPVPEPENNLOFOIRYGLSGKEIOWKMYDVYDAKSKSVSLPV 598  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
| : : : : :  
Db 599 PDFCAVYAVQVRCKRSDGLGLMSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658



QY 661 TLIMKPLMKNDLSCVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 659 TLIMKPLMKNESLSCVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 718  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 719 GASVANENLTFSPMSKVNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 778  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSDA 840  
DB 779 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHONDA 838  
QY 841 GLYVIVPVIISILLGLTLLISHQRMKLFWEDEVNPNKNSWAQGLNFOR 891  
DB 839 GLYVIVPVIISILLGLTLLISHQRMKLFWEDEVNPNKNSWAQGLNFOR 898  
QY 892 -----PETFEHLFIKHTASVTCGPLLEPETISEDISVDTSMK 929  
DB 899 LVLNSQAQVHPRRPKYLELQPETFEHLFIKHTASVTCGPLLEPETISEDISVDTSMK 958  
QY 930 NKDEMPPTVVSLLSTLDLEKGSVCISDOFNSVNFSEAEGETEVTYEDESQKOPFVKYATL 989  
DB 959 NKDEMPPTVVSLLSTLDLEKGSVCISDOFNSVNFSEAEGETEVTYEDESQKOPFVKYATL 1018  
QY 990 ISNSKPSETGEEGLINSSVTKCFSSKNSPLKDSFNSNSWEIEQAFFILSDQHPNIISP 1049  
DB 1019 ISNSKPSETGEEGLINSSVTKCFSSKNSPLKDSFNSNSWEIEQAFFILSDQHPNIISP 1078  
QY 1050 HLTPEGLDELLEKGNFPEENNDKSIYLGVTISIKKRESGVLLTDKSRVSCPFPAPCL 1109  
DB 1079 HLTPEGLDELLEKGNFPEENNDKSIYLGVTISIKKRESGVLLTDKSRVSCPFPAPCL 1138  
QY 1110 FTDIRVLQDSCHFEVENNINIGTSSKKTFFASYMPOFOTCSTOTHKIMENKCDLTV 1165  
DB 1139 FTDIRVLQDSCHFEVENNINIGTSSKKTFFASYMPOFOTCSTOTHKIMENKCDLTV 1194

RESULT 4  
ID 002671 PRELIMINARY; PRT; 1165 AA.  
AC 002671;  
DT 01-JUL-1997 (Tremblrel. 04, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE TRANSMEMBRANE LEPTIN RECEPTOR.  
GN LEPR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.-F.,  
RA Murphy B.D.;  
RT "Porcine leptin (Ob) receptor complete coding sequence."  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 408-470 FROM N.A.  
RX MEDLINE=97222487; PubMed=9069130;  
RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;  
RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";  
RL Mamm. Genome 8:226-226(1997).  
DR EMBL; AF092422; AAC61766.1; -.  
DR HSSP; U72070; AAC48707.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.

DR PROSITE; PS01353; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Transmembrane.  
SQ SEQUENCE 1165 AA; 132548 MW; 1BBE562FEA282F12 CRC64;  
Query Match 84.3%; Score 5269; DB 6; Length 1165;  
Best Local Similarity 84.0%; Pred. No. 0;  
Matches 980; Conservative 73; Mismatches 110; Indels 4; Gaps 4;  
QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPKFKLSCMPNSTYDYLPLAGLSKNTSNS 60  
DB 1 MTCPKFSVALLHMEFIYVITAFDLAYPTPKFKLSCMPNTTYD-FLIPAGISKNTSTL 59  
QY 61 NGHYETAPEPKNSSGTHFSNL-SKTFHCCTFSEQDRNCSLCADNIEGKTFVSTNSLV 119  
DB 60 NGHDEAVETELNIGTYLSNLSKKTFFHCCTFSEEDKNSVHADNIAKAFVSAVNSLV 119  
QY 120 FQOIDANWNIDQWLKGLKLFICYVESLFRNRYNYKVHLLVLPVEVLEDSPLVPQKG 179  
DB 120 FQOTGANWNIDQWKKEDLKFICYMESLFRNPKNYDLKVLHLLVYLLVLEGGSPLLPQKG 179  
QY 180 SFQMVHCNSVHECCCLVPPVPTAKLNDTLMLCKITSGVIFQSPIMSVQPINVKPDP 239  
DB 180 SFQSVQCNSARECECHVPVSAKLNFTLMLKITSGAVFHSPLMSVQPINVKPDP 239  
QY 240 PLGLHMEITDDGNLKSMSSPPLVPFPLOQYKYSNSTVIREADKIVSATSLLVDSIL 299  
DB 240 PLGLHMEITDGNLKSMSSPPLVPFPLOQYKYSNSTVIREADKIVSATSLLVDSVL 299  
QY 300 PGSSYEYQVRGRRLDGPIMSDWSTPRVFTQDYIYFPKILTSVGSNVSFHCYKKNK 359  
DB 300 PGSSYEYQVRGRRLDGPIMSDWSTPRVFTQDYIYFPKILTSVGSNVSFHCYKKNK 359  
QY 360 IVPSEKIYMMNLAEKIPQSQDYDVSDHVSATFENLNETKPRGKFTYDAVCCNEHECH 419  
DB 360 IVPSEKIYMMNLAEKIPQSQDYDVSDHVSATFENLNETKPRGKFTYDAVCCNEHECH 419  
QY 420 HRYAELVIDVNNINISCEITDGYLTMTCRMSTSIQSLAESTLQLRHSSLYCSDIPSI 479  
DB 420 HRYAELVIDVNNINISCEITDGYLTMTCRMSTSIQSLVGLSTLQLRHSSLYCSDVPSV 479  
QY 480 HPISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSLSGLDSEPTCVLPDSVKKPLP 539  
DB 480 HPISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSLSGLDSEPTCVLPDSVKKPLP 539  
QY 540 PSSVKAETITNIGLLKISWEKVPFENNLOQIRYGLSGKEYQWKIYEVYDTKLKSTSLP 599  
DB 540 PSSVKAETITNIGLLKISWEKVPFENNLOQIRYGLSGKEYQWKIYEVYDTKLKSTSLP 599  
QY 600 VPDLCAVYAVOVRCKRLDGLGYSNMSNPATVYMDIKVPMRGPEFWRINGDTMKKEKN 659  
DB 600 VPDLCAVYAVOVRCKRLDGLGYSNMSNPATVYMDIKVPMRGPEFWRINGDTMKKEKN 659  
QY 660 VTLWKPLMKNDLSCVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 719  
DB 660 VTLWKPLMKNDLSCVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 719  
QY 720 IGASVANENLTFSPMSKVNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 779  
DB 720 IGASVANENLTFSPMSKVNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 779  
QY 780 DGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSD 839  
DB 780 DGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSD 839  
QY 840 AGLYVIVPVIISILLGLTLLISHQRMKLFWEDEVNPNKNSWAQGLNFOR 899  
DB 839 AGLYVIVPVIISILLGLTLLISHQRMKLFWEDEVNPNKNSWAQGLNFOR 898  
QY 900 IKHTASVTCGPLLEPETISEDISVDTSMKKNKDEMPPTVVSLLSTL-DLEKGSVCISDQ 958  
DB 899 IKHTASVTCGPLLEPETISEDISVDTSMKKNKDEMPPTVVSLLSTL-DLEKGSVCISDQ 958

[illegible]

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RESULT      5
092920
ID      092920      PRELIMINARY;      PRT;      958 AA.
AC      092920;
DT      01-FEB-1997 (TREMBLrel. 02, Created)
DT      01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      LEPTIN RECEPTOR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96398968; PubMed=8805376;
RA      Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RT      Matthews W.;
RL      "A role for leptin and its cognate receptor in hematopoiesis.";
      Curr. Biol. 6:1170-1180(1996).
DR      EMBL: U66496; AAB07496.1; -.
DR      HSSP: P16471; 1BP3.
DR      InterPro: IPR002996; CRIA.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003529; Hematopo_receptor_L_F2.
DR      InterPro: IPR003531; Hematopo_receptor_S_F1.
DR      Pfam: PF00041; fn3. 2.
DR      SMART: SM00060; FN3. 1.
DR      PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR      PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KM      Receptor.
SQ      SEQUENCE      958 AA;      109392 MW;      3F65BC5A187E803A CRC64;

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Query Match	77.38;	Score 4831.5;	DB 4;	Length 958;
Best Local Similarity	94.48;	Pred. No. 0;		
Matches 904; Conservative	5;	Mismatches 24;	Indels 25;	Gaps 3;

QY	1	MICORECVLLHMEFIYVITAFNLSTYPTPWRFKLSCMPPNSTYDYFLLBAGLSKNTSNS	60
Db	1	MICORFCVLLHMEFIYVITAFNLSTYPTPWRFKLSCMPPNSTYDYFLLBAGLSKNTSNS	60
QY	61	NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTEVSTVNSLVE	120
Db	61	NGHYETAEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTEVSTVNSLVE	120
QY	121	QOIBANNIQCWLKGDCLKFCYVESLEFKNLFRNRYNKVHLLVLPVELEDSPLVPQKGS	180
Db	121	QOIBANNIQCWLKGDCLKFCYVESLEFKNLFRNRYNKVHLLVLPVELEDSPLVPQKGS	180
QY	181	FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGGVI FQSP LMSVQPINMKPDP	240
Db	181	FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGGVI FQSP LMSVQPINMKPDP	240
QY	241	IGLHMETDDGNLKISWSSPPLVPEPLOYKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	241	IGLHMETDDGNLKISWSSPPLVPEPLOYKYSENSTTVIREADKIVSATSLLVDSILP	300

QY	301	GSSYEVOVRCKRLDGP	GIWSDWSTPRVFTTQDVI	FPFKILTSVGSNVSEHC	IYKKNKI	360		
Db	301	GSSYEVOVRCKRLDGP	GIWSDWSTPRVFTTQDVI	FPFKILTSVGSNVSEHC	IYKKNKI	360		
QY	361	VPSKEIVMMNLAEKIP	OSQYDVASDHAKVTEF	FNLNETKPRGKF	TYDAVCCNEHCH	420		
Db	361	VPSKEIVMMNLAEKIP	OSQYDVASDHAKVTEF	FNLNETKPRGKF	TYDAVCCNEHCH	420		
QY	421	RYAELVIDVINISCE	TGDLTKMTCRNST	TIQSLAESTLQLR	HRSSLYCSDIPS	480		
Db	421	RYAELVIDVINISCE	TGDLTKMTCRNST	TIQSLAESTLQLR	HRSSLYCSDIPS	480		
QY	481	PISEPKDCYLOSDFE	YECIFOPIFLLSGY	MMIRINHSLGSLD	SPICVLPDSVYKPL	540		
Db	481	PISEPKDCYLOSDFE	YECIFOPIFLLSGY	MMIRINHSLGSLD	SPICVLPDSVYKPL	540		
QY	541	SSYKAEITINIGLLK	ISWEKPVFPENNLO	EQIRYGLSGKEVOW	KIYEVYDAKSYS	600		
Db	541	SSYKAEITINIGLLK	ISWEKPVFPENNLO	EQIRYGLSGKEVOW	KIYEVYDAKSYS	600		
QY	601	PDLCAVYAVOVRCR	KLDELGLGYMSNWS	NPAYTVMDIKVPMR	GPBEFWIRLINGD	TMKKEKNV	660	
Db	601	PDLCAVYAVOVRCR	KLDELGLGYMSNWS	NPAYTVMDIKVPMR	GPBEFWIRLINGD	TMKKEKNV	660	
QY	661	TLLWPKMLKNDLS	CSVQRYVINHHTSC	NGTWSEDEVGNHTK	FTFLWTLOAHTV	LAINSI	720	
Db	661	TLLWPKMLKNDLS	CSVQRYVINHHTSC	NGTWSEDEVGNHTK	FTFLWTLOAHTV	LAINSI	720	
QY	721	GASVANENLTFSP	MPMSKVNIQSL	SAYPLNSSCVIVS	WILSPSDYKLM	YFIIEKMNED	780	
Db	721	GASVANENLTFSP	MPMSKVNIQSL	SAYPLNSSCVIVS	WILSPSDYKLM	YFIIEKMNED	780	
QY	781	GEIKWLRISSVKK	YIYIHDHFIPIEK	YQFSLYPIFMEG	VGPKIINSFTQD	DIERHOSDA	840	
Db	781	GEIKWLRISSVKK	YIYIHDHFIPIEK	YQFSLYPIFMEG	VGPKIINSFTQD	DIERHOSDA	840	
QY	841	GLYVIVYVYIISS	SILLGLTLLISHQ	RMKLEWEDV	PNPKNC	SWAQGLNFOK	-----PE	893
Db	841	GLYVIVYVYIISS	SILLGLTLLISHQ	RMKLEWEDV	PNPKNC	SWAQGLNFOK	-----PE	893
QY	894	TFEHLTKHT-AS	VTGP-----	LLLEPETISED	ISVDTS	SKNKDE	933	
Db	901	SHHSLISTOGH	KHCGRPOGPLH	KRTDCLSLV	LLTLPPLLSYD	PAKSPSV	RNTQOE	958

RESULT	6
0929219	
ID	0929219
AC	PRELIMINARY;
DT	01-FEB-1997 (TREMBlrel. 02, Created)
DT	01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	LEPTIN RECEPTOR.
GN	DB.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID-9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA	Matthews W.;
RL	Curr. Biol. 6:0-0(0).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-97215244; Pubmed-9061609;
RA	Luoh S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
RA	Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
RT	"Cloning and characterization of a human leptin receptor using a
RT	biologically active leptin immunoadhesin."
RL	J. Mol. Endocrinol. 18:77-85(1997).
EMBL	U66495; AAB07495.1; -

DR EMBL; U50748; AAC23650.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
SQ SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CRC64;

Query Match 77.2%; Score 4826; DB 4; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERPKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSL 120  
DB 61 NGHYETAVERPKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSL 120  
QY 121 QQIDANMNIQCWLKGLDKLFICYVESLFKNLFRNRYNYKVHLLYVLEVLDSPLVPQKS 180  
DB 121 QQIDANMNIQCWLKGLDKLFICYVESLFKNLFRNRYNYKVHLLYVLEVLDSPLVPQKS 180  
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVQPINMVKPDP 240  
DB 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPLVPFPLOYQVKYSENSTVIREADKIVATSLLVDSILP 300  
DB 241 LGLHMETDDGNLKLISWSSPLVPFPLOYQVKYSENSTVIREADKIVATSLLVDSILP 300  
QY 301 GSSYEVOYRGKRDLDPGIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
DB 301 GSSYEVOYRGKRDLDPGIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIVYDVNINISCEITDGYLTMTQCRWSTSTIQSLAESTLQLRHRSLSYCSDDIPSIH 480  
DB 421 RYAEIVYDVNINISCEITDGYLTMTQCRWSTSTIQSLAESTLQLRHRSLSYCSDDIPSIH 480  
QY 481 PISEPKCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLRP 540  
DB 481 PISEPKCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISWEKPVFENNLOFQIRYGLSGKEVQMKYEVYDAKSQSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKPVFENNLOFQIRYGLSGKEVQMKYEVYDAKSQSVSLPV 600  
QY 601 PDLCAVYAVQVRKRLDGLGYSWNSNPATVYMDIKVPMRGPFRIRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRKRLDGLGYSWNSNPATVYMDIKVPMRGPFRIRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSQVRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVALINSI 720  
DB 661 TLLMKPLMKNDSLCSQVRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVALINSI 720  
QY 721 GASVANNLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 780  
DB 721 GASVANNLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSTNAOGLNFQK 891  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVDPNPKNCSTNAOGLNFQK 891

RESULT 7  
Q13592  
ID Q13592 PRELIMINARY; PRT; 958 AA.  
AC Q13592;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; PubMed=8616721;  
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RA Platika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
RT hematopoiesis and reproduction.";  
RL Nat. Med. 2:585-589(1996).  
DR EMBL; U52912; AAC50509.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.  
SQ SEQUENCE 958 AA; 109419 MW; C7E0EBD18428677B CRC64;

Query Match 77.1%; Score 4819.5; DB 4; Length 958;  
Best Local Similarity 94.1%; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERPKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSL 120  
DB 61 NGHYETAVERPKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSL 120  
QY 121 QQIDANMNIQCWLKGLDKLFICYVESLFKNLFRNRYNYKVHLLYVLEVLDSPLVPQKS 180  
DB 121 QQIDANMNIQCWLKGLDKLFICYVESLFKNLFRNRYNYKVHLLYVLEVLDSPLVPQKS 180  
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVQPINMVKPDP 240  
DB 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPLVPFPLOYQVKYSENSTVIREADKIVATSLLVDSILP 300  
DB 241 LGLHMETDDGNLKLISWSSPLVPFPLOYQVKYSENSTVIREADKIVATSLLVDSILP 300  
QY 301 GSSYEVOYRGKRDLDPGIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
DB 301 GSSYEVOYRGKRDLDPGIMSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420

QY 421 RYAEIYVIDVININISCETDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVININISCETDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTRKFTFLMTEQAHTVTLAINSI 720  
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTRKFTFLMTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFMEDVNPKNCSMAOGLNFQK-----PE 893  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFMEDVNPKNCSMAOGLNFQK-----PE 893  
QY 894 TREHFIKHT-ASVTCGP-----LLEPETISEDIVSDTSWKNKDE 933  
Db 901 SHHSLISSTQGHKHCGRPGPLHRKTRDLCSLVYLLTLPPLSLYDPAKSPSVRNTQE 958

RESULT 8  
Q13593  
ID Q13593 PRELIMINARY; PRT; 906 AA.  
AC Q13593;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; PubMed=8616721;  
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RA Platika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
RT hematomiasis and reproduction.";  
RL Nat. Med. 2:585-589(1996).  
DR EMBL: U52913; AAC50510.1; -  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam: PF000041; fn3; 2.  
DR SMART: SMO0060; FN3; 1.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.  
SQ SEQUENCE 906 AA; 103487 MW; 6D51126F33076626 CRC64;

Query Match 77.0%; Score 4816; DB 4; length 906;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 MICQFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYELLPAGLSKNTSNS 60  
Db 1 MICQFCVLLHMEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYELLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPENSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLYF 120  
Db 61 NGHYETAVERPENSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLYF 120  
QY 121 QOIDANMNIOQWLKGLDKLFICVESLEFKNLFRNRYNKHLLVLPVLEDSPLVPQKGS 180  
Db 121 QOIDANMNIOQWLKGLDKLFICVESLEFKNLFRNRYNKHLLVLPVLEDSPLVPQKGS 180  
QY 181 FQVHNCNVHCECECLVPVPTAKLNDTLMLCKITSGGYTFQSPILMSVOPINMKPDP 240  
Db 181 FQVHNCNVHCECECLVPVPTAKLNDTLMLCKITSGGYTFQSPILMSVOPINMKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPLVFPLOQYVKYSENSTYVREADKIVSATSLVDSILP 300  
Db 241 LGLHMETDDGNLKLISWSSPLVFPLOQYVKYSENSTYVREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPISWDSWTPVFTQDVYFPFKILTSVGSNVSEHCYKKEKNI 360  
Db 301 GSSYEYQVRGKRLDGPISWDSWTPVFTQDVYFPFKILTSVGSNVSEHCYKKEKNI 360  
QY 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFNLETGPRKFTYDAVYCCNEHECH 420  
Db 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFNLETGPRKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVININISCETDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVININISCETDGYLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFYECIFOPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTRKFTFLMTEQAHTVTLAINSI 720  
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTRKFTFLMTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFMEDVNPKNCSMAOGLNFQKMPGTKEKL 900  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFMEDVNPKNCSMAOGLNFQKMPGTKEKL 900

RESULT 9  
Q13594  
ID Q13594 PRELIMINARY; PRT; 896 AA.  
AC Q13594;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; PubMed=8616721;  
RA Clotfi J.A., Shafter A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RT Platica D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
hematopoiesis and reproduction.";  
RT Nat. Med. 2:585-589(1996).  
RL EMBL; U52914; AAC50511.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.  
SQ SEQUENCE 896 AA; 102516 MW; 73C431F8C578CD07 CRC64;

Query Match 77.0%; Score 4814; DB 4; Length 896;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVYLLHWEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVYLLHWEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLDKLFTCYVESLFKNLFERNYNYKVHLLVYLPEVLLEDSPVLPQKGS 180  
DB 121 QOIDANMNIOQWLKGLDKLFTCYVESLFKNLFERNYNYKVHLLVYLPEVLLEDSPVLPQKGS 180  
QY 181 FQMVHCNCSVHECCCECLVPPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKPDP 240  
DB 181 FQMVHCNCSVHECCCECLVPPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINMKPDP 240  
QY 241 LGLHMETDDGNLKISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSTLP 300  
DB 241 LGLHMETDDGNLKISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSTLP 300  
QY 301 GSSYEVOYRGKRLDGPGLMSDWSIPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVOYRGKRLDGPGLMSDWSIPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVWMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIVWMNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
QY 421 RYAEELVIDVNINISCEIDGYLTKMTCRMSTSTIQSLAESTIQLRHYRSSLYCSDIPSIH 480  
DB 421 RYAEELVIDVNINISCEIDGYLTKMTCRMSTSTIQSLAESTIQLRHYRSSLYCSDIPSIH 480  
QY 481 PISEKDCYLQSDGFYECIFQPIFLISGYTMMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
DB 481 PISEKDCYLQSDGFYECIFQPIFLISGYTMMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQMKYEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQMKYEYDAKSKSVSLPV 600

DB 541 SSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQMKYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCRRLDGLGYWSNWSNPAVTVMDIKVPMRGPEYRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCRRLDGLGYWSNWSNPAVTVMDIKVPMRGPEYRIINGDTMKKEKNV 660  
QY 661 TLLWPKPLMKNDLSQVQRYVINHHTSCNGTWSQEDVGNHTKFTFLTEQAHVTVLAINSI 720  
DB 661 TLLWPKPLMKNDLSQVQRYVINHHTSCNGTWSQEDVGNHTKFTFLTEQAHVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKLINFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKLINFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVITISSILLGLTLLISHQRMKLLFWEDVPNPKNCNSVAQGLNFQK 891  
DB 841 GLYVIVPVITISSILLGLTLLISHQRMKLLFWEDVPNPKNCNSVAQGLNFQK 891

RESULT 10  
Q9QWG3 PRELIMINARY; PRT; 1162 AA.  
AC Q9QWG3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR B.  
GN LEPR OR LEPRB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KK OBESE; TISSUE=BRAIN, HYPOTHALAMUS;  
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Harberg L.,  
RA Joost H.G.;  
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,  
hyperinsulinemic KK mouse strain.";  
RT J. Endocrinol. 21:337-345(1998).  
RL EMBL; Y10296; CAA71342.1; -.  
DR HSSP; P16471; 1BP3.  
DR MGD; MGI:104993; Lepr.  
DR InterPro; IPR002996; Lepr.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 3.  
DR SMART; SM00060; FN3; 3.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
FT VARIANT 600 600 N -> D.  
SQ SEQUENCE 1162 AA; 130787 MW; 541E77CBB46EC00D CRC64;

Query Match 76.1%; Score 4761.5; DB 11; Length 1162;  
Best Local Similarity 75.3%; Pred. No. 0;  
Matches 878; Conservative 116; Mismatches 167; Indels 5; Gaps 5;

QY 1 MICQKFCVYLLHWEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVYLLHWEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCALTDNTEGKTLASVVKASVF 120  
QY 121 QOIDANMNIOQWLKGLDKLFTCYVESLFKNLFERNYNYKVHLLVYLPEVLLEDSPVLPQKGS 180  
DB 121 QOIDANMNIOQWLKGLDKLFTCYVESLFKNLFERNYNYKVHLLVYLPEVLLEDSPVLPQKGS 180



121 ROLGVNWDIECWMKGDLEFLICHEMELPKNPFKNYDSKVHLLYDLPEVIDDSPLEPKDS 180  
QY 181 FOMVHCNCSVHECCFCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMYKPDPP 240  
Db 181 FQTVQCNCSLRG-CECHYVPVRAKLNYALMLYLEITSAGVSFQSPILMSLQPMVLVYKPDPP 239  
QY 241 LGLHMETDDGNLKISWSSPPLVPPLOQYKVSNSQTVIREADKIVSATSLLVDSILP 300  
Db 240 LGLHMEVTDGDLKISWSDQTMARPPLOQYKYLENS-TIVREAETVSATSLVDSVLP 298  
QY 301 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTQDVITYFPFKILTSVGSNSVFHCITYKKNKI 360  
Db 299 GSSYEVOVRGKRLDGSQVWSDMSSPOVFTQDVITYFPFKILTSVGSNASFHCITYKNENOI 358  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 359 ISSKQIVWMRNLAEKIPEIQYISVSDRVSKVTFESNLKATPRGKFTYDAVYCCNEQACHH 418  
QY 421 RYAEIYVIDVNNINISCEFDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSLSLYCSDIPSIH 480  
Db 419 RYAEIYVIDVNNINISCEFDGYLTMTKCRWSPSTIQSLVGSVTVQLRYHRSLSLYCSDIPSIH 478  
QY 481 PISEPKDCYIQSDGFYECLFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVYKPLPP 540  
Db 479 PISEPKDCYIQSDGFYECLFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVYKPLPP 538  
QY 541 SSVKAEITINIGLKISWEKVPFENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPY 600  
Db 539 SSVKAEITINIGLKISWEKVPFENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPY 598  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFWRRIINGDTMKKEKNY 660  
Db 599 SNIQAVYVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFWRRIINGDTMKKEKNY 658  
QY 661 TLLMKPLMKNDLSQVQRYVNHHTSCNGTWSEDEVGNHTKFTPLMTEQANTVYLAINSI 720  
Db 659 TLLMKPLMKNDLSQVQRYVNHHTSCNGTWSEDEVGNHTKFTPLMTEQANTVYLAINSI 718  
QY 721 GASVANENLTFSPWMSKVNIQSLAYPLNSSCVIIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 719 GASVANENLTFSPWMSKVNIQSLAYPLNSSCVIIVSWILSPSDYKLMYFIEMKNLNE 778  
QY 781 GEIKWLRISSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDTEKHQSDA 840  
Db 779 DGMKWLRISSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDTEKHQSDA 838  
QY 841 GLYIVPVISSSILLGLTLLSHQRMKKLEWEDVNPKNCSWAQGLNFQKPEFHEHLE 900  
Db 839 GLYIVPVISSSILLGLTLLSHQRMKKLEWEDVNPKNCSWAQGLNFQKPEFHEHLE 898  
QY 901 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPITYVSLSTT-DLEKGSVCISDOF 959  
Db 899 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPITYVSLSTT-DLEKGSVCISDOF 958  
QY 960 NSVNFSEAEGETEYTEDSQRPVVKYATLISNSKPSFTEGEOGLINSSVTKCFSSKNSP 1019  
Db 959 NSVNFSEAEGETEYTEDSQRPVVKYATLISNSKPSFTEGEOGLINSSVTKCFSSKNSP 1018  
QY 1020 LKDSFSSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITY 1079  
Db 1019 LKDSFSSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITY 1077  
QY 1080 LGVTSIKKRESGVLLTOKSRVCPFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFA 1139  
Db 1078 LGVTSIKKRESGVLLTOKSRVCPFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFA 1136  
QY 1140 SYMPOFOTCSTQTHKIMENKCDLTV 1165  
Db 1137 SYMPOFOTCSTQTHKIMENKCDLTV 1162

RESULT 11

Q9MYK9 ID Q9MYK9 PRELIMINARY; PRT; 925 AA.  
AC Q9MYK9;  
DT 01-OCT-2000 (Tremblrel, 15, Created)  
DT 01-OCT-2000 (Tremblrel, 15, last sequence update)  
DT 01-DEC-2001 (Tremblrel, 19, last annotation update)  
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADIPOSE TISSUE;  
RX MEDLINE=98408931; PubMed=9738551;  
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA  
RT expression in the adipose tissue of normal, hyperinsulinemic, and type  
RT 2 diabetic rhesus monkeys."  
RL Obes. Res. 6:353-360(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADIPOSE TISSUE;  
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF225875; AAF35389.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;  
  
Query Match 73.4%; Score 4591; DB 6; length 925;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 850; Conservative 15; Mismatches 28; Indels 2; Gaps 1;  
  
QY 1 MICQKFCVLLHMEFYITAFNLSYPTTPWRFKLSKMPNPNSTYDYFLLPAGLSKNTS 60  
Db 1 MICQKFCVLLHMEFYITAFNLSYPTTPWRFKLSKMPNPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVE--FNSSDTHFNSLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSVF 120  
Db 61 NGHYETAVE--FNSSDTHFNSLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSVF 118  
QY 121 QQIDANNIQQWLKGLDKLFCYVESLFKNLFRNRYKVHLLYVLEVLDSPLVPQKS 180  
Db 119 QQIDANNIQQWLKGLDKLFCYVESLFKNLFRNRYKVHLLYVLEVLDSPLVPQKS 178  
QY 181 FOMVHCNCSVHECCFCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMYKPDPP 240  
Db 179 FOMVHCNCSVHECCFCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMYKPDPP 238  
QY 241 LGLHMETDDGNLKISWSSPPLVPPLOQYKVSNSQTVIREADKIVSATSLLVDSILP 300  
Db 239 LGLHMETDDGNLKISWSSPPLVPPLOQYKVSNSQTVIREADKIVSATSLLVDSILP 298  
QY 301 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTQDVITYFPFKILTSVGSNSVFHCITYKKNKI 360  
Db 299 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTQDVITYFPFKILTSVGSNSVFHCITYKKNKI 358  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 359 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 418  
QY 421 RYAEIYVIDVNNINISCEFDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSLSLYCSDIPSIH 480

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Db 419 RYAEIYIDVNIINISCEIDGHLTKMTCRMSTNTIQLAGSTLQLRARRSSLYCFDIPSIH 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540
Db 479 PISKPKDCYLQSDGFYECVQPIFLSGYTMIRINHPGLSLDSPPTCYLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKKMEYVDKAKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEIOWKKMYDYDAKSVSLPV 598
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCKRSDGLGLWSNWSNPAYTVMDIKVPMRGPEFWRRIINGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTLAINSI 720
Db 659 TLLWKPLMKNESLCSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTLAINSI 718
QY 721 GASVANFNLFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFTIEMKNLNE 780
Db 719 GASVANFNLFSPMSKVNIVQSLSAVPLNSSCVILSWILSPDYKLMYFTIEMKNLNE 778
QY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKTIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKTIINSFAQDNTTEKHQND 838
QY 841 GLYIVPVYIISSSILLGLTLLISHQRMKLLFWEVDVPPNPKNCMSWAQGLNFQKPETF 895
Db 839 GLYIVPVYIISSSILLGLTLLISHQRMKLLFWEVDVPPNPKNCMSWAQGLNFQKIRGF 893

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RESULT 12
Q9MYL1 PRELIMINARY; PRT; 894 AA.
ID Q9MYL1
AC Q9MYL1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys."
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225873; AAF35387.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRA1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAF032238BAFB9 CRC64;

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Query Match 73.48; Score 4590; DB 6; Length 894;
Best Local Similarity 95.3%; Pred. No: 0;
Matches 849; Conservative 15; Mismatches 25; Indels 2; Gaps 1;

QY 1 MICQKFCVYLLHWEFTYVITAFNLSTYPTPWRFKLSGMPNPNSTYVYFLLPAGLSKNTS 60
Db 1 MICQKFCVYLLHWEFTYVITAFNLSTYPTPWRFKLSGMPNPNSTYVYFLLPAGLSKNTS 60
QY 61 NGHYETAPEPKENSSGTHFSNLSTKFTFCERSEQDRNCSLACADNIEGTFVSTVNSLVF 120
Db 61 NGHYETAPE - FNSSDTHFSNLSTKFTFCERSEQDRNCSLACADNIEGTFVSTVNSSVF 118
QY 121 QQIDANNNIQWLKGLDKLFICYVESLEKKNLERNYNYKVHLLYVLREVLDSPLVPQKS 180
Db 119 QQMGANNNIQWLKGLDKLFICYVESLEKKNPEKNYKHVHLLYVLREVLDSPLVPQKS 178
QY 181 FQWVHCNCSVHECCGLVPVPTAKLNDTLMLCLKITSQGVIFQSPPLMSVQPINMKPDP 240
Db 179 FQWVHCNCSVHERCEGLVPVPTAKLNDTLMLCLKITSQGVIFQSPPLMSVQPINMKPDP 238
QY 241 LGLHMETDDGNLKISWSSPPLVPFPLOYKYSENSTTVIREADKIVSATSLVDSILP 300
Db 239 LGLRMEITDDGNLKISWSSPPLVPFPLOYKYSENSTTVIREADKIVSATSLVDSILP 298
QY 301 GSSYEVOVGRKRLDGPGLSWDSTPRVFTQDVLYFPKILTSVGSNVSFHCYKKEKN 360
Db 299 GSSYEVOVGRKRLDGPGLSWDSTPRVFTQDVLYFPKILTSVGSNVSFHCYKKEKN 358
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 359 VSSKRIYWMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 418
QY 421 RYAEIYIDVNIINISCEIDGHLTKMTCRMSTNTIQLAGSTLQLRARRSSLYCFDIPSIH 480
Db 419 RYAEIYIDVNIINISCEIDGHLTKMTCRMSTNTIQLAGSTLQLRARRSSLYCFDIPSIH 478
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540
Db 479 PISKPKDCYLQSDGFYECVQPIFLSGYTMIRINHPGLSLDSPPTCYLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKKMEYVDKAKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEIOWKKMYDYDAKSVSLPV 598
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
Db 599 PDFCAVYAVQVRCKRSDGLGLWSNWSNPAYTVMDIKVPMRGPEFWRRIINGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTLAINSI 720
Db 659 TLLWKPLMKNESLCSVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHTVTLAINSI 718
QY 721 GASVANFNLFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFTIEMKNLNE 780
Db 719 GASVANFNLFSPMSKVNIVQSLSAVPLNSSCVILSWILSPDYKLMYFTIEMKNLNE 778
QY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKTIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKTIINSFAQDNTTEKHQND 838
QY 841 GLYIVPVYIISSSILLGLTLLISHQRMKLLFWEVDVPPNPKNCMSWAQGLNFQK 891
Db 839 GLYIVPVYIISSSILLGLTLLISHQRMKLLFWEVDVPPNPKNCMSWAQGLNFQK 889

RESULT 13
Q9MZS2 PRELIMINARY; PRT; 848 AA.
ID Q9MZS2
AC Q9MZS2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).

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GN OBR.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Hu X., Dai R., Li N., Wu C.;  
RT "Expression, Detection, and Partial Cloning of Porcine Leptin Receptor  
RT (OBR) Gene.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF167719; AAF89633.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
FT NON\_TER 1 1  
FT SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;  
SQ

Query Match 63.5%; Score 3970.5; DB 6; Length 848;  
Best Local Similarity 86.5%; Pred. No. 6.9e-285;  
Matches 735; Conservative 43; Mismatches 69; Indels 3; Gaps 3;

QY 7 CTVLLHWEFIVITAFNLSPYTPWRFKLSGMPNSTYDYFLPAGISKNTSNGHYET 66  
DB 1 CTVLLHWEFIVITAFDLAYPTPWKFKLSGMPNNTTYD-FLPAGISKNTSTLNGHDEA 59  
QY 67 AVEPKFNSSGTHFSNL-SKTFHCCFRSDQDRNCSLCADNIEGKTFVSTVNSLVFQIDA 125  
DB 60 VVEMELNSSGTYLSNLSSKTFHCCFSESEKNCVHADNIAKAFVAVNSLVFOOTGA 119  
QY 126 NMNIQCWLKGLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGSFQMVH 185  
DB 120 NMNIQCWMKEDLKFICYMESLFKNPFKNYDLKVHLLVLLVLEGSPLLPQKGSFQSVQ 179  
QY 186 CNCVHCECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMKPDPPLGLHM 245  
DB 180 CNCVARECECHVPSAAKLNLYTLMLYKITSGAVFHSPLMSVQPINVKKPDPPLGLHM 239  
QY 246 EITDDGNLKISWSSPPLVPPLQYQVKSSENSTTVIREADKIVATSILVDSILPGSSYE 305  
DB 240 EITDTGNLKISWSSPPLVPPLQYQVKSSENSTTNMRKADEIVSDTSLVDSVLPGSSYE 299  
QY 306 VQVRGKRLDGPGLWSDWSTPRVFTQDVYIFPPKILTSVGSNVSEHCYKKNKIIVPSKE 365  
DB 300 VQVRGKRLDGPGLWSDWSTPRFTTQDVYIFPPKILTSVGSNISLHCYKKNKIIVPSKE 359  
QY 366 IYMMNLAELKIPQSQDYVDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHHRYAEL 425  
DB 360 IYMMNLAELKIPQSQDYVDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHHRYAEL 419  
QY 426 YVIDVNINISCTDGYLTMTKCRWSTSTQSLAESTLQRLYHRSLSYCSDDIPSIHIPISEP 485  
DB 420 YVIDVNINISCTDGYLTMTKCRWSTSTQSLAESTLQRLYHRSLSYCSDDIPSIHIPISEP 479  
QY 486 KDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSIGSLDSPPTCVLPDSVVKPLPSSVKA 545  
DB 480 KDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSIGSLDSPPTCVLPDSVVKPLPSSVKA 539  
QY 546 EITINIGLKISWKKVPFENNLOQIRYGLSGKEVQWKMYEYDAKSKSVSLPVPDLCA 605  
DB 540 EITAKIGLKISWKKVPFENNLOQIRYGLSGKEVQWKMYEYDTKLKSTSLPVPDLCA 599  
QY 606 VYAVQVRCKRLDGLGYWSNMSNPATYVVMIDIKVPMRGPEFWRIINGDTMKKEKNVTLLMK 665

DB 600 VYAVQVRCKRLDGLGYWSNMSNPATYVVTVDYKVPIRGPEFWRIINGDTMKKEKNVTLLMK 659  
QY 666 PLMKNDLSICVQRYVINHTSCNGTWSEEDVGNHTKFTFLWTEQAIIVTLAINSIGASVA 725  
DB 660 PLMKNDLSICVRSYVVKHHTSRHGTWSEEDVGNHTKFTFLWTEQAIHSTVLAVNSIGASSA 719  
QY 726 NFNLTFSPWPKVNIIVOSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNEDEGIKW 785  
DB 720 NFNLTFSPWPKVNIIVOSLSAYPLNSCVGLSWLLSPSDYNLMYFIEMKILNEDEGIKW 779  
QY 786 LRISSVKKYIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDDIEKHQSDAGLYVI 845  
DB 780 LRISSVKKYIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDC-EKHNDAGLYVI 838  
QY 846 VPVITSSSIL 855  
DB 839 VPVITSSSIL 848

RESULT 14  
Q62960  
ID 062960 PRELIMINARY; PRT; 895 AA.  
AC 062960;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR.  
GN ROB-R.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RA Wang M.-Y., Unger R.H.;  
RT "Characterization of leptin receptors in normal and Zucker diabetic  
RT fatty rats.";  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U53144; AAB03088.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;

Query Match 59.6%; Score 3729; DB 11; Length 895;  
Best Local Similarity 76.5%; Pred. No. 5.4e-267;  
Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;

QY 1 MICQPCVVLHWEFIVITAFNLSPYTPWRFKLSGMPNSTYDYFLPAGISKNTSNS 60  
DB 1 MICQPCVVLHWEFIVITAFNLSPYTPWRFKLSGMPNSTYDYFLPAGISKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNL-SKTFHCCFRSDQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 KGASEALVEAKFNSGTIVSELSKTFHCCFRSGNEDGQNCALTGNETKTLASVVKPLVF 120  
QY 121 QOIDANMNIQCWLKGLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180  
DB 121 ROLGVNMDIECMKGDLLTFICHMEPLKNPFKNYDSKVHLLYDLPEVIDDLPLPKDS 180  
QY 181 FQMVHNCVHCECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPINMKPDP 240  
DB 181 FQTVQCNCVRF-CECHVVPVPRAKVNYALMLYLTITSAGVVSFQSPILMSVQPINMKPDP 239

OY	241	LGLHMETDDGNLKLISWSSPPLVFPFLODYOKYSNSTVTIREADKIVSATSLVDSTLP	300
Db	240	LGLRMEETDDEGNLKISWDSQTKAPFLQYOXYLENS-TIVREAELIVSDTSLVDSVLP	298
OY	301	GSSYEVOYGKRLDGPGIWSDMSTPRVFOTODVIYEPFKILTSVGSNVSFHCIYKKENKI	360
Db	299	GSSYEVOYRSKRLDGSGVMSDWMLPOLFTQTQDVMYFPFKILTsvgsnasfcCiyKENOCT	358
OY	361	VPSKEIVMMNLAEKIPQSQYDVVSDSHVSKYTFENLNETHPKRGKFTYDAVAYCCNEHCCH	420
Db	359	ISSKOIYWMNMNLAEKIPETOYNVSDHSIKYTFENLNKATRPRGKFTYDAVAYCCNEQCCH	418
OY	421	RVAELYVIDVININISCETDGYLTfKMTCRMSTSTIQSLAESTLQLRYHRSSLYCSDTPSIH	480
Db	419	RYADLYVIDVININISCETDGYLTfKMTCRMSESTIQSLVGSTVOLRYHRSSLYCPEDNPSIR	478
OY	481	PISEPRDCYLQSDGFYECIFOPIFLLSGTYMIRINHSLGSLDSPPTCVLPDSVVKPLPP	540
Db	479	PTESELKNVCYLQTDGLYECVSOPIPLLGGTYMIRINHSLGSLDSPPTCVLPDSVVKPLPP	538
OY	541	SSVKAELITINIGLLKISWEKVPFPENNLOFOIRYGLSGKEVQMKEYEYDAKSASVSLPV	600
Db	539	SNNKAELITINTGLLKVSWEKVPFPENNLOFOIRYGLNGKEIQWKTHEVFDAKSASASLPV	598
OY	601	POLCAVYA VOYRCRKRLDGLGYWSMNSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	599	SDLCAVYVVQYRCORLDGLGYWSMNSSPAYTLVMDVKVPMRGPEFWRIIMGDITTKERNV	658
OY	661	TLLMKPLMKNDLSCSVQRYYVINHHTSCNGTWSEDVGNHTKFTFLMTQAHTVYLAINSI	720
Db	659	TLLMKPLMKNDLSCSVRRYVVKHRTAHNGTWQDVGNQTNLTFLSGESAHTVYVLIDINSI	718
OY	721	GASVANFNLTFSWPMSKVNIQVSLAYPINSSCVIVSWILSPSDYKLMYFIEMKNLINED	780
Db	719	GASIVNFNLTFESWPMSKVNGWQSLAYSPLSSCVILSWTLSPNDYSILYLVIEKMLIND	778
OY	781	GEIKWLRISSSVKKYYIHDFIPIEKYQSFSLYPIEMEGVGPKIINSFTQDDIEKHQSDA	840
Db	779	DGMKMLRIPSNVNKYIHDNFIPIEKYQSFSLYPVEMGVGPKIINGFTKDIKAOQNDA	838
OY	841	GLYVIVPYIISSSILLGLTLLISHQRMKKLFMEDVPNPKNCswAGLNfQK	891
Db	839	GLYVIVPYIISSCYLLGLTLLISHQRMKKLFMDVDPNPKNCswAGLNfQK	889
RESULT 15			
Q9DDK1 ID Q9DDK1 PRELIMINARY; PRT: 1147 AA.			
AC	Q9DDK1;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR.		
GN	OB-R.		
OS	Melagris gallopavo (Common turkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
OX	NCBI_Taxid=9103;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	.TISSUE=BRAIN;		
RA	Richards M.P., Poch S.M., Ashwell C.M.;		
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF321982; AAG40323.1; .		
DR	HSSP; P40189; 1BQU.		
DR	InterPro; IPR002996; CRA1.		
DR	InterPro; IPR003961; FN_III.		
DR	pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 4.		
KM	Receptor.		
FT	VARIANT 1133 1133 Q -> R.		
SEQ	SEQUENCE 1147 AA; 129131 MW; 34197B7908F734F4 CRC64;		

[illegible]

```
QY 1022 D$F$N$S$W$E$I$A$Q$F$F$I$L$S$D$---H$P$---N$I$S$H$L$T$F$E$G$L$D$E$L$L$K$L$E$G$N$F$P$E$N$N$D$K 1074
      | | | | : : : : | | | | : : | | | | : : : :
Db 1011 G$V$C$G$S$S$W$E$L$G$E$E$F$F$L$L$P$D$Q$G$S$R$P$C$K$L$S$L$I$S$-----S$E$G$F$E$P$S$D$Q$D$A$F$T$D$G$S$P$E 1065
      | | | | : : : : | | | | : : | | | | : : : :
QY 1075 K$I$Y$Y$L$G$V$T$S$I$K$K$R$E$S$G$V$L$L$T$D$K$S$R$V$S$C$P$E$P$A$C$L$E$T$D$I$R$V$L$Q$D$S$C$H$F$V$E$N$N$I$N$-L$G$T$S 1133
      : : | | | : | | : : : : | | : : | | : : | | : :
Db 1066 R$G$L$C$Y$L$I$G$T$S$L$D$K$R$E$N$A$I$F$L$T$E$S$R$L$M$C$H$F$H$T$A$D$L$L$R$G$V$F$L$O$N$T$-----P$P$L$N$A$F$L$Q$S 1120
      : : | | | : | | : : : : | | : : | | : : | | : :
QY 1134 S$K$T$F$A$S$Y$M$P$Q$F$Q$T$C$S$T$Q$T$H$K$I$M$E$N 1158
      | | | | : : | | | | : : : : | |
Db 1121 S$I$K$A$I$V$P$Y$P$Q$F$Q$M$T$A$K$V$Q$E$T$T$E$N 1145
      | | | | : : | | | | : : : : | |
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Search completed: May 18, 2002, 07:01:59  
Job time: 543 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:18:00 ; Search time 122.79 Seconds  
(without alignments)  
1053.840 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 6254  
Sequence: 1 MICQKFCVLLHMEFIYIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*  
1: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	6254	100.0	1165	AAW24051	Human WSX receptor
2	6254	100.0	1165	AAE12609	Human OB receptor
3	6254	100.0	1220	AAW34500	Obesity receptor D
4	6250	99.9	1165	AAE12551	Human OB receptor
5	6246	99.9	1165	AAV13474	Peptide Seq ID No:
6	6240	99.8	1165	AAW19116	Human Ob receptor.
7	5809	92.9	1221	AAW62544	Human ob-receptor
8	4831.5	77.3	970	AAW34499	Obesity receptor C
9	4826	77.2	896	AAW24052	Human WSX receptor
10	4826	77.2	923	AAW24053	Human WSX receptor
11	4826	77.2	972	AAW34497	Obesity receptor A

12	4826	77.2	999	18	AAW34498	Obesity receptor B
13	4819.5	77.1	958	18	AAW38214	Human OB-R variant
14	4819.5	77.1	958	18	AAW31911	Human OB-R leptin
15	4819.5	77.1	958	18	AAW19535	Human OB-R leptin
16	4819.5	77.1	958	18	AAW22773	Human haematopoiet
17	4816.5	77.0	960	17	AAW88910	Haematopoietin rec
18	4814	77.0	896	18	AAW50003	Human OB-R variant
19	4814	77.0	904	18	AAW50002	Human OB-R variant
20	4813	77.0	908	17	AAW88911	Haematopoietin rec
21	4811	76.9	898	17	AAW88912	Haematopoietin rec
22	4799	76.7	908	18	AAW19536	Variant form of hu
23	4785	76.5	896	18	AAW14841	Human haematopoietin
24	4784.5	76.5	1162	18	AAW34257	Rat wild-type ob r
25	4784.5	76.5	1162	18	AAW23398	Rat ob receptor (w
26	4778.5	76.4	1162	18	AAW23399	Rat ob receptor (f
27	4770.5	76.3	1162	18	AAW19115	Murine long form O
28	4770.5	76.3	1162	22	AAE12615	Murine long form O
29	4766.5	76.2	1162	20	AAV13473	Peptide Seq ID No:
30	4574	73.1	883	19	AAW62543	Human ob-receptor
31	4554	72.8	839	18	AAW34502	Obesity receptor P
32	4421	70.7	815	20	AAV05701	Human OB receptor
33	4337	69.3	804	18	AAW34501	Obesity receptor P
34	4214.5	67.4	1015	18	AAW34259	Rat ob receptor is
35	3793	60.6	900	18	AAW22105	Murine leptin rece
36	3787	60.6	892	18	AAW34260	Rat ob receptor is
37	3787	60.6	894	18	AAW37337	Ob protein recepto
38	3787	60.6	895	18	AAW34258	Rat ob receptor is
39	3785	60.5	894	18	AAW24064	Murine WSX recepto
40	3785	60.5	894	18	AAW19114	Murine short form
41	3785	60.5	894	22	AAE12608	Murine short form
42	3781	60.5	894	18	AAW37338	Ob protein recepto
43	3479	55.6	842	18	AAW22102	Murine leptin rece
44	3340	53.4	805	18	AAW22106	Murine leptin rece
45	3143	50.3	783	18	AAW24054	Murine WSX recepto

ALIGNMENTS

RESULT 1	AAW24051	standard; Protein: 1165 AA.
ID	AAW24051;	
XX	AAW24051;	
AC	AAW24051;	
XX	AAW24051;	
DT	17-MAR-1998	(first entry)
XX	17-MAR-1998	(first entry)
DE	Human WSX receptor variant 13.2.	
XX	Human WSX receptor; variant 13.2; identification; purification;	
KW	ligand; activator; antibody; agonist; proliferation; obesity;	
KW	differentiation; anaemia; treatment; neoplasia; arteriosclerosis;	
KW	Type II diabetes; polycystic ovarian disease;	
KW	cardiovascular disease; osteoarthritis; dermatological disorder;	
KW	hypertension; insulin resistance; hypercholesterolaemia;	
KW	hypertriglyceridaemia; cancer; cholelithiasis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9725425-A1.	
XX		
PD	17-JUL-1997.	
XX		
PF	07-JAN-1997;	97WO-US00325.
XX		
PR	20-JUN-1996;	96US-0667197.
PR	08-JAN-1996;	96US-0585005.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;	
PI	Rodrigues ML;	
XX		

DR WPI: 1997-372864/34.  
DR N-PSDB; AAT85575.  
XX MSX receptor and related antibodies and ligands - used to develop  
PT products for diagnosis and therapy, e.g. for improving  
PT haematopoiesis or for treating tumours  
XX  
PS Claim 2; Pages 81-85; 219pp; English.  
XX  
CC The present sequence is the human MSX receptor variant 13.2,  
CC which can be used to identify and purify ligands and activators.  
CC An anti-MSX receptor antibody can be used as an agonist to activate  
CC the MSX receptor, leading to enhanced proliferation or  
CC differentiation of a cell expressing the MSX receptor. It can also  
CC be used to decrease body weight and/or fat-depot weight and/or food  
CC intake in an obese mammal. MSX receptor ligands can be used to  
CC enhance proliferation or differentiation of lymphoid, myeloid or  
CC erythroid blood cell lineages. This is useful when a mammal,  
CC especially a human, is suffering from decreased blood cell levels,  
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone  
CC marrow transplantation therapy. It can also be used to repopulate  
CC blood cells in a mammal. The products can also be used to treat,  
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,  
CC polycystic ovarian disease, cardiovascular diseases,  
CC osteoarthritis, dermatological disorders, hypertension, insulin  
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer  
CC and cholelithiasis.  
XX  
SQ Sequence 1165 AA:  
  
Query Match 100.0%; Score 6254; DB 18; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTPWRFKLSCMPNSTYDYELLPAGLSKNTSNS 60  
DB 1 micqkfcvllhwefiyvitafnlsyptpwrfklscompnstydyellpaglskntsns 60  
  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNTEGKTFVSTVNSLVE 120  
DB 61 nghyetavepkfnssgthfnslnsktfhccfrseodrnscslcadntegktfstvnsli 120  
  
QY 121 QOIDANWNIQWLKGDCLKFCYVESLEKFNFRNYKVHLLYVLEVEDSPLVPQKGS 180  
DB 121 qqidanwniqwlgdclkfcyveslefkfnfrnykvhllylvlevedsplvpqkgs 180  
  
QY 181 FQMVHNCVSVECCCECLVPVPTAKLNDTLLMCLKITSGVIFOSPINSVQPINVKKDDP 240  
DB 181 fgmvhncvsveccceclvpvptaklndtllmclkitsgvifgsplmsvqpinmvkddpp 240  
  
QY 241 LGLHMETDGDNLKISWSSPPLVPFPIQYQVKYSENSTVIREADKIVSATSLLVDSILP 300  
DB 241 lglhmetdgdnlkiswsspplvpfpilqyqvkyseentvireadkivsatsllvdsilp 300  
  
QY 301 GSSYEVQVRGKRLDGPGLSDWSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 gssyevqvrgrldgpglswdstprvfttqdvityfppkiltsvgsnvsfhcikykenki 360  
  
QY 361 VPSKEIYWMNMNLAEKIPQSQYDVVSVSHVSKVTFPNLNETKPRGFTYDAVYCCNEHECHH 420  
DB 361 vpskeiywmnmlaekipqsqydvsvshvskvtfpnlnetkprgftydavycnehechh 420  
  
QY 421 RYAEIYVIDVNNINISCEIDGYLTKMTCRWSSTSTIOSLAESTLOLRHRSLSLYCSDIPSIH 480  
DB 421 ryaelyvldvnniniscetdgyltkmtcrwststioslaestlqlrhrsslycsdipsih 480  
  
QY 481 PISEPKDCYLQSDGFYEYECIFQPIFLSGYTMWIRINHSLSGLSDPPTCYLPDSVVKPLRP 540  
DB 481 pisepkdcylqsdgfyecifqipiflsgytmwirinhsigsldspptcylpdsvvkplrp 540  
  
QY 541 SSVKAETITINIGLKLISWEKPVFEPENLQFQIRYGLSGKEVOMKMEVYDAKSKSVSLPV 600  
DB 541 ssvkaetitinigllkliswekpvfepennlqfqiiryglsgkevomkmevydaksksvslpv 600

DB 541 ssvkaetitinigllkliswekpvfepennlqfqiiryglsgkevqkmyevydaaksksvslpv 600  
QY 601 PDLCAVAVQVRCRRLDGLGYWSNWSNPATVVMMDIKVPMRGPETWRIINGDTMKKEKNV 660  
DB 601 pdlcavavqvrckrlldglgywsnwsnpaytvmmdikvpmrgpetwriingdtmkkekvn 660  
  
QY 661 TLLWKPMLKNDSLCSVQRYVINHHHTSCNGTWSVDGNHTKFTFLTEQAHTVTVLAINSI 720  
DB 661 tllwkpmlkndslcsvqryvinhhhtscngtwsedvgnhtkftflteqahvtvlainsi 720  
  
QY 721 GASVANFNLFESWPMKSKVINVOQLSAYPLNNSCVIVSWILSPSDYKUMYFIIEWKNLNE 780  
DB 721 gasvanfnlftswpmkskvinvoqlsayplnnsccvsvilspdykumyfiilewknlned 780  
  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDA 840  
DB 781 geikwlri:sssvkkyyihdhfipiekyslypifmegvgkpkilnsftqddlekhsda 840  
  
QY 841 GLYVIVPVLISSSILLGLTLLISHQRMKLFMEDVNPKNKNSNAGLNFQKPEFELFLI 900  
DB 841 glyvivpvli:sssillgltllishqrmklfmedvnpknknsnaglnfqkpetfehlfli 900  
  
QY 901 KHTASVTCGPELLPEPITISEDIVDSKMKNDMPPTVVSLLSTTDLEKGSVCISDQFN 960  
DB 901 khtasvtcgplllepetisedivdsknkndempptvvsllstdlekgsvcisdqfn 960  
  
QY 961 SVNFSAEGETEVTYEDESQRPVFKYATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
DB 961 svnfseagtevttyedesqrpfvfyatlisnkspssetgeeglinsvvtckfssknspl 1020  
  
QY 1021 KDSFNSNSWEIEAOAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
DB 1021 kdsfnsnsweieaafilisdqhpniisphlftfsegidellklegnfpeenndksiiyy 1080  
  
QY 1081 GVTSIKKRESGVLTLTKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
DB 1081 gvtsikresgvltltksrsvcfpapclftdirvlqdschshfveenninlgtsskktffas 1140  
  
QY 1141 YMPQFQTCSTQTHKIMENKMCIDLTV 1165  
DB 1141 ympqfqtcsqthkimenkmcidltv 1165  
  
RESULT 2  
AAE12609  
ID AAE12609 standard; Protein; 1165 AA;  
XX  
AC AAE12609;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Human Ob receptor (OBR) protein.  
XX  
KW Human; obese receptor; OBR; anorectic; anabolic; body weight disorder;  
KW therapy; obesity; cachexia; anorexia.  
OS  
XX Homo sapiens.  
XX  
FH Key  
FT Peptide 1..20  
FT Protein /label- signal\_peptide 21..1165  
FT /label- Human\_mature\_OBR\_protein 21..839  
FT Domain /label- Extracellular\_domain 23..25  
FT /note- "Asn is N-glycosylated" 41..43  
FT /note- "Asn is N-glycosylated" 56..58  
FT /note- "Asn is N-glycosylated" 59..61  
FT /note- "Asn is N-glycosylated"

FT Modified-site 73..75 /note- "Asn is N-glycosylated"  
FT Modified-site 98..100 /note- "Asn is N-glycosylated"  
FT Modified-site 187..189 /note- "Asn is N-glycosylated"  
FT Modified-site 206..208 /note- "Asn is N-glycosylated"  
FT Modified-site 276..278 /note- "Asn is N-glycosylated"  
FT Modified-site 347..349 /note- "Asn is N-glycosylated"  
FT Modified-site 319..323 /note- "Asn is N-glycosylated"  
FT Region /note- "Conserved motif of cytokine I receptor family"  
FT Modified-site 397..399 /note- "Asn is N-glycosylated"  
FT Modified-site 433..435 /note- "Asn is N-glycosylated"  
FT Modified-site 516..518 /note- "Asn is N-glycosylated"  
FT Modified-site 622..626 /note- "Asn is N-glycosylated"  
FT Region /note- "Conserved motif of cytokine I receptor family"  
FT Modified-site 624..626 /note- "Asn is N-glycosylated"  
FT Modified-site 659..661 /note- "Asn is N-glycosylated"  
FT Modified-site 670..672 /note- "Asn is N-glycosylated"  
FT Modified-site 688..690 /note- "Asn is N-glycosylated"  
FT Modified-site 697..699 /note- "Asn is N-glycosylated"  
FT Modified-site 728..730 /note- "Asn is N-glycosylated"  
FT Modified-site 750..752 /note- "Asn is N-glycosylated"  
FT Modified-site 840..862 /note- "Asn is N-glycosylated"  
FT Domain /label- Transmembrane\_domain  
FT Domain 863..1165 /label- Cytoplasmic\_domain  
XX  
PN US6287782-B1.  
XX  
PD 11-SEP-2001.  
XX  
PF 29-APR-1998; 98US-0069781.  
XX  
PR 27-NOV-1995; 95US-0562663.  
PR 04-DEC-1995; 95US-0566622.  
PR 08-DEC-1995; 95US-0569485.  
PR 11-DEC-1995; 95US-0570142.  
PR 28-DEC-1995; 95US-0583153.  
PR 22-JAN-1996; 96US-0599455.  
PR 26-APR-1996; 96US-0638524.  
PR 03-SEP-1996; 96US-0708123.  
PR 28-MAY-1997; 97US-0864564.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
XX  
DR WPI; 2001-624489/72.  
DR N-PSDB; AAD20509.  
XX  
PT Identifying compounds for treating body weight disorder, e.g. obesity,  
PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob  
PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test  
PT compound -  
XX  
PS Claim 1; Fig 3; 109pp; English.  
XX  
CC The patent discloses obese receptor (Obr) proteins and nucleic acids  
CC encoding them. Obr protein participates in the regulation of mammalian

CC body weight. The invention also relates to a method of identifying  
CC therapeutic compounds for the treatment of a body weight disorder.  
CC The method involves contacting a cell that expresses a mammalian Obr  
CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test  
CC compound. The method is useful for identifying compounds which modulate  
CC Obr gene expression and gene product activity, which can be used as  
CC agents to control body weight particularly as therapeutic agents for  
CC treating body weight disorders, including obesity, cachexia and anorexia.  
CC The present sequence is Obr protein from human.  
XX  
SQ Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 22; Length 1165;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFIYVITAEFLNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 mlcqkfcvllhweftvltafnlstypiltpwrflksmpnstydyfllpaglskntsns 60  
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTFHCFCFRSEODRNCSCADNTEGKTFVSTVNSLVR 120  
Db 61 nghyetavepkfnssgthfnsksctfhccfrseqdncscadnlgkftvstvnslvr 120  
QY 121 QQIDANNNIQCWLKGDCLKFICVESLSFKNLFERNYKHYLLVLPVELDSDPLVPQKGS 180  
Db 121 qqidannniqcwlkgdclki fcyveslfnklnfrnykhyllvlpvelsdplvpqkgs 180  
QY 181 FQWVHCNCSVHCECECLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP 240  
Db 181 fgwvhcnscsvhcececlvpvptaklndtlmlckitsggvifqspilmsvqpinmkpdp 240  
QY 241 LGLHEITDDGNLKSISWSSPLVPPLQYOVKYSNSTYVIREADKIVSATSLVDSILP 300  
Db 241 lglhemitddgnlksiswssplvpplqyovkysnstyvirreadkivsatslvdsilp 300  
QY 301 GSSYEVOYRGKRLDGPISWDSWTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKEKNI 360  
Db 301 gssyevoyrgkrlldgpiswdsdwtpvftqdvityfpkiltsvgsnvsfhcitykkekni 360  
QY 361 VPSKEIYWMNLAEKIPQSQDYDVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 vpskeiywmnlaekipqsqdydvsdhsvskvtfeflnetkprgkfttydavycnehechh 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTGRWSTSTIQSLAESTLOLRHYRSSLYCSDIPSIH 480  
Db 421 ryaeliyvidvininisceitdgyltkmtgrwststisqlaestlqlrhyrsslycsdipsh 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLRP 540  
Db 481 pisepkdcylqsdgfyecifqpfllsgytmwirinhsisglspptcvlpdsvvkplrp 540  
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
Db 541 ssvkaeitinigllkiswekpvfpennlqfiryglsgkevqmkyyevydaksksvslpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNNSNPATVVMIDIKVPMRGPEFWITINGDTMKKEKNV 660  
Db 601 pdlcavyavqvrckrldglgywsnnsnpatvvmidikvpmrgpewfwtngdtmkkekvnv 660  
QY 661 TLWKPMLKNDLSQVORYVINHHSCNGTWSSEVDGNHTKFTPLMTGOAHTVTVLAINSI 720  
Db 661 tlwkpmlkndlsqvgryvinhhscngtwsedvgnhtkftplmtgoahvtvvlainssi 720  
QY 721 GASVANFLTFSPMSKVNIVQSIASAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780  
Db 721 gasvanfltfspmskvnivqsisayplnsscvivswilspdyklymfiiwknlned 780  
QY 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 geikwlriSSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSILLGLTLLISHQRMKLFMEDVNPKNCSMAOGLNFQKPEFHELF 900  
DB 841 glyvivpviasslllgltllishqrmklfmedvnpknscwaglnfqkpetfehlf 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVSLSTDLKSGVCSISDQFN 960  
DB 901 khtasvtcgpillepetisedisvdtswknkdemptltvslstdlekgsvcisdfn 960  
QY 961 SVNFSEAGTEVTEDESOQOPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 svnfseagtevyedesqrpfvkyaatlisnskpssetgeeglinssvtckfssknspl 1020  
QY 1021 KDSFSNSSWEIEAQAFETLSDQHPNIIISPHLTFSEGLDELKLEGNPEENNKKSIYYL 1080  
DB 1021 kdsfnsnwelaeaqafllsdqhpniisphltfsegldekllegnpfeennkksiyyl 1080  
QY 1081 GVTSIKKRESGYLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINLGTSKKTFFAS 1140  
DB 1081 gvtsikkrsgvlltdksrvscfpapclftdirvlqdschfvenninlgtskktffas 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 ympqfqtcstqthkimenkmdltv 1165

RESULT 3

AAW34500 AAW34500 standard; protein; 1220 AA.

AC AAW34500;

DT 18-MAR-1998 (first entry)

DE Obesity receptor D protein.

KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

KW high blood lipid level; obesity; diabetes; high cholesterol level;

KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

Location/Qualifiers

FT Misc-difference 1..1165 /note="encoded by AAT98531"

FT Misc-difference 1166 /label="unknown" /note="encoded by stop codon"

FT Misc-difference 1169 /label="unknown" /note="encoded by stop codon"

FT Misc-difference 1187 /label="unknown" /note="encoded by stop codon"

FT Misc-difference 1207 /label="unknown" /note="encoded by stop codon"

FT Misc-difference 1..1165 /note="encoded by stop codon"

FT Misc-difference 1..1165 /note="encoded by AAT98531"

PN WO9725424-A1.

PD 17-JUL-1997.

PE 02-JAN-1997; 97WO-US00128.

PR 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

PI Chang M, Fletcher FA, Welcher AA;

DR WPI; 1997-384981/35.

DR N-PSDB; AAT98531.  
XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels  
XX  
PS Claim 31; Page 76; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor D protein. This  
CC sequence has one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 1220 AA:

Query Match 100.0%; Score 6254; DB 18; Length 1220;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVYLLHMEFIYVITAENLSXPITPWRFKLSGMPNSTRDYFLLPAGLSKNTSNS 60  
DB 1 micqkfcvylhweifyvitaenlsypitpwrfkiscmpnstydyfllpaglskntns 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLKTTTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 nghyetavepkfnssgthfsnlskttfhccfrseodrnscalcadniegkctfvstvnslvf 120  
QY 121 QQIDANMNIQCWLKGDILKLFICYESLFKNLFERNYKVNLLVLPVLEDSPLVPQKS 180  
DB 121 qqidanwniqcwlkgdilklficyeslfnklnfrnykvnllvlpvledsplvpqkgs 180  
QY 181 FQWVHCNSVHECCCLVPVPTAKNDLLMCLKITSGGVIFQSPLMVQPINMVKPDP 240  
DB 181 fqwvhcnsvheccclvpvptakndllmclkitsggyvfqsplmvqpinmvkpdpp 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPPLOQYQVYSENSTVIREADKIVSATSLVDSILP 300  
DB 241 lglhmeitddgnlkiswsspplvpploqyvqysenstviradkivsatslvdslip 300  
QY 301 GSSYEQVGRKRLDGPGLWSDMSTRVFTTQDVIFYFPKILTSVGSNVSFHCYKKEKNI 360  
DB 301 gssyevqvrgrldgpglwsdmsrvtfttdvifyfprkiltsvgsnvsfhciykkenki 360  
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSXVTFENLNETRPRGFTYDAVYCCNEHECHH 420  
DB 361 vpskeiywmnlaekipsgydvvsdhvskvtfenlnetprgkftydavycnehechh 420  
QY 421 RYAEIYVIDVININISCEPDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
DB 421 ryaelvyidvinniscedgyltmcrwststiqslaestlqlrhrsslycsdpsih 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVYKPLPP 540  
DB 481 pisepkdcylqsdgyfecifqpfllsgytmwirinhsldspsptcvlpdsavkplpp 540  
QY 541 SSVKAEITINIGLLKISWEKPYEPENNLFQIRYGLSGKEVQWKMYEYVDAKSKVSILPV 600  
DB 541 ssvkaeitinigllkiswekpyepennlfqirylsgkevqwkmyevydakskvsilpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWMSNMPATYVMDIKYPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 pdlcavayavvrckrldglgyswnsnmpatylvmdikypmrgpewfwiingdtmkkeknv 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWEDEVGNHTKFTFLWTEQAHVTYVLAINSI 720  
DB 661 tllmkplmkndslcsvqryvinhhtscngtwsedvgnhtkftflwteqahvtvylainsi 720  
QY 721 GASVANENLTFSPMKSXVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLED 780  
DB 721 gasvanenltfspmksxvniqslayplnsscvivswilspdyklmfyiemknled 780





CC from the wild-type human OBR protein shown in Figure 3 of the  
CC specification (AAE12609).

XX	Sequence	1165 AA;
SQ		

**SQ Sequence 1165 AA:**

Query Match	99.98;	Score 6250;	DB 22;	Length 1165;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 1164; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MICQKFCVLLHMEPIVITAEFLNSYPITPMREKLSICMPNPSTYDFLLPAGISKNTSNS	60
Db	1	micqkfcvllhwefflyitafinsylpwr fklscmpnstydfllpagiskntsns	60
QY	61	NGHETAVEPKFNSSGTHFNSLKTFFHCCFRSEQDRNCSLADNIEGKTFEVSVNSLVF	120
Db	61	nghetavepkfnssgthfnslksctfhccfrseqdrncslcadniegkltfvsvnslvf	120
QY	121	QOIDANMNIQOEWLKGDKLFCICYVESLEKNLFRNRYNKVHLLVYLPEVLEDSPLVPQKS	180
Db	121	qoidanwniqcwllkgdklfcicyveslfnlfrnyknkvhllylpevledsplvpqks	180
QY	181	FQWVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIPOSPLMSPQPINMKPDP	240
Db	181	fqwvhcnscsvhecceclvpvptaklndtlmclkitsggviqspmlsvqpinmkpdp	240
QY	241	LGLHMEITDDGNLKISWSSPPLVPEPLQYQYKSENSTVIREADKIVSATSILVDSILP	300
Db	241	lglhmeitddgnlkiswsspplvpplqyqyksenstvi readkivsatsilvdsilp	300
QY	301	GSSYEVQVRGKRLDGPGISWSDSTPRVETTQDVIFPPKILTSVGSNVSFHCYKKEKNI	360
Db	301	gssyevqvrgrldgpgiwsdstp rvefttdvlyfppkiltsvgsnvsfhcykkenki	360
QY	361	VPSKEIWMWMLAEKIPQSOYDVVSDHVSKVTEFNLNETKPRGKFTYDAYVCCNEHECH	420
Db	361	vpskeiwmwnlaekipqsodyvvsdhvskvtefnlnetkprgkftdayvccnehech	420
QY	421	RYAELVYIDVNNINISCEITDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCSDIPI	480
Db	421	ryaelvldvnniniscetdgy ltkmtcrwststislaestiolryhrslycsdipih	480
QY	481	PISEPKDCYLOSDFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSYVKPLP	540
Db	481	pisepkdcylosdgyfye cifqipifllsgytmwirinhslsglsdspptcvlpdsvvpklpp	540
QY	541	SSVKAETINIGLLKISWEKRVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV	600
Db	541	ssvkaeitinigllkiswekvpfpennlqfiryglsgkevqwkmyevdaksksvslpv	600
QY	601	PDLCAVYAVQVRCKRLDGLGYSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	601	pdlcavyavqvrckrldglgyswnsnpayltvmdikvpmrgpewriingdtmkkeknv	660
QY	661	TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSEDEVGNHTKFTFLWTEQAHVTVALINSI	720
Db	661	tlwmkplmkndlsqsvqryvinhhtscngtwsedevgnhtkftflwteqahvtvalinsi	720
QY	721	GASVANENLTFSWPMKSVNIQSLSAYPLNSSCVIVSWILSPSDYKLMFTIEMKNLNE	780
Db	721	gasvanenlftswpmksvniqslsayplnsscvivswilspdyklmfтиемкnlне	780
QY	781	GEIKWLRISSSVKKYYIHDFPIEKQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA	840
Db	781	geikwlri ssvkkyyihdhfpi ekqfslypifmegvgkpkii nsftoddiekhgsda	840
QY	841	GLYIVIVPIIISSSILLGTLISHQMKKLFMEDVPNPKNCSSWAQGLNFOKPEFHEHFI	900
Db	841	glyivivpiissillgtllishqmkklfmedvpnpknccswaqglnfokpelfehlf	900
QY	901	KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN	960
Db	901	khtasvtcgpillepetisedisvdtswknkdempttvsllsttlekgsvcisdqfn	960

QY	961	SVNSEAEGETVTEDESOQOPFVKYATLISNSKPSETGEEGLINSSVTCKCRSSKN SPL	1020
Dd	961	svnfseagtevttyedesqgpfvkyaatlisnskpseltgeegjlinssvckcissknsp l	1020
QY	1021	KDSFSNSSWEIEAQAFILSDQHPIIISPHLTFEGDELKLEGNFPRENNDKRSIYYL	1080
Dd	1021	kdsfnsnwseieagaftllsdqhpnllsphlttfsegldelklklegnfprenndkkslyl l	1080
QY	1081	GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFEVENNINIGTSSKKT FAS	1140
Dd	1081	gvtsikkresgvlltdksrvscfpapclftdirvlqgdscshfevenninigtsskk tfas	1140
QY	1141	YMPOFOCTSTQTHKIMENKMCDLT V 1165	
Dd	1141	ympofqtctstqthkimenkmcdlt v 1165	

## RESULT 5

AAV13474

ID AA13474 standard; Protein; 1165 AA.

AC AAY13474;

DT 26-JUL-1999 (first entry)

DE Peptide Seq ID No: 4 of W09923493.

\*\*\*  
KW Leptin: phosphorylated leptin receptor; tyrosine phosphatase ID; PTP-1B;  
KW modulator; drug; weight loss; adiposity; hypertension; heart disease;  
KW type II diabetes; cancer; AIDS; agriculture.

PN W09923493-A1

PD 14-MAY-1999.

PF 27-OCT-1998; 98WO-US22797.

PR 26-OCT-1998; 98US-0178691.

PR 31-OCT-1997; 97US-0961809.

PA (UYRQ ) UNIV ROCKEFELLER.

PI Friedman JM, Li C

DR WPI: 1999-327025/27.

DR N-PSDB; AAX55588.

PT Identifying modulators agents that modulate leptin activity

PS Disclosure; page 77-84; 96pp; English.

The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine phosphatase 1D (PTP-1D). The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-1D or its fragment in the presence and absence of a candidate agent under conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-1D or its fragment can be detected; and (b) detecting the binding of the phosphorylated leptin receptor and PTP 1D; where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin receptor-dependent PTP-1D phosphorylation are useful as drugs in weight loss diet regimens. The drugs identified can regulate adiposity and fat content of animals, particularly in mammals. Disorders that can be treated by PTP-1D modulators include obesity and its associated diseases, e.g. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally, the agents identified may be useful in agriculture where body weight of domestic animals can be



FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	433	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	516	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	624	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	658	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	670	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	688	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	697	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	728	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
FT	750	
FT	/label=	Glycosylation
FT	/note=	"potential N-linked glycosylation site"
XX	WO9719952-A1.	
XX	05-JUN-1997.	
XX	27-NOV-1996;	96WO-US19128.
XX	03-SEP-1996;	96US-0708123.
PR	27-NOV-1995;	95US-0562663.
PR	04-DEC-1995;	95US-0566622.
PR	08-DEC-1995;	95US-0569485.
PR	11-DEC-1995;	95US-0570142.
PR	28-DEC-1995;	95US-0583153.
PR	22-JAN-1996;	96US-0599455.
PR	26-APR-1996;	96US-0638524.
XX	(MILL-) MILLENNIUM PHARM INC.	
PA	Culpepper JA, Tartaglia LA, Tepper RI, White DW;	
XX	WPI; 1997-310525/28.	
DR	N-PSDB; AAT69592.	
XX	Isolated Ob receptor genes and polypeptide(s) - useful to develop	
PT	products for diagnosis or treatment of body weight disorders, e.g.	
PT	obesity, cachexia, anorexia and bulimia	
XX	Example; Fig 3; 265pp; English.	
PS	Human Ob receptor (OBR) (AAW19116) is a novel polypeptide that	
XX	participates in the control of body weight and which is involved in	
CC	signal transduction triggered by the binding of its natural ligand,	
CC	Ob (leptin). It is a member of the class I cytokine receptor	
CC	family. Its amino acid sequence was deduced from a foetal brain	
CC	cDNA clone (AAT69592). The receptor corresponds to the long form	
CC	mouse OBR (AAW19115). OBR proteins, peptides, antibodies, agonists	
CC	and antagonists can be used in the diagnosis and treatment of body	
CC	weight disorders such as obesity, cachexia and anorexia.	
XX	Sequence 1165 AA;	
XX	99.8%; Score 6240; DB 18; Length 1165;	
XX	Best Local Similarity 99.8%; Pred. No. 0;	

	Matches	1163; Conservative	0; Mismatches	2; Indels	0; Gaps	0.7
QY	1	MICQKCECVLLHMEFIYVITAFNLSPYTPPWRFKLSCMPNPSTYDYFLLPAGLSKNTS	60			
Db	1	micqkcecvllhweiflyitafnlspypwrfklscmpnpstydyfllpaglsknts	60			
QY	61	NGHYEAVEPKFNSSGTHFSNLKPTWHCCFRSEODRNCSLCADNTEGKTFVSTVNSLVF	120			
Db	61	nghyeavepkinssgthfslsktcthccfrseodrnscslcadnlegktfvstvnslvf	120			
QY	121	QQIDANNNIQCWLKGDCLKFICYVESLFKNLFERNYNKYKHLLVLPPEVLDSPLVPQKS	180			
Db	121	qqidannniqcwlkgdklificyveslfknlfrnykvhllylpevledsplvpqkgs	180			
QY	181	FQWVHNCVSVHECCCECLVPVPPTAKLNDTLMLCKLITSGCVIFOSPLMSVOPIMVKKPDP	240			
Db	181	fqmvhncsvheccceclvpvptaklndtlmlcklitsgcvifgsplmsvqplmvmkdpdp	240			
QY	241	LGLEHMETDDGNLKLISWSSPPLVPFPLOYQVKYSENSTVIREADKIVSATSLLDVSI	300			
Db	241	lgllmetddgnlkiswssplvpfploqvkysenstlvireadkivsatsllvdsilp	300			
QY	301	GSSYEQVQRKRLDGPGLMSDWSTPRVFTQDVIYFPFKILTSVGSNVSFHCYKKEKNI	360			
Db	301	gssyeqvqrgkrlpgplmsdwstprvftqdvlyfppklltsvgsnvshciykkenki	360			
QY	361	VPSKEIYWMNNLAEKIPQSQYDVVSDHYSKVTFENLNETKPRGKFTYDAVYCCNEHECH	420			
Db	361	vpskelvwmnlaekipqsqydvvsdhyskvtfnlnetkprgkftcydavycnehech	420			
QY	421	RYAELVIDVININISCETDGYLTRKMCRMSTSTIQSLAESTLQLRHRSLSLYCSDIPS	480			
Db	421	ryaelvidvnniniscetdgyltrkmcrcmststiqslaestlqlrhrslycsdipsh	480			
QY	481	PISEPRDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCYLLPDSVKKPLP	540			
Db	481	piseprdcylqsdgfyecifqpfllsgytmwirinhsllsglsdldpplcvlpdsvkkplsp	540			
QY	541	SSVKAETINIGLKLISWEKPVFPENNLOFQIRYGLSGKEVQWKVEYDAAKSQSVLPV	600			
Db	541	ssvkaetinnigllklswekpvfpennlqfdirylsgkewqwkmyevydaaksqsvslpv	600			
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMIDIKVPMRGPEFWRLINGDTMKKEKNV	660			
Db	601	pdlcavyavqvrckrldglgywsnwnpaytvvmidikvpmrgpewrllngdtmkkekvn	660			
QY	661	TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSSEDEVGNHTKFTFLWTEQAHTVTVLA	720			
Db	661	tlwkpmlkndslscsvqryvinhhtscngtwsedvgnhtkftflwteqahvtvlatnsi	720			
QY	721	GASVANFNLTFSWPMKSVNIVOSLSAYPLNSSCVIVSWILSPSPDKMLYFIIEWKNLNED	780			
Db	721	gasvanfnltfswpmksvnivglsayplnsscvivswilspsgklymyflliewknlnded	780			
QY	781	GEIKMLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIDIEKHQSDA	840			
Db	781	gelkwlriissvkkyyihdhfpielkyqfslpylfmegvgkpkilnsftqddiekhsda	840			
QY	841	GLYIVIVPIIISSSILLGLTLISHQRMKLLFWEDEVNPNPKNCNMAOCLNFQKPEFHEHFT	900			
Db	841	glyivivpiliissilllgltlisqrmkklfwedevnpnknswagqlnfqkpetfehlf	900			
QY	901	KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPPTVWSLSTDLLEKGSVCISDQFN	960			
Db	901	khtasvtcgpilllepetisedivdtswknkdempttvsllstdlekgsvclsdqfn	960			
QY	961	SVNFSAEGETEVTYEDESQRPFYKATLISNSKPSSETGEGGLINSSVTCKCFSSKNSPL	1020			
Db	961	svnfseaegetevtyedesqrpfvkyatlinsnkspssetgeegglinsvtckcfssknspl	1020			
QY	1021	KDSFNSSSWEIEAOAFILSDQHPNIISPHLTFSEGLDELKLEGNPPEENNDKKSITYL	1080			
Db	1021	kdsfnssweieaafilisdqhnllsphlftseglldelklegnppeenndkksityl	1080			

QY	1081	GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSSKRYEAS	1140
Db	1081	gvtsikkresgvlltdksrvscpfpapclftdirvlqdschfvenninlgtsskrtas	1140
QY	1141	YMPQFQTCSTQTHKIMENKMDLTV	1165
Db	1141	ympqfqtctstqthkimenkmcdltv	1165

RESULT 7  
AAW62544

ID AAW62544 standard; protein; 1221 AA.

AC AAW62544;

DT 12-OCT-1998 (first entry)

DE Human ob-receptor replacement mutant.

KW ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;

KW anorexia; cachexia.

OS Homo sapiens.

PN W09824881-A1.

PD 11-JUN-1998

PF 26-NOV-1997; 97WO-US22165.

PR 02-DEC-1996; 96US-0032367.

PA (MERI ) MERCK & CO INC.

PI Fong TM, Huang RC, Van Der Ploeg L.

DR WPI; 1998-333304/29.

PT New mutant ob receptor(s) - used to develop products for drug

PT anorexia

PT anorexia

PS Claim 6; Fig 2; 27pp; English.

The ob-receptor (OB-R), a member of the cytokine receptor family is transcribed in the hypothalamus and is involved in obesity. The replacement mutant has had amino acids 420-496 the second CK-F3 module in OB-R deleted and replaced by amino acids 500-632. The replacement mutant together with mutants lacking a functional first CK-F3 module or a functional intracellular domain can be used in assays for the detection of ligands, agonists, antagonists and ligand mimetics. The leptin agonists identified can be used in situations where leptin insufficiency causes obesity, diabetes or infertility. The leptin antagonists identified can be used in the treatment of anorexia and cachexia. The mutant receptor nucleic acids can also be used in gene therapy for weight control, e.g. for treating obesity or anorexia.

50 Sequence . 1221 AA;

Query Match	92.98;	Score 5809;	DB 19;	Length 1221;
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Best Local Similarity 90.68; Pred. No. 0;

Matches 1110; Conservative 17; Mismatches 34; Indels 64; Gaps 8;

QY 1 MICKFCVLLHWEFIYVITAFNLSTPTPWRFKLSGMPNPSTYDYFLLPAGLSKNTSNS 60  
 Db 1 micqfcvllhweftiyvitafnlstptpwrfklscmpnpstydyfllpaglskntsns 60  
 QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCEPSEODRNCISLCADNIEGKTFVSTVNSLVF 120  
 Db 61 ngyetavepknssgthfshnlsktthfcccseodrnscisladniegkthfsvtnslvf 120

QY	121	QOJDANWNIQCWLKGDLEKFCIVESLEFKNLEFRNMYKVHLLYLPEVLEDSPLVPQKS	180
Db	121	qgidanwniqcwlkgdlekfcivyseslfknlefrnykvhllylvilevledsplvpqks	180
QY	181	FOMVHNCNSVHECCCECLVPVPTAKLNDTLMLCKLTHSGGVIFQSPLSNVQPIPNVKKPDP	240
Db	181	fomvhncnsvhcccclvppvptaklndtlmlcklthsggvifqspmsvqplnmvkkpdp	240
QY	241	LGHEMITDDGNLKSISWSPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLVDSTLP	300
Db	241	lgheimitddgnlkiswsspplvpfploqvyksensttvireadkivsatsllvdstlp	300
QY	301	GSSYEVOVRGKRLDGPISWDMSTPRVFTTODVITYEPPKILTSVGSNVSFHCITYKKENKI	360
Db	301	gsseyevovrgkrl dgprgswdstprvfttgdvlyfppkiltsvgsnvsfhclykkenki	360
QY	361	VPSKEIWMNMNLAEKIPQSQYDVYSDHVSXVTFENLNETHKPRGKFTYDAVYCCNEHECHH	420
Db	361	vpskeiwmnmnlaekipqsgydvysdhvskvtfenlnethkprgkftydavycnehechf	420
QY	421	RYAEL--YVIDVNINISCTDGYL-TKMTGRWSTSTIQSL-----AESTL-----	462
Db	421	qpfllsgytmwirinhs---gslspsptcvlpdsavvxpilpssvkaeltinlglikis	477
QY	463	-----QLRYHRS-----SLYCSUPISHPISEPKDCYL	490
Db	478	wekpyfpeennlqfgrgyslgskveqwkmyevydaaksksvslpvpdlcayav-qvrcrkrl	536
QY	491	QSDGEY-----ECIFOPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP	540
Db	537	dglgyswnsnpaytveciqlpfilisgytmwirinhsigslspsptcvlpdsavvxpilpp	596
QY	541	SSVKAETITINIGLKISWEKPYEPENNLOFOIRYGLSCKEVOQWKMEVYDAKSYSLSLV	600
Db	597	ssvkaeltiniglkwiswepvfpennlqfgrgyslgskveqwkmyevydaaksksvslpv	656
QY	601	PDLCAVYAVOVRCRKLDELGYTWSNWSNPAYTVVMDIKYPMRGPEFWRIINGDIMKEKNV	660
Db	657	pdlcayavovrcrkrl dglgyswnsnpaytvvmdikypmrgpewrilingdimkeknv	716
QY	661	TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTVYLAINSI	720
Db	717	tlwkpmlkndslscsvgrvynhhtscngtwsedvgnhbkftflwteqahvtvylainst	776
QY	721	GASVAFENLTFSPMSKVNIVQSLAYPLNSCVTVSWLISPSDYKLMYFITEKNUNED	780
Db	777	gasvanfnltfswpmskvnivqslsayplnsscvtswlispdyklmyfillewknlned	836
QY	781	GEIKWIRISSVKKYVIHDFPIEKKYQFSLYPIFMEVGKPKIINSFTODDIEKHQSDA	840
Db	837	geikwirissvkkyyihdfpiefekyqfslpifmegykpkinsftgddiekhqsd	896
QY	841	GLYVIVPVITISSSILLGLTLLISHQRMKKLFMEDVPNPKNCSNAQGLNFQKPETFEHLFT	900
Db	897	glyvivpvilssslilgltllishqrmkklfmedvpnpknscswagqlnfqkpetfelnfl	956
QY	901	KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPITYVSLSTLDLEKGSVCISDOFN	960
Db	957	khtasvtcgpillepeticisedisvdtswknkdemptvsvslstldlekgsvcisdqfn	1016
QY	961	SVNFSAEGETEVTYEDESQROPEVKYATLISNSKPSSETGEEGLINSVTKCFSSKN SPL	1020
Db	1017	svnfseagtevttyeaesqrpfvkyatlinsnkspssetgeegqlinsvtcktsknsp	1076
QY	1021	KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELTLKLGNEPEENNDRKSTIYLL	1080
Db	1077	kdsfnssweieaqaffilisdqpnliisphltfseglidelklegnfpeenndrkstlyll	1136
QY	1081	CVTSIIKKRESGVLLTDKSRVSCPEFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS	1140
Db	1137	cvtsiikresgvlltdksrvscpfpapclftdirvlqdseshfvenninlgtskktffas	1196
QY	1141	YMPQFQTCSTQTHKIMENKMDLTV	1165



```
Db 1197 ymptqfqtctgtkimenkmccltv 1221
|||||
RESULT 8
AAW34499
ID AAW34499 standard; protein; 970 AA.
XX
AC AAW34499;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor C protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 959 /label= unknown
FT /note= "encoded by stop codon"
XX
PN WO9725424-A1.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
PI Chang M, Fletcher FA, Welcher AA;
XX
DR WPI; 1997-384981/35.
DR N-PSDB; AAT98530.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 2; Page 72; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor C protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 970 AA;

Query Match 77.3%; Score 4831.5; DB 18; Length 970;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

QY 1 MICQFCVVLHWEFIYVITAFNLSTPTPWRKLSCMPNSTYDYFLLPAGLSKNTS 60
Db 1 micqfcvvlhwefiyvitafnlstptpwrklscompnstydyfillpaglsknts 60
QY 61 NGHYETAVEKFNSSGTHFSNLSKTPHCPRSEODRNCSLCADNIEGKTFVSTVNSLV 120
Db 61 nghyetavekfnssgthfnslnsktphcprseodrnscslcadniegkktfstvnslvf 120
QY 121 QOIDANWNIQGWLKGDLKLFICYVESLFRNLYRNYKVHLVLPVLEDSPLVPQKGS 180
Db 121 qoidanwniqgwlkgdlklficyveslfrnlyrnykvhlvlpvledsplvpqkgs 180
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```
QY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLKCLKITSQGVIFQSPILMSVQPINMKPDP 240
Db 181 fgmvhcnscsvhececlvpvptaklndtlkclkitsqgvifqspilmsvqpinmvpkdpdp 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLQYQVYKSENSTTVIREADKIVSATSLLDVSLP 300
Db 241 lglhmeitddgnlkswsppplvpfpplqyqvkyseenttviireadkivsatslldvslp 300
QY 301 GSSYEQVRGKRDLGPGIWSDMSTPRVFTTQDVLYFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 gssyevqvrgrldgpgiwsdstprvfttqdvlyfppklltsvgsnvsfhcltykkenki 360
QY 361 VPSKEIVMMNLAEKIPQSYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeivwmnlakqipsgydvdsdhvskvtfnltnetkprgkftydavycnehechh 420
QY 421 RYAEIYVIDVNNISCE TDGYLTRKMTCRMSTSTIQSLAESTLQRLRHRSLLYCS DIPSIH 480
Db 421 ryaelyvldvnniscedtdgyltrkmtcrwststiqslaestlqlryhrsslycsdipsih 480
QY 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMIRINHSLSGLSDSPICVLPDSVVKPLPP 540
Db 481 pisepkdcylqsdgfyecifqpfifllsgytmirinhslsglsdspdpcvlpdsvvpklpp 540
QY 541 SSVKAEITINIGLKLISWEKVPFPENNIOQIRYGLSGKEVQWKMEVYDAKSYSVSLPV 600
Db 541 ssvkaeittinigllkliswekvpfpennioqirylsgkevqwkmevydaksksvslpv 600
QY 601 PDLCAVYAVQYRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFVITINGDTMKKEKNV 660
Db 601 pdlcavayavqrckrldglgywsnwsnpaytvmdikvpmrgpefvtlingdtmkkekvn 660
QY 661 TLWKPLMKNDLSQVQRYVINNHTSCNGTWSQSDVGNHTKFTPLNTEQAHTVTLAINSI 720
Db 661 tlwkplmkndlsqvgryvinhntscngtwsedvgnhtkftplntegahvtvtaainst 720
QY 721 GASVANFNLTFSWPMKSVNIVQSLAYPLNSSCVIVSWILSPSDYKLMFTIEMKNLNE 780
Db 721 gasvanfnltfswpmksvniqvslsayplnsscvivswilspdyklmfyiemknlne 780
QY 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 geikwlri:ssvkkyyihdhfipiekyslypifmegvgkpkinsftqddiekhsda 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSMAQGLNEOK-----PE 893
Db 841 glyvivpvi:sssillgltllishqrmklfwedvnpknkcswaeglntfkmlegsmfvk 900
QY 894 TFEHLFIKHT-ASVTGP-----LLLEPETISEDTSVDTSMKNKDE 933
Db 901 shhslsistqghkhcgrpgpplrktirdclslylltllppllsydpakpsavrvntqe 958

RESULT 9
AAW24052
ID AAW24052 standard; Protein; 896 AA.
XX
AC AAW24052;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human WSX receptor variant 6.4.
XX
KW Human; WSX receptor; variant 6.4; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
```

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XX WO9725425-A1.
PN
XX 17-JUL-1997.
PD
XX
XX 07-JAN-1997; 97WO-US00325.
PF
XX 20-JUN-1996; 96US-0667197.
PR 08-JAN-1996; 96US-0585005.
XX
XX (GETH ) GENENTECH INC.
PA
XX Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
PI
XX WPI; 1997-372864/34.
DR N-PSDB; AAT85576.
XX
XX MSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
PS Claim 2; Pages 86-89; 219pp; English.
XX
XX The present sequence is the human MSX receptor variant 6.4,
CC which can be used to identify and purify ligands and activators.
CC An anti-MSX receptor antibody can be used as an agonist to activate
CC the MSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the MSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. MSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
XX Sequence 896 AA;
SQ
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Query Match 77.2%; Score 4826; DB 18; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICOKFCVLLHWEFIYVITAFNLSTPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60
Db 1 micqkfcvllhweifyvitafnlstypitpwrfklscompnstydyfllpaglsknsns 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
Db 61 nghyetavepkfnssgthfnslnskttfhccfrseqdrcnslcadniegkttfvstvnslvf 120
QY 121 QOIDANMNIOQWLKGLDKLFICIVESLFLKNLFRNRYKVVHLLVLPVLEDSPLVPQGS 180
Db 121 qqidanwniqcwlkgdlkificyveslflknlfrynrykvhllvlpvledsplvpqgys 180
QY 181 FOMVHCNCSVHECCCLVPVPYPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMKPDP 240
Db 181 fgmvhcnscsvheccclvpvptaklndtlmlclkitsqgvifqspilmsvqpinmkpdp 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPEPLOYOVKYSNSTVYIREADKIVSATSLVDSILP 300
Db 241 lglhmeitddgnlkiwswspplvpeployovkysnstvrireaddkivsatslvdsilp 300
QY 301 GSSYEYQVGRKRLDGPITWSDMSTPRVFTTQDVIVFPFKILTSVGSNVSFHCITYKENKI 360
Db 301 gssyeyqvgrkrlldgpitwsdmsprvfttqdvivfpfkiltsvgnsvfhciykenki 360
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QY 361 VPSKEIWMNMNLAERIPQSOYDVSDHVSQKYTFNLTNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 vpskeiwmnmnlaekipqsydvdsdhvskvtfnlnetkprgkfttydavycnehechh 420
QY 421 RYAEIYVIDVNNINISCEITDGYLT/KMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480
Db 421 ryaeliyvidvnniniscedtgylltkmtrwststlqslaestllqlyhrsslycsdipsih 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylqsdgfyecifqipifllsgytmirinhslsglsdspptcvlpdsvvpklpp 540
QY 541 SSVKAEITINIGLKIWEKVPPENNLOFIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 541 ssvkaeitiniglkiswekvppennlofiryglsgkevqwkmyevydaksksvslpv 600
QY 601 PDLCAVYAVOVRCKRDLGIGYWSNMSNPATVVMIDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavyavvrckrldglgywsnmsnpaytvmidikvpmrgpelwrlingdtmkkeknv 660
QY 661 TLLMKPLMKNDSLCSQVRVINHTSCNGTWSQEDVGNHTKFTFLNTEQAHVYVLAINSI 720
Db 661 tllmkplmkndslcsqvrvinhntscngtwsedvgnhtkftflwteqahvylaansi 720
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLNE 780
Db 721 gasvanenlftswpmskvnivqslsayplnsscviyswilspsdyklymfieknlned 780
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 geikwlri:sssvkkyihdhfipiekyslypifmegvgkpkinsftqddiekhsda 840
QY 841 GLYIVPVIISISILLGLTLLISHQRMKLLFWEVDVNPKNCSWAQGLNFQK 891
Db 841 glyivpviissillgltilishqrmkllfwevdvnpknscswaqglnfqk 891
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RESULT 10  
AAW24053  
ID AAW24053 standard; Protein; 923 AA.  
XX  
AC AAW24053;  
XX  
DF 17-MAR-1998 (first entry)  
XX  
DE Human MSX receptor variant 12.1.  
XX  
KW Human; MSX receptor; variant 12.1; identification; purification;  
KW ligand; activator; antibody; agonist; proliferation; obesity;  
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;  
KW Type II diabetes; polycystic ovarian disease;  
KW cardiovascular disease; osteoarthritis; dermatological disorder;  
KW hypertension; insulin resistance; hypercholesterolaemia;  
KW hypertriglyceridaemia; cancer; cholelithiasis.  
XX  
OS Homo sapiens.  
XX  
PN WO9725425-A1.  
XX  
PD 17-JUL-1997.  
XX  
PF 07-JAN-1997; 97WO-US00325.  
XX  
PR 20-JUN-1996; 96US-0667197.  
PR 08-JAN-1996; 96US-0585005.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;  
PI Rodrigues ML;  
XX  
DR WPI; 1997-372864/34.

DR N-PSDB; AAT85577.  
XX  
PT WSX receptor and related antibodies and ligands - used to develop  
PT products for diagnosis and therapy, e.g. for improving  
PT haematopoiesis or for treating tumours  
XX  
PS Claim 2; Pages 89-93; 219pp; English.  
XX  
CC The present sequence is the human WSX receptor variant 12.1,  
CC which can be used to identify and purify ligands and activators.  
CC An anti-WSX receptor antibody can be used as an agonist to activate  
CC the WSX receptor, leading to enhanced proliferation or  
CC differentiation of a cell expressing the WSX receptor. It can also  
CC be used to decrease body weight and/or fat-depot weight and/or food  
CC intake in an obese mammal. WSX receptor ligands can be used to  
CC enhance proliferation or differentiation of lymphoid, myeloid or  
CC erythroid blood cell lineages. This is useful when a mammal,  
CC especially a human, is suffering from decreased blood cell levels,  
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone  
CC marrow transplantation therapy. It can also be used to repopulate  
CC blood cells in a mammal. The products can also be used to treat,  
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,  
CC polycystic ovarian disease, cardiovascular diseases,  
CC osteoarthritis, dermatological disorders, hypertension, insulin  
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer  
CC and cholelithiasis.  
XX  
XX Sequence 923 AA;  
SQ

Query Match 77.2%; Score 4826; DB 18; Length 923;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICRRCVVLHWEFIYVITAFNLSYPTPWRFKLSQMPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 micrkcfcvllhweilyvitafnlsyptpwrfklsqmpnstydyfllpaglskntns 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 nghyetavepkfnssgthfnslnskttfhccfrseodrnscslcadniegkftfstvnslvf 120  
QY 121 QQIDAMNIOQWLKGDCLKFCICYESLFLKLFNRYNKVHLVLPVLEDSPLVPQKS 180  
Db 121 qqidanwniqcwlkgdclkficyeslflklnfrnykvhllylpevledsplvpqkgs 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKINDTLMLCLKITSGGVIFQSPLMVQPIIMVKKPDP 240  
Db 181 fgmvhcnscsvheccclvpvptakindtlmlclkitsgvlifqspimsvqipimvkkpdp 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVFPPLQYQVKYSENSTTVIREADKIVSATSLVDSILP 300  
Db 241 lglhmeitddgnlkiswsspplvfpplqyqvkysesttvireadkivsatsllvdsilp 300  
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 gssyeqvrgrldgpglswdsprvfttqdvlyfppkiltsvgsnvsfnciykknki 360  
QY 361 VPSKEIYVWNNLAEKIPQSQYDVVSDHVSQVTFNLTNETKPRGKFTYDAYVCCNEHECHH 420  
Db 361 vpskeiyvwmnlaekipqsgydvvsdhvskvtffnlnetkprgkftdayvcnehechh 420  
QY 421 RYAEIYVIDVNNINISCEIDGYLTKMTCRWSTSTIQSLAESTLQLRHRSRLYCS DIPSIH 480  
Db 421 ryaeliyvidvnniniscedgyltkmcrwststisqlaestlqlrhrssrlycsdipsh 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPTCVLPDSVVKPLPP 540  
Db 481 pisepkdcylqsdgfyecifqpfllsgytmwirinhsrlsglsdpsptcvlpdsvvkplpp 540  
QY 541 SSVKAEITINIGLTKISWEKVPENNLOQOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 541 ssvkaeitinigltkiswekvpennlqfqlirylsgkevqwkmyevydaksksvslpv 600

QY 601 PDLCAVAVQVRCRLDGLGYSNMSNPAYTVVMDIKVPMGDEFWRIINGDTMKKEKNV 660  
Db 601 pdlcavavqvrckrldglgysnmsnpaytvvmdikvpmgdefwriingdtmkkeknv 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWESEVDGNHTKFTFLNTEQAHVTVLAINSI 720  
Db 661 tllwplmkndslcsvqryvinhtscngtwsedvgnhtkftflwteqahvtvlainsi 720  
QY 721 GASVANFNLTFSWPMKSVKNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 gasvanfnltfswpmksvknivqslayplnsscvivswilspdyklmyfiemknlne 780  
QY 781 GEIKMLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 781 geikmlrissvkkyyihdhfipiekysfslypifmegvgkpkkinsftqddiekhsda 840  
QY 841 GLYVAVPYIISILLGTLTISHQRMKKLWEDVPPNPKNGSMAOGLNFOK 891  
Db 841 glyvavpyiissillgtlshqrmkklfwedvpnpknsgswaaglnfoqk 891

RESULT 11  
AAW34497  
ID AAW34497 standard; protein; 972 AA.  
AC AAW34497;  
XX  
DT 18-MAR-1998 (first entry)  
XX  
DE Obesity receptor A protein.  
XX  
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;  
KW high blood lipid level; obesity; diabetes; high cholesterol level;  
KW weight loss; therapy; weight maintenance.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 897 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 919 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 925 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 939 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 948 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 952 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 971 /label- unknown  
FT /note- "encoded by stop codon"  
PN WO9725424-A1.  
XX 17-JUL-1997.  
PD  
XX  
PE 02-JAN-1997; 97WO-US00128.  
XX  
PR 31-DEC-1996; 96US-0774414.  
PR 04-JAN-1996; 96US-0582825.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Chang M, Fletcher FA, Welcher AA;

XX WPI: 1997-384981/35.  
DR N-PSDB; AAT98528.  
XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight  
PT disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels  
XX  
PS Claim 1; Page 64; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor A protein. This  
CC sequence has one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 972 AA;

Query Match 77.2%; Score 4826; DB 18; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MICOKFCVLLHWEIYITAFNLSPITPWRFKLSGMPNSTYDYFLPAGLSKNSNS 60  
DB 1 micqkfcvllhweifyitafnlslpypwrflksmpnstydyflpagslksnts 60  
OY 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGTFVSTVSLVF 120  
DB 61 nghetavepkfnssgthfnsksktfhccfrseqdrcnscadniegktfstvsnslvf 120  
OY 121 QOIDANMNIIQCMWLGDLKIFIGYVESLFEKNLFRNRYKVHLLVLPVLEDSPLVPQGS 180  
DB 121 qoidanmniiqcmwlgdlkifigyseslfeknlfrnrykvhllvlpvledsplvpqgs 180  
OY 121 qgidanwniqcmwlgdlkifigyseslfeknlfrnrykvhllvlpvledsplvpqgs 180  
OY 181 FQWVHCNCSVHECCCLVPEVPTAKLNDTLMLCKITSGVIFQSPMLMSVOPINWVPRDP 240  
DB 181 fgmvhcnscsvheccclvpevptaklndtlmlckitsgvifqspmlmsvopinwvprdp 240  
OY 241 LGLHMEITDDGNLKIWSPPPLVPELOYOXVYSENSTVIREADKIVSATSLVDSILP 300  
DB 241 lglhmeitddgnlkiwsppplvpplpoyoxvyseinstvireadkivsatslvdsilp 300  
OY 301 GSSYEVOVRGKRLDGPFIWSDMSTPRVFTTQDVIFPPKILTVSGSNVSFHCITYKKENKI 360  
DB 301 gssyevovrgkrlldgpfiswdsstprvfttdvifppkiltvsgsnvsfhciykkenk 360  
OY 361 VPSKEIWMNMNLAEKIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 vpskeiwmnmnlaekipqsgydvsvdhvskvtfenlnetkprgkftydavycnehech 420  
OY 421 RYAEIYVIDVNNINISCEIDGILTKMTCRWSTSTIOSLAESTLQRYHRSSLYCSDIPSIH 480  
DB 421 ryaelyvidvnninisceidqyltkmtrwststioslaestlqlyhrsslycsdipsih 480  
OY 481 PISEPKDCYLOSDFEYECIFQPIFLISGYTWMIRINHSIGLSDSPTCVLPDSVVKPLPP 540  
DB 481 pisepkdcylsdfeyecifqpfiflisgytmwirinhsiglsdpsptcvlpdsvvkplpp 540  
OY 541 SSVKAEITINIGLKIWSKPEVPENNLOFOIRYGLSGKEVQWKMVEVYDAKSKSVSLPV 600  
DB 541 ssvkaeitiniglkiwskepvepennlofoirylsgkevqwkmyevydaaksksvslpv 600  
OY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRITINGDTMKKENV 660  
DB 601 pdlcavayavvrckrldglgwsnmsnpatytvmdikvpmrgpefwrirtingdtmkkenv 660  
OY 661 TLLMKPLMKNDLSLCSVQRIYINHTSCNGTWSSEDCVGNHTKFTFLMTBOAHYTVLAINSI 720  
DB 661 tllmkplmkndslslcsvqriyinhtscngtwssedcvgnhtkftflmtboahyvtvlainsi 720

OY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 gasvanenlftswpmskvnivqslaysayplnsscvivswilspdyklymyfielwknlned 780  
OY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
DB 781 geikwlri:sssvkkyihdhfi:piekyqfsl:yplfme:vgkpk:insftqdd:iekhsda 840  
OY 841 GLYVIVPVIISSSIIIGTLLISHORMKFLFWEVDPNPKNSWAQGLNFQK 891  
DB 841 glyvivpvil:ssslllgllishqrmkklf:wedvpnpkn:cswaqgl:nfqk 891

RESULT 12

AAW34498  
ID AAW34498 standard; protein; 999 AA.  
XX  
AC AAW34498;  
XX  
DT 18-MAR-1998 (first entry)  
XX  
DE Obesity receptor B protein.

XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;  
KW high blood lipid level; obesity; diabetes; high cholesterol level;  
KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 905 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 933 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 971 /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 988 /label- unknown  
FT /note- "encoded by stop codon"

PN W09725424-A1.

PD 17-JUL-1997.

PF 02-JAN-1997; 97WO-US00128.

PR 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

PI Chang M, Fletcher FA, Welcher AA;

XX WPI: 1997-384981/35.

DR N-PSDB; AAT98529.

XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight  
PT disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels

PS Claim 2; Page 68; 151pp; English.

XX  
CC This sequence represents the obesity (OB) receptor B protein. This  
CC sequence has one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.

SO Sequence 999 AA:

Query Match 77.2%; Score 4826; DB 18; Length 999;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFYVITAFNLSYPTTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 micqkfcvllhweifyvitafnlsypttpwrfrklscompnstydyfllpaglskntsns 60  
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 nghyetavepkfnssgthfnslnskttfhccfrseqdrcnslcadniegkttfstvnslvf 120  
QY 121 QOIDANWNIQCWLKGLKLFICYVESLEFKNLERNYKVVHLLVLEPELSDPLVPQKGS 180  
DB 121 qqidanwniqcwlkgdklficyveslfknlfrrnykvhllylpevledsplvpqkgs 180  
QY 181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKPDP 240  
DB 181 fgmvhncnsvhceccclvpvptaklndtllmclkitsgvifqspplmsvqpinmkpdp 240  
QY 241 LGLHMETDDGNLTKISWSSPPLVPFLOQYQVKYSENSTVIREADKIVATSLSLVDSILP 300  
DB 241 lglhmeitddgnlkwsspplvpfloqyqvkysenstvirreadkivsatsllvdsilp 300  
QY 301 GSSYEVOYRGKRLDGPISDWSPTPVTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 gssyevoyrgkrlldgpiisdwstptvttqdvityfppkiltsvgsnvsfhciykkenki 360  
QY 361 VPSKEIYVMMNLAEKIPQSQYDVAVSDHVSQVTFPNLNETKPRGKFTYDAYVCCNEHECH 420  
DB 361 vpskeiyvmmnlakeipqsqydvavsdhvsqvtfplnetkprgkftydayvccnehech 420  
QY 421 RYAEIYVDVNNINISCESTDGYLTAKTCRMWSTSTIOSLAESTLOLRHRSLSYCSDIPS 480  
DB 421 ryaeliydvnniniscetdgyltaktcrmwststioslaestlolrrhsslycsdips 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTWMIRINHSLSGSDSPPTCVLPDSVVKPLP 540  
DB 481 pisepkdcylqsdgfyecifqipflisgytwmirinhslsgsdspptcvlpdsvvkplp 540  
QY 541 SSVKAEITINIGLTKISWEKPVFPPENLQFQIRYGLSGKEVQWMEVYDAKSKSVSLPV 600  
DB 541 ssvkaeitinigltkiswekpvfppenlqfqiiryglsgkevqwmeyvdaaksksvslpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNNSNPATTVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660  
DB 601 pdlcavayavqrckrldglgywsnnsnpattvmdikvpmrgpefwrriingdtmkkeknv 660  
QY 661 TLLMKPLMKNDLSQVQRYVINNHNTSCNGTWSSEVDGNHTKFTFLTEQAHTVTVLAINSI 720  
DB 661 tllmkplmkndlsqvqryvinnhntscngtwssevdgnhtkftflteqahtvtvlainssi 720  
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIIEKMLNED 780  
DB 721 gasvanfnltfswpmksnivqslayplnnsccvsvswilspdyklymyfiiekwmlned 780  
QY 781 GEIKWLRISSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 geikwlriSSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLSHQRMKLLFWEDEVNPNPKNSWAQGLNFOK 891  
DB 841 glyvivpviSSSILLGLTLLSHQRMKLLFWEDEVNPNPKNSWAQGLNFOK 891

RESULT 13  
AAW38214  
ID AAW38214 standard; Protein; 958 AA.  
XX  
AC AAW38214;

XX 11-JUN-1998 (first entry)  
XX Human OB-R variant Form 1.  
DE  
XX Detection; defective obese protein receptor; defective OB-R; human;  
KW defective leptin receptor; variant Form 1; infertility.  
XX Homo sapiens.  
OS  
XX WO9741263-A1.  
PN  
XX 06-NOV-1997.  
PD  
XX 28-APR-1997; 97WO-US07676.  
PE  
XX 29-APR-1996; 96US-0640389.  
PR  
XX (PROG-) PROGENITOR INC.  
PA  
XX Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;  
PI WPI; 1997-549757/50.  
PT N-PSDB; AAT95779.  
DR  
XX Detecting defective obese protein or leptin receptor in reproductive  
PT cells - using variant receptor gene specific probes  
XX  
XX Disclosure; Fig 3; 40pp; English..  
XX  
XX The present sequence was used in the development of a novel method  
CC for detecting a defective obese protein or leptin receptor (OB-R)  
CC in cells. This method comprises contacting RNA extracted from a  
CC cell population (preferably an ovary, prostate, testis, sperm, ova,  
CC ovarian follicular or blood cell population) with an  
CC oligonucleotide derived from a portion of the human OB-R variant  
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are  
CC associated with infertility, as they are unable to correctly  
CC transduce signals from leptin binding. The detection method can be  
CC used to diagnose infertility, or predisposition to infertility,  
CC while treatments that inhibit or down regulate the variants, gene  
CC therapy to replace them in homozygotes or direct activation of  
CC downstream signal transduction can be used to improve fertility.  
CC Also described is the use of labelled DNA probes based on the OB-R  
CC sequence to screen for other variants.  
CC  
XX  
XX Sequence 958 AA:

Query Match 77.1%; Score 4819.5; DB 18; Length 958;  
Best Local Similarity 94.1%; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFYVITAFNLSYPTTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 micqkfcvllhweifyvitafnlsypttpwrfrklscompnstydyfllpaglskntsns 60  
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 nghyetavepkfnssgthfnslnskttfhccfrseqdrcnslcadniegkttfstvnslvf 120  
QY 121 QOIDANWNIQCWLKGLKLFICYVESLEFKNLERNYKVVHLLVLEPELSDPLVPQKGS 180  
DB 121 qqidanwniqcwlkgdklficyveslfknlfrrnykvhllylpevledsplvpqkgs 180  
QY 181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKPDP 240  
DB 181 fgmvhncnsvhceccclvpvptaklndtllmclkitsgvifqspplmsvqpinmkpdp 240  
QY 241 LGLHMETDDGNLTKISWSSPPLVPFLOQYQVKYSENSTVIREADKIVATSLSLVDSILP 300  
DB 241 lglhmeitddgnlkwsspplvpfloqyqvkysenstvirreadkivsatsllvdsilp 300



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QY 301 GSSYEYVQVRGKRLDGPGLWSDMSTPRVFTQDVLYEPFKILTSVGSNVSEFCIKYKKNKI 360
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Db 301 gssyeqvrvgrldgpglwsdstprvftcqvdyfppkiltsvgsnvsefcikykknki 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVCCNEHECHH 420
    |||
Db 361 vpskeivwmmnlakipsgydvsvdhvskvtfenlnetkprgkftdyavccnehechh 420
QY 421 RYAEIYVIDVNIINISCTEDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCDIPSIH 480
    |||
Db 421 ryaelvidvniiniscetdgyltkmtcrwststiqslaestlqlrhrsslycsdipsih 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCLPDSVVKPLPP 540
    |||
Db 481 pisepkdcylsqdgfyecifqpfllsgytmwirinhslyslsdspptclpdsvvpklpp 540
QY 541 SSVKAEITINIGLIKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
    |||
Db 541 ssvkaeitniglikiswekvpfpennlofqirylsgkevqwmveydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
    |||
Db 601 pdlcavayavvrckrldglgywsnmsnpatvymdikvpmrgpefwringdtmkkekuv 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEVGNHTKFTPLMTEQAHRYVLAINSI 720
    |||
Db 661 tllmkplmkndlsqvqryvinhtscngtsevgnhtkftplmteqahrvlainsi 720
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSCVIWSILSPSDYKIMYFIEMKNLNE 780
    |||
Db 721 gasvanfnltfswpmkvnivqslayplnscv iwswilspdykilmfyiemknlne 780
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
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Db 781 geikwlri:sssvkryihdhfipiekqfslypifmegvgkpkilnsftqddiekhsda 840
QY 841 GLYVIVPVISSSILLGLLISHQRMKTLFWEDEVNPNKNCWAGLNFQK-----PE 893
    |||
Db 841 glyvivpvi:sssillgl:llishqrmk:tlfwe:dev:pn:kn:cw:ag:ln:fm:qk:leg:sm:fv:k 900
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSMKNKDE 933
    |||
Db 901 shhslisstqghkncgrpgpplrhrktrdicslylltllppllsydpakspsvrntqte 958

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RESULT 14
AAW31911
ID AAW31911 standard; Protein; 958 AA.
XX
AC AAW31911;
XX
DT 02-FEB-1998 (first entry)
XX
DE Human OB-R leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 85 /note- "variation from published sequence"
FT Misc-difference 109 /note- "variation from published sequence"
FT Misc-difference 223 /note- "variation from published sequence"
FT Domain 845..862 /label- Transmembrane_domain
FT Misc-difference 892..938 /note- "divergence from published sequence"
XX
PN W09726370-A1.

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XX
PD 24-JUL-1997.
XX
PF 17-JAN-1997; 97WO-US00570.
XX
PR 18-JAN-1996; 96US-0588190.
XX
PA (PROG-) PROGENITOR INC.
XX
PI Cioffi J, Shafer AW, Snodgrass HR, Zupancic TJ;
XX
DR WPI; 1997-385353/35.
XX
DR N-PSDB; AAT89193.
XX
PT Detecting defective leptin receptor by hybridisation assay - and
PT receptor, also screening for compounds that inhibit the defective
PT activity
XX
PS Claim 12; Fig 1A-E; 26pp; English.
XX
CC This polypeptide comprises a variant of the human leptin receptor
CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
CC derived from overlapping clones isolated from a human foetal liver
CC library. The sequence shows near identity to a published OB-R
CC sequence in the extracellular domain, with the exception of 3 amino
CC acids, but there is extensive diversity in the intracellular
CC cytoplasmic domain at the C-terminal end. A claimed method for
CC detection of OB-R in cells comprises extraction of RNA and testing
CC this for hybridisation to an oligonucleotide (1) derived from the
CC OB-R variant gene, especially from the region beyond nucleotide
CC 2770. Also claimed are methods of: (1) treating obesity by
CC administration of an agent that inhibits expression of the OB-R
CC variant gene; and (2) identification of a compound that can
CC supplement activity of leptin by: (1) incubating cells expressing
CC OB-R variant first with leptin and then with a test compound, and
CC (11) comparing activation signals between cells treated and not
CC treated with the test compound. Inhibition/down-regulation of the
CC variant OB-R (found in obese people) improves response of cells to
CC weight regulation by leptin. Replacing variant OB-R by gene therapy
CC (in homozygous individuals) can be used to treat obesity. Labelled
CC probes based on the gene can be used to isolate other variant forms
CC of the receptor gene or to detect the variant gene (e.g. for
CC determining predisposition to obesity), while the OB-R gene can be
CC used to express recombinant OB-R (optionally as fusion protein) and
CC in standard hybridisation assays. The OB-R gene can also be used
CC therapeutically in cases of overexpression of functional OB-R
CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.
XX
SQ Sequence 958 AA;

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Query Match 77.1%; Score 4819.5; DB 18; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

```

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QY 1 MICOQFCVLLHWEFIYVTAENLSYPTTPWRFKLSGMPNSTYVFLPAGLSKNTSNS 60
    |||
Db 1 micqkfcvllhwe:fiyta:enlsy:pttpwr:fk:ls:gm:pn:st:yv:fl:pa:gl:sk:nt:sn:s 60
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADHIEGKTFVSTVNSLVF 120
    |||
Db 61 nghyeta:pepkfn:ssgth:fsn:lsk:ttf:hcc:fr:se:qd:rn:cs:lc:ad:hie:gt:fv:st:vn:sl:vf 120
QY 121 QOIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLYVLPVELDSDPLVPQKGS 180
    |||
Db 121 qoidanwniqcwlkglk:lficy:vesl:fk:nl:fr:nry:kv:hll:yv:lp:vel:ds:pl:vp:qk:gs 180
QY 181 FQMVHCNCSVHECCELVPEPTAKLNDTLMLCKITSGCVIFQSPILMSVQPIINWVKPDPP 240

```



```
|||||
Db 61 nghyetavepkfnsgthfnlskcatfhccfrsegdncslcadniegrtfvstvnsivf 120
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QY 241 LGLHMEITDDGNLKISWSSPPLVPPLQYQVYSENSTVIREADKIVSATSLVDSILP 300
Db 241 lglhmeitddgnlkiswsspplvplqyqvkysestlvireadkivsatslvdslp 300
QY 301 GSSYEVQVRGKRLDGPGIWSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
Db 301 gssyevqvrgrldgpgiwsdmstprvfttqdvlyfppklltsvgsnvsfhclykknk 360
QY 361 VPSKEIWMWMLAEKIPQSQYDVVSDHVSXVTFPMLNETKPRGKFTYDAVYCCNEHCCH 420
Db 361 vpskeiwmwmlaekipqsgydvvsdhvskvtfpmlnetkprgkftydavycnech 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCRMSTSTIOSLAESTLOLRHRSIYCSIDIPSIH 480
Db 421 ryaelvidvniiniscetdgyltmtcrwststiqslaestlqlrhrslycsdipsih 480
QY 481 PISEPKDCYLOSDFYECIFQPIFLLSGYFMWIRINHSLSGLDSPPTCVLPDSVVKPLP 540
Db 481 pisepkdcylsgdfyecifqipifllsgyfmwirinhsisglsdspptcvlpdsvvpklp 540
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Db 541 ssvkaeitiniglkiswekvpfpennlqfdiryglsgkevqwkmyevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSMNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKENV 660
Db 601 pdlcavayavvrckrldglgywsnspaytlvmdlkvpmrgpewrlingdtmkkenv 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHTSCNGTWESEDVGNHTKFTLWTEQAHVTVLAINST 720
Db 661 tllwkpmlkndslcsvqryvinhtscngtwsedvgnhtkftlwteqahvtvlainst 720
QY 721 GASVANFNLTFSWPMKYNIVQSLASAYPLNSSCVIYVSWILSPSDYKLMYFIIEWKNLND 780
Db 721 gasvanfnltfswpmkynivqslasayplnsscvlyvswilspdyklymyfiiewknlnd 780
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Db 781 geikwlri:sssvkyyihdhfipiekyslypifmegvgkpkiiinsftqddiekhgsda 840
QY 841 GLYVIVPVIISSSILLLGLLISHQRMKLLFWEDVPNPKNCSWAQGLNFQK-----PE 893
Db 841 glyvivpviisssilllglilishqrmkllfwedvpnpknscswaqglnfqkmlsgsfvk 900
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933
Db 901 shhsllsstgqhkcgfpgpplhrktrdlslyllitlppllsydpakspsvrntge 958
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Job time: 5693 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 06:47:52 ; Search time 230.02 Seconds  
(without alignments)  
1782.703 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICQKFCVLLHMEFTVIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	6254	100.0	1165	9	US-08-585-005-2
4	6254	100.0	1165	10	US-08-638-524B-4
5	6254	100.0	1165	10	US-08-667-197-2
6	6254	100.0	1165	11	US-08-708-123D-4
7	6254	100.0	1165	11	US-08-779-457-2

8	6254	100.0	1165	11	US-08-780-562-2	Sequence 2, Appli
9	6254	100.0	1165	14	US-09-094-410-4	Sequence 4, Appli
10	6254	100.0	1165	15	US-09-137-132-4	Sequence 4, Appli
11	6254	100.0	1165	23	US-09-950-149-4	Sequence 4, Appli
12	6254	100.0	1216	11	US-08-774-414-7	Sequence 7, Appli
13	6254	100.0	1216	20	US-09-671-049-7	Sequence 7, Appli
14	6247	99.9	1167	23	US-09-948-933-284	Sequence 284, App
15	6247	99.9	1167	23	US-09-948-947-87	Sequence 87, Appl
16	6246	99.9	1165	9	US-08-599-974C-56	Sequence 56, Appl
17	6246	99.9	1165	11	US-08-713-296-11	Sequence 11, Appl
18	6246	99.9	1165	13	US-08-961-809-4	Sequence 4, Appli
19	6246	99.9	1165	15	US-09-178-691-4	Sequence 4, Appli
20	6246	99.9	1165	21	US-09-700-813-10	Sequence 10, Appl
21	6246	99.9	1165	23	US-09-948-933-256	Sequence 256, App
22	6246	99.9	1165	23	US-09-948-947-73	Sequence 73, Appl
23	6246	99.9	1165	24	US-10-095-929-11	Sequence 11, Appl
24	6240	99.8	1165	9	US-08-583-153-4	Sequence 4, Appli
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26	6240	99.8	1165	10	US-08-638-524A-4	Sequence 4, Appli
27	6240	99.8	1165	11	US-08-708-123C-4	Sequence 4, Appli
28	6240	99.8	1165	12	US-08-864-564A-4	Sequence 4, Appli
29	6240	99.8	1165	24	US-10-079-625-4	Sequence 4, Appli
30	6236	99.7	1165	9	US-08-570-142B-4	Sequence 4, Appli
31	6236	99.7	1165	9	US-08-570-142C-4	Sequence 4, Appli
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33	6032	96.5	1137	9	US-08-569-485-4	Sequence 4, Appli
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36	4831.5	77.3	969	9	US-08-582-825A-5	Sequence 5, Appli
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43	4826	77.2	896	9	US-08-585-005-3	Sequence 3, Appli
44	4826	77.2	896	10	US-08-667-197-3	Sequence 3, Appli
45	4826	77.2	896	11	US-08-779-457-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1

US-08-570-142D-4

Sequence 4, Application US/08570142D

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

TITLE OF INVENTION: OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/570,142D

FILING DATE: 11-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622



FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meikie John, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-570-142D-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFTYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHWEFTYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120  
DB 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVF 120  
QY 121 QOIDANWNICWLKGLKLFICYVESLFEKLFNFRNRYKVLHLLVLPVELEDSPLVPQKGS 180  
DB 121 QOIDANWNICWLKGLKLFICYVESLFEKLFNFRNRYKVLHLLVLPVELEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINWKPDP 240  
DB 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINWKPDP 240  
QY 241 LGLHMEITDDGNLKSISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLLVDSILP 300  
DB 241 LGLHMEITDDGNLKSISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 360  
DB 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVLYFPFKILTSGVSNVSPHCITYKKENKI 360  
QY 361 VPSKEIWMNMNLAEKIPQSQYDVSDHVSQVFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIWMNMNLAEKIPQSQYDVSDHVSQVFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSLCSDDIPSIH 480  
DB 421 RYAEIYVIDVNNISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSLCSDDIPSIH 480  
QY 481 PISEPKDCYLOSDGYECIFQPIFLLSGYTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDGYECIFQPIFLLSGYTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKSWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKSWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLNGDITMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLNGDITMKKEKNV 660  
QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHVTVLAINSI 720  
DB 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSVNIVQSLASAPPLNSSCVIVSWILSPSDYKLMFTIEKKNLND 780  
DB 721 GASVANFNLTFSWPMKSVNIVQSLASAPPLNSSCVIVSWILSPSDYKLMFTIEKKNLND 780  
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSTQDDIEKHQSDA 840  
QY 841 GLYIVPVISSSTILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFOKPEFHEHFLI 900  
DB 841 GLYIVPVISSSTILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFOKPEFHEHFLI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVSLSTTDLEKGSVCISDOFN 960  
DB 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVSLSTTDLEKGSVCISDOFN 960  
QY 961 SVNFSEAGTEVYEDESQROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAGTEVYEDESQROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEAFAFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080  
DB 1021 KDSFSSNSWEIEAFAFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLITDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
DB 1081 GVTSIKKRESGVLITDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 2  
US-08-583-153A-4  
Sequence 4, Application US/08583153A  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meikie John, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-583-153A-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSCLMPNSTYDYFLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSCLMPNSTYDYFLPAGLSKNTS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLKFLTCYVESLFKNLFRNYNYKVHLLVYLPEVLDSPLVPQKGS 180  
Db 121 QOIDANMNIOQWLKGLKFLTCYVESLFKNLFRNYNYKVHLLVYLPEVLDSPLVPQKGS 180  
QY 181 FQVYHNCVSHECCCLVPPVPAKINDTLLMCLKITSGGVTFQSPILMSVQPINMVKPDP 240  
Db 181 FQVYHNCVSHECCCLVPPVPAKINDTLLMCLKITSGGVTFQSPILMSVQPINMVKPDP 240  
QY 241 IGLHMEITDDGNLKSWSPLVPFLQYQVKYSENSTVIRADKIVATSLSLVDSILP 300  
Db 241 IGLHMEITDDGNLKSWSPLVPFLQYQVKYSENSTVIRADKIVATSLSLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPGLMSDMSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVQVRGKRLDGPGLMSDMSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKETIWMNLAEKIPQSQDYVSDHVSQVTFNLTNETKRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKETIWMNLAEKIPQSQDYVSDHVSQVTFNLTNETKRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDYNINISCTDGYLTKTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDYNINISCTDGYLTKTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCYLPDSVVKPLRP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCYLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISWEKPYFPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISWEKPYFPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYMSNNSPAYTVMDIKVPMRGDEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYMSNNSPAYTVMDIKVPMRGDEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDISCSVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720  
Db 661 TLLMKPLMKNDISCSVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNED 780  
QY 781 GEIKMLRISSSVKKYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKKYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYIVPVIISILLGLTLLISHORMKLLFWEDVPPNPKNCSWAQGLNFQKPETFEHLFI 900  
Db 841 GLYIVPVIISILLGLTLLISHORMKLLFWEDVPPNPKNCSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSISDPFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTDLKSGVCSISDPFN 960  
QY 961 SVNFEAEGETEVTYEDESQROPVRYATLISNSKPSSETGEQGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFEAEGETEVTYEDESQROPVRYATLISNSKPSSETGEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQSDCSHVEVNNINLGTSSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQSDCSHVEVNNINLGTSSKKTFFAS 1140  
QY 1141 YMPQOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQOTCSTQTHKIMENKMDLTV 1165

RESULT 3  
US-08-585-005-2  
Sequence 2, Application US/08585005  
GENERAL INFORMATION:  
APPLICANT: Matthews, William  
APPLICANT: Bennett, Brian  
TITLE OF INVENTION: MSX RECEPTOR  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,005  
FILING DATE: 08-Jan-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-585-005-2

Query Match 100.0%; Score 6254; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSCLMPNSTYDYFLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSCLMPNSTYDYFLPAGLSKNTS 60

QY 61 NGHETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQWLGDKDLKFLICYVESLEFKNLFERNYKVVHLLVLPVELEDSPVLPQKS 180  
DB 121 QOIDANMNIOQWLGDKDLKFLICYVESLEFKNLFERNYKVVHLLVLPVELEDSPVLPQKS 180  
QY 181 FOMVHCNCSVHECECLVPVPTAKLNDTLMCLKITSGVIFQSPLMSVOPINMVKPDP 240  
DB 181 FOMVHCNCSVHECECLVPVPTAKLNDTLMCLKITSGVIFQSPLMSVOPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOYQKXSENSTTVIREADKIYSAISLLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFLOYQKXSENSTTVIREADKIYSAISLLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPGLWSDMSTPRVFTQDVIYFPFKILTSGVSNVSPHCITYKKENKI 360  
DB 301 GSSYEVQVRGKRLDGPGLWSDMSTPRVFTQDVIYFPFKILTSGVSNVSPHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKEYFPENLNETKPRGKFYDAVYCCNEHECH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSKEYFPENLNETKPRGKFYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVNNISCETDGYLTMTCRMSTSTIQSLAESTLQLRHRSLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNNISCETDGYLTMTCRMSTSTIQSLAESTLQLRHRSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLP 540  
DB 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLP 540  
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLP 600  
DB 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLP 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLNGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLNGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSQVORYVINHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDSLCSQVORYVINHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANENLTFSPWMSKVINIQLSAYPLNSSCVIVSWILSPSDYKLMFIIEMKNLNE 780  
DB 721 GASVANENLTFSPWMSKVINIQLSAYPLNSSCVIVSWILSPSDYKLMFIIEMKNLNE 780  
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNKCSWAQGLNFOKPEFHEHFI 900  
DB 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNKCSWAQGLNFOKPEFHEHFI 900  
QY 901 KHTASVTCGPLEPETISEDISVDTSMKNDEMPTTVVSLSTDLIEKGSVCISDQFN 960  
DB 901 KHTASVTCGPLEPETISEDISVDTSMKNDEMPTTVVSLSTDLIEKGSVCISDQFN 960  
QY 961 SVNFSAEGETEYTYEDESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSAEGETEYTYEDESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELKLEGNPEENNDDKSIYYL 1080  
DB 1021 KDSFNSNSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELKLEGNPEENNDDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLETDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLETDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
RESULT 4  
US-08-638-524B-4  
Sequence 4, Application US/08638524B  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,524B  
FILING DATE: 26-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/018001  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-638-524B-4  
Query Match 100.0%; Score 6254; DB 10; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTFPWRFKLSKMPNSTDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTFPWRFKLSKMPNSTDYFLLPAGLSKNTSNS 60  
QY 61 NGHETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120

QY 121 QOIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180  
Db 121 QOIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240  
Db 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTVIYREADKIVATSLSLVDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTVIYREADKIVATSLSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPGLMSDMSPTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKEKNI 360  
Db 301 GSSYEYQVRGKRLDGPGLMSDMSPTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKEKNI 360  
QY 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIVYDVNINISCEFDGVLTKMTCRSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480  
Db 421 RYAEIVYDVNINISCEFDGVLTKMTCRSTSTQSLAESTLQLRHRSLSYCSIDPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFOPFILLSGYTMWIRINHSLSGLDPTCVLPDSVVKPLP 540  
Db 481 PISEPKDCYLQSDGFYECIFOPFILLSGYTMWIRINHSLSGLDPTCVLPDSVVKPLP 540  
QY 541 SSVKAEITINIGLKLISWEKPYFPPENNLQOIRYGLSGKEVQWKMEYVDKSKSVSLP 600  
Db 541 SSVKAEITINIGLKLISWEKPYFPPENNLQOIRYGLSGKEVQWKMEYVDKSKSVSLP 600  
QY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNY 660  
Db 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNY 660  
QY 661 TLLMKPLMKNDLSCSVQRYVNHHTSCNGTWESEVGNHTKFTFLMTEQAHVTVLAINSI 720  
Db 661 TLLMKPLMKNDLSCSVQRYVNHHTSCNGTWESEVGNHTKFTFLMTEQAHVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKIMYFIEMKNLNE 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKIMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVPNPKNCMAOGLNFQKPEFHEHFT 900  
Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVPNPKNCMAOGLNFQKPEFHEHFT 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTVVSLSLSTDLKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTVVSLSLSTDLKGSVCISDQFN 960  
QY 961 SVNFEABGTEVTEYEDESQROPVRYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFEABGTEVTEYEDESQROPVRYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFILSDQHNITISPHLTFSEGLDELKLEGNFPEENNDKSTIYL 1080  
Db 1021 KDSFNSSSWEIEAQAFILSDQHNITISPHLTFSEGLDELKLEGNFPEENNDKSTIYL 1080  
QY 1081 GVTSTKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHVEENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSTKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHVEENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 5  
US-08-667-197-2  
; Sequence 2, Application US/08667197  
; GENERAL INFORMATION:  
; APPLICANT: Matthews, William  
; TITLE OF INVENTION: USES FOR WSX LIGANDS  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,197  
; FILING DATE: 20-Jun-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585005  
; FILING DATE: 01/08/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: P-40,378  
; REFERENCE/DOCKET NUMBER: P0986P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9861  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-667-197-2  
  
Query Match 100.0%; Score 6254; DB 10; length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MICQKFCVYLLHMEFIYVITAFNLSTPITPWRFKLSCMPNNTYDYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVYLLHMEFIYVITAFNLSTPITPWRFKLSCMPNNTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYF 120  
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYF 120  
QY 121 QOIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180  
Db 121 QOIDANWNIQCWLKGLKLFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240  
Db 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTVIYREADKIVATSLSLVDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYQVKSSENSTVIYREADKIVATSLSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPGLMSDMSPTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKEKNI 360  
Db 301 GSSYEYQVRGKRLDGPGLMSDMSPTPRVFTQDVITYFPFKILTSVGSNVSFHCITYKKEKNI 360  
QY 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420

Db 361 VPSKEIWMNMNLAEKIPQSOQYDVSDHVSQVTFEENLNKTPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDNINISCEITDGYLTMTCRWSTSTIOSLAESTLOLRHRSLSYC6DIPSIH 480

Db 421 RYAEIYVIDNINISCEITDGYLTMTCRWSTSTIOSLAESTLOLRHRSLSYCSDIPSIH 480

QY 481 PISEPKDCYLOSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540

Db 481 PISEPKDCYLOSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540

QY 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSYSPLPV 600

Db 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSYSPLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSMSPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 601 PDLCAVYAVQVRCKRLDGLGYSWNSMSPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLMKPLMKNDSLCSQVRYVINHHTSCNGTWESEVGNHTKFTFLWTEQAHVTVLAINSI 720

Db 661 TLLMKPLMKNDSLCSQVRYVINHHTSCNGTWESEVGNHTKFTFLWTEQAHVTVLAINSI 720

QY 721 GASVANENLTFSPWMSKYNIVQSLAYPLNSSCVIYVSWILSPSDYKLMYFIEMKNLNE 780

Db 721 GASVANENLTFSPWMSKYNIVQSLAYPLNSSCVIYVSWILSPSDYKLMYFIEMKNLNE 780

QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSEFTODDIEKHQSDA 840

Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSEFTODDIEKHQSDA 840

QY 841 GLYVIVPVIISSSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFKRETFEHLFI 900

Db 841 GLYVIVPVIISSSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFKRETFEHLFI 900

QY 901 KHTASVTCGPLLEPTISEDISVDTSMKNKDEMPPTVSLSTTDLEKGSYCISDOFN 960

Db 901 KHTASVTCGPLLEPTISEDISVDTSMKNKDEMPPTVSLSTTDLEKGSYCISDOFN 960

QY 961 SVNFSEAGTEVTEDESQROQPFVKYATLISNSKPSSETGEEOGLINSSVTKCHSSKNSPL 1020

Db 961 SVNFSEAGTEVTEDESQROQPFVKYATLISNSKPSSETGEEOGLINSSVTKCHSSKNSPL 1020

QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080

Db 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080

QY 1081 GVTISIKKRESGVLLTDSKRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSSKKTFFAS 1140

Db 1081 GVTISIKKRESGVLLTDSKRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSSKKTFFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 6

US-08-708-123D-4

; Sequence 4, Application US/08708123D

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; APPLICANT: White, David W.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

FILING DATE: US/08/708,123D

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Melklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/019001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-708-123D-4

Query Match 100.0%; Score 6254; DB 11; Length 1165;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAENLSYPTPWRKLSGMPNNTYDFLLPAGLSKNTSNS 60

Db 1 MICQKFCVLLHWEFIYVITAENLSYPTPWRKLSGMPNNTYDFLLPAGLSKNTSNS 60

QY 61 NGHYETAVERPKFNSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGTFVSTVNSLVF 120

Db 61 NGHYETAVERPKFNSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGTFVSTVNSLVF 120

QY 121 QOIDANWNIQGWLKGDLKLFICYVESLFKNLFRNRYNKVHLLVYLPEVLEDSPLVPQGS 180

Db 121 QOIDANWNIQGWLKGDLKLFICYVESLFKNLFRNRYNKVHLLVYLPEVLEDSPLVPQGS 180

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMVKPDP 240

Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMVKPDP 240

QY 241 LGLHMEITDGNLKISWSSPPLVPFPLQYQKYSNSTVIREADKIYATSLSLVDISLP 300

Db 241 LGLHMEITDGNLKISWSSPPLVPFPLQYQKYSNSTVIREADKIYATSLSLVDISLP 300

QY 301 GSSYEYQVRGKRLDGPGLMSDSTPRVETQDVIYFPKILTSVGSNVSFHCYKKEKNI 360

Db 301 GSSYEYQVRGKRLDGPGLMSDSTPRVETQDVIYFPKILTSVGSNVSFHCYKKEKNI 360

QY 361 VPSKEIWMNMNLAEKIPQSOQYDVSDHVSQVTFEENLNKTPRGKFTYDAVYCCNEHECHH 420

Db 361 VPSKEIWMNMNLAEKIPQSOQYDVSDHVSQVTFEENLNKTPRGKFTYDAVYCCNEHECHH 420



QY 421 RYAEIVIDNINISCTEDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIPSIH 480  
Db 421 RYAEIVIDNINISCTEDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLP 540  
QY 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVLPV 600  
Db 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVLPV 600  
QY 601 PDLCAVYAVQVRCRKLGLGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCRKLGLGYWSNMSNPATYVMDIKVPMRGPEFRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINNHTSCNGTWSGNGHTKFTPLMTEQAHTVYLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINNHTSCNGTWSGNGHTKFTPLMTEQAHTVYLAINSI 720  
QY 721 GASVANFNLTFSWPMKYNIVQSLAYPLNSSCVIYMWILSPSDYKLMYFIEMKMNED 780  
Db 721 GASVANFNLTFSWPMKYNIVQSLAYPLNSSCVIYMWILSPSDYKLMYFIEMKMNED 780  
QY 781 GEIKWLRISSSVKKYIHDHPIEIKYQSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHPIEIKYQSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVIPVITISSILLGLTLLISHQRMKLFMEDVPRNPKNSWAQGLNFQKPEFHEHLEI 900  
Db 841 GLYIVIPVITISSILLGLTLLISHQRMKLFMEDVPRNPKNSWAQGLNFQKPEFHEHLEI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPITYVSLSTDLKSGSVCTISQFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPITYVSLSTDLKSGSVCTISQFN 960  
QY 961 SVNFSEAEGETEYDESOQRPVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETEYDESOQRPVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPLTFSEGLDELKLEGNFPEENNDRKSIYLL 1080  
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPLTFSEGLDELKLEGNFPEENNDRKSIYLL 1080  
QY 1081 GYTSIKKRESGVLTLTKSRVSCPFPAPCLFTDIRVLQDSCHFEVENNINLGTSKRTFAS 1140  
Db 1081 GYTSIKKRESGVLTLTKSRVSCPFPAPCLFTDIRVLQDSCHFEVENNINLGTSKRTFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 7  
US-08-779-457-2  
; Sequence 2, Application US/08779457  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Chiang, Nancy Y.  
; APPLICANT: Kyung, Jin Kim  
; APPLICANT: Matthews, William  
; APPLICANT: Rodrigues, Maria L.  
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,457  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/667197  
; FILING DATE: 06/20/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585005  
; FILING DATE: 01/08/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0986P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-779-457-2

Query Match 100.0%; Score 6254; DB 11; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICOKFCVLLHMEFIYVITAFNLSPYTPWRFKLSQMPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 MICOKFCVLLHMEFIYVITAFNLSPYTPWRFKLSQMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCAONIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCAONIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPOKGS 180  
Db 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPOKGS 180  
QY 181 PQMVHNCNSVHECCCLVPPVPTAKLNDPLMLCKLITSGVIFQSPPLMSVQPINMKRDP 240  
Db 181 PQMVHNCNSVHECCCLVPPVPTAKLNDPLMLCKLITSGVIFQSPPLMSVQPINMKRDP 240  
QY 241 LGLHMETDDGNLKSISWSSPLVPEPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMETDDGNLKSISWSSPLVPEPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPQISWDSNTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEYQVRGKRLDGPQISWDSNTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKETVMMNLAEKIPQSQDYVSDHVSQVTFEFLNETKRGKITYDAVYCCNEHECHH 420  
Db 361 VPSKETVMMNLAEKIPQSQDYVSDHVSQVTFEFLNETKRGKITYDAVYCCNEHECHH 420  
QY 421 RYAEIVIDNINISCTEDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIPSIH 480  
Db 421 RYAEIVIDNINISCTEDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLP 540  
QY 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVLPV 600  
Db 541 SSVKAEITINIGLTKISWEKPVPEENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVLPV 600

QY 601 PDLCAVAVAVQVRCRDLGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVAVAVQVRCRDLGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
DB 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGPKIINSETODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGPKIINSETODDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFEHLFI 900  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVSLSTDLKESVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVSLSTDLKESVCISDQFN 960  
QY 961 SVNFSEAGTEVEYDEDSQROFVKYATLISNSKPSSETGEQGLINSSVTRCFSSKNSPL 1020  
DB 961 SVNFSEAGTEVEYDEDSQROFVKYATLISNSKPSSETGEQGLINSSVTRCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
DB 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
QY 1081 GVTISIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
DB 1081 GVTISIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 8  
US-08-780-562-2  
Sequence 2, Application US/08780562  
GENERAL INFORMATION:  
APPLICANT: Matthews, William  
APPLICANT: Bennett, Brian  
TITLE OF INVENTION: WSX RECEPTOR  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780.562  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/  
FILING DATE: 01/08/97  
ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-780-562-2  
Query Match 100.0%; Score 6254; DB 11; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSMPNNTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSMPNNTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERKFNSSGTHFNSLSKTFHCCFRSEQDRNCSLCAADNIEGTFVSTVNSLVF 120  
DB 61 NGHYETAVERKFNSSGTHFNSLSKTFHCCFRSEQDRNCSLCAADNIEGTFVSTVNSLVF 120  
QY 121 QQIDANWNIQCNLKGDKLFCICYVESLFKNLFRNRYKVVHLLVYLPEVLEDSPLVPQKS 180  
DB 121 QQIDANWNIQCNLKGDKLFCICYVESLFKNLFRNRYKVVHLLVYLPEVLEDSPLVPQKS 180  
QY 181 FQVHNCNSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
DB 181 FQVHNCNSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPQYQYKYSNSTVIVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFPQYQYKYSNSTVIVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOVRGRDLGPGIWSMDSTPRVFTQDYIYFPKILTSVGSNVSFHCYKKEKNI 360  
DB 301 GSSYEVOVRGRDLGPGIWSMDSTPRVFTQDYIYFPKILTSVGSNVSFHCYKKEKNI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNINISCTDGYLTKMTCRMSTIQLAESTIQLRHRSSLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNNINISCTDGYLTKMTCRMSTIQLAESTIQLRHRSSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLSGTYMMIRINHSLSGLSDSPPTCYLLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLSGTYMMIRINHSLSGLSDSPPTCYLLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600  
QY 601 PDLCAVAVAVQVRCRDLGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVAVAVQVRCRDLGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
DB 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGPKIINSETODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGPKIINSETODDIEKHQSDA 840

Db 781 GEIKWLRISSVKKYYIHDFIPIEKYQFSLYPIFMWGVGPKTINSFTQDDIEKHQSDA 840  
QY 841 GLVYIVPVIISSSILLGLTLLSHQRMKLFMEDVDPNPKNSWAQGLNFQKPEFHEHLFI 900  
Db 841 GLVYIVPVIISSSILLGLTLLSHQRMKLFMEDVDPNPKNSWAQGLNFQKPEFHEHLFI 900  
QY 901 KHTASVTCGPIILLEPETISEDISVDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPIILLEPETISEDISVDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960  
QY 961 SVNFSAEGETEVTYEDESQROPVYKATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
Db 961 SVNFSAEGETEVTYEDESQROPVYKATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEAQAFFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYLL 1080  
Db 1021 KDSFSSNSWEIEAQAFFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYLL 1080  
QY 1081 GVTSTKKRESGLTLDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSTKKRESGLTLDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 9  
US-09-094-410-4  
; Sequence 4, Application US/09094410  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/094,410  
; FILING DATE: 09-JUN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-094-410-4

Query Match 100.0%; Score 6254; DB 14; length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSCMPPNSTYDYFLLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSCMPPNSTYDYFLLPAGLSKNTS 60

QY 61 NGHYETAPEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAPEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120

QY 121 QOIDANWNIQWLKGDCLKFICVESLEFRNRYKVVHLLYVLEVEDSPLPVOKGS 180  
Db 121 QOIDANWNIQWLKGDCLKFICVESLEFRNRYKVVHLLYVLEVEDSPLPVOKGS 180

QY 181 FQMVHNCVSHECCCLVPPTAKLNDFTLMCLKITSGVIFQSPILNSVQPIVMKPPDP 240  
Db 181 FQMVHNCVSHECCCLVPPTAKLNDFTLMCLKITSGVIFQSPILNSVQPIVMKPPDP 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOYQVYKSENSTVIREADKIVSATSLVDSTLP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLOYQVYKSENSTVIREADKIVSATSLVDSTLP 300

QY 301 GSSYEVOVRGKRLDGPGLWSWSTPRVFTQDVIYFPFKILTSV;SNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPGLWSWSTPRVFTQDVIYFPFKILTSV;SNVSFHCITYKKENKI 360

QY 361 VPSKEIWMWMLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMWMLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVNNISCEETDGYLTMTCRNSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480  
Db 421 RYAEIYVIDVNNISCEETDGYLTMTCRNSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480

QY 481 PISEPKDCYLOSDFYECIFQPIFLSGTYMIRINHSLSGLSDSPPCVLLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDFYECIFQPIFLSGTYMIRINHSLSGLSDSPPCVLLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKNEYDYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKNEYDYDAKSKSVSLPV 600

QY 601 PDLCAVAYAVOYRCKRLDGLGWSNWSNPATVVMIDIKVPMRGPEFWRLINGDTMKKEKNV 660  
Db 601 PDLCAVAYAVOYRCKRLDGLGWSNWSNPATVVMIDIKVPMRGPEFWRLINGDTMKKEKNV 660

QY 661 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSDEVGNHTKFTFLVTAQHTVTLAINSI 720  
Db 661 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSDEVGNHTKFTFLVTAQHTVTLAINSI 720

QY 721 GASVANFNLFSPWMSKVINIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANFNLFSPWMSKVINIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780

QY 781 GEIKWLRISSVKKYIHDHFIPIEKYQPSLYPIEMEGVGKPKIINSFTODDIEKHOSDA 840  
DB 781 GEIKWLRISSVKKYIHDHFIPIEKYQPSLYPIEMEGVGKPKIINSFTODDIEKHOSDA 840  
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQKPEFEHLFI 900  
DB 841 GLYIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQKPEFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVSLSTDLKSGVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVSLSTDLKSGVCISDQFN 960  
QY 961 SVNFSEAEGETEYEDESQORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAEGETEYEDESQORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIQAFFILSDQHPNIIISPHLTSEGLDELKLEGNPEENNDDKSIYYL 1080  
DB 1021 KDSFNSSSWEIQAFFILSDQHPNIIISPHLTSEGLDELKLEGNPEENNDDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNIMLGTSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 10  
US-09-137-132-4  
: Sequence 4, Application US/09137132  
: GENERAL INFORMATION:  
: APPLICANT: Tartaglia, Louis A.  
: APPLICANT: Tepper, Robert I.  
: APPLICANT: Culpepper, Janice A.  
: APPLICANT: White, David W.  
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
: TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
: TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fish & Richardson, P.C.  
: STREET: 225 Franklin Street  
: CITY: Boston  
: STATE: MA  
: COUNTRY: US  
: ZIP: 02110-2804  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: Windows95  
: SOFTWARE: FASTSEQ for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/137,132  
: FILING DATE: 18-AUG-1998  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/864,564  
: FILING DATE: 28-MAY-1997  
: APPLICATION NUMBER: 08/708,123  
: FILING DATE: 03-SEP-1996  
: APPLICATION NUMBER: 08/638,524  
: FILING DATE: 26-APR-1996  
: APPLICATION NUMBER: 08/599,455  
: FILING DATE: 22-JAN-1996  
: APPLICATION NUMBER: 08/583,153  
: FILING DATE: 28-DEC-1995  
: APPLICATION NUMBER: 08/570,142  
: FILING DATE: 11-DEC-1995  
: APPLICATION NUMBER: 08/569,485  
: FILING DATE: 08-DEC-1995  
: APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-137-132-4

Query Match 100.0%; Score 6254; DB 15; length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPTWRFKLSGMPNSTVYVLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSTPTPTWRFKLSGMPNSTVYVLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKRNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTEFVSTVNSLVE 120  
DB 61 NGHYETAVEPKRNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTEFVSTVNSLVE 120  
QY 121 QOIDANMNIOCKLKGDKLFICYVESLEKLNFRNRYKVHLLVYIPEVLEDSPLVPQKGS 180  
DB 121 QOIDANMNIOCKLKGDKLFICYVESLEKLNFRNRYKVHLLVYIPEVLEDSPLVPQKGS 180  
QY 181 FQMVHCNCSVHECCCLVPPVPTAKLNDILMLCKITSGGVTFQSPMSVQPINMKPDP 240  
DB 181 FQMVHCNCSVHECCCLVPPVPTAKLNDILMLCKITSGGVTFQSPMSVQPINMKPDP 240  
QY 241 LGLHMEITDGNLKSISWSSPPLVPFLOYQVYKSENSTVIREAKIVASATSLVDSILP 300  
DB 241 LGLHMEITDGNLKSISWSSPPLVPFLOYQVYKSENSTVIREAKIVASATSLVDSILP 300  
QY 301 GSSYEYQVRGRLDGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSEHCYKKNKI 360  
DB 301 GSSYEYQVRGRLDGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSEHCYKKNKI 360  
QY 361 VPSKEIYWMNLAEKIPQSDYDVSDHYSKVTFENLNETKPRGKIYDAVYCCNEHECHH 420  
DB 361 VPSKEIYWMNLAEKIPQSDYDVSDHYSKVTFENLNETKPRGKIYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDYNINISCEITDGYLTMTCKRSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
DB 421 RYAEIYVIDYNINISCEITDGYLTMTCKRSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
QY 481 PISEPKDYIQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDPPTCVLPDSVVKPLPP 540  
DB 481 PISEPKDYIQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAETITINIGLLKISWEKVPFPENNIOFQIRYGLSGKEVQWKNYEYDAKSKSVSLPV 600  
DB 541 SSVKAETITINIGLLKISWEKVPFPENNIOFQIRYGLSGKEVQWKNYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOYRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVOYRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660  
QY 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLUTEQAHTVTLAINSI 720  
DB 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLUTEQAHTVTLAINSI 720

QY 721 GASVANFNLTFSWPMKVNIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLTFSWPMKVNIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYIYHDFIPIEKFQSLYPIEMEGVGKPKIINSTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYIYHDFIPIEKFQSLYPIEMEGVGKPKIINSTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFTEHLEFI 900  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFTEHLEFI 900  
QY 901 KHTASVTCGPPLLEPETISEDISVDTSMKNKDEMPPTTVSLSTDLKSGVCISDQFN 960  
DB 901 KHTASVTCGPPLLEPETISEDISVDTSMKNKDEMPPTTVSLSTDLKSGVCISDQFN 960  
QY 961 SVNFSEAGTEVYTEDSQRQPFVKATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAGTEVYTEDSQRQPFVKATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISHLTFSEGLDELKLEGNPEENNDKKSITYL 1080  
DB 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISHLTFSEGLDELKLEGNPEENNDKKSITYL 1080  
QY 1081 GVTSIKKREGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
DB 1081 GVTSIKKREGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQCTSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQCTSTQTHKIMENKMDLTV 1165

RESULT 11  
US-09-950-149-4  
Sequence 4, Application US/09950149  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
Tepper, Robert I.  
Culpepper, Janice A.  
White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
THE OB DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/950,149  
FILING DATE: 10-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,781  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: US 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: US 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: US 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: US 08/570,142  
FILING DATE: 11-DEC-1995

APPLICATION NUMBER: US 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: US 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: US 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-950-149-4

Query Match 100.0%; Score 6254; DB 23; length 1165;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAPEPKFNSSGTHESNLSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAPEPKFNSSGTHESNLSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANWNIQCKLGDLCFICVESLEKMLFRNRYKVALLYLPEVLEDSPLVPQKGS 180  
DB 121 QQIDANWNIQCKLGDLCFICVESLEKMLFRNRYKVALLYLPEVLEDSPLVPQKGS 180  
QY 181 FQMVHNCNSVHECCCELYVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMYKBDPP 240  
DB 181 FQMVHNCNSVHECCCELYVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMYKBDPP 240  
QY 241 LGLHMEITDDGNLKISNSPPLVPFPLOYQVKYSENSTYVIREADKIVATSLSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISNSPPLVPFPLOYQVKYSENSTYVIREADKIVATSLSLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTODVITFPFKILTSVGSNVSFHCITYKKEKI 360  
DB 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTODVITFPFKILTSVGSNVSFHCITYKKEKI 360  
QY 361 VPSKEIVWMNLAEKIPOSQYDVSDHVSQVTFENLNETKPRCKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIVWMNLAEKIPOSQYDVSDHVSQVTFENLNETKPRCKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVININISCTDGLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSDFPSIH 480  
DB 421 RYAEIYVIDVININISCTDGLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSDFPSIH 480  
QY 481 PISEPKDCYLQSDGFYEICFQPIFLLSGYTMWIRINHSLSGLSDSPICVLPDSVYKPLPP 540  
DB 481 PISEPKDCYLQSDGFYEICFQPIFLLSGYTMWIRINHSLSGLSDSPICVLPDSVYKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQMKTEVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQMKTEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKYPMRGPEFWIRINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKYPMRGPEFWIRINGDTMKKEKNV 660



QY 661 TLLMKPLMKNDLSVQRYVINHHHTSCNGTWSERVEDVGNHTKFTFLMTQEAHTVTVALAINSI 720  
Db 661 TLLMKPLMKNDLSVQRYVINHHHTSCNGTWSERVEDVGNHTKFTFLMTQEAHTVTVALAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKMLRISSSVKKYIYHDFPIEIKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKKYIYHDFPIEIKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDEVNPNKCSWAQGLNFQKPEFHEHLEFI 900  
Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDEVNPNKCSWAQGLNFQKPEFHEHLEFI 900  
QY 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLLEKGSVCISDQFN 960  
QY 961 SVNFEAEGETEVTYEDESQRPVKYATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFEAEGETEVTYEDESQRPVKYATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFSNSSWEIEAQAFFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1080  
Db 1021 KDSFSNSSWEIEAQAFFILSDQHNIIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVENNINLGTSKKTFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVENNINLGTSKKTFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTY 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTY 1165

RESULT 12  
US-08-774-414-7  
; Sequence 7, Application US/08774414  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; APPLICANT: WELCHER, ANDREW A.  
; APPLICANT: FLETCHER, FREDERICK A.  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,414  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382-A  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1216 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-774-414-7  
Query Match 100.0%; Score 6254; DB 11; Length 1216;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHMEFIYVITAFNLSPYITPWRKFLSCMPNPNSTYVYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHMEFIYVITAFNLSPYITPWRKFLSCMPNPNSTYVYFLLPAGLSKNTSNS 60  
QY 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANWNIQWLKGLKFLICYVESLFKNLFERNYNYKVHLLYVPEVLEDSPLVPQKGS 180  
Db 121 QOIDANWNIQWLKGLKFLICYVESLFKNLFERNYNYKVHLLYVPEVLEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCLVVPPTAKLNDTLLMCLKITSGVIFOSPLMSVOPINMVKPDP 240  
Db 181 FQWVHCNCSVHECCCLVVPPTAKLNDTLLMCLKITSGVIFOSPLMSVOPINMVKPDP 240  
QY 241 LGLHMETDDGNLKSISWSSPPLVPFPLOYQVYKSENSTVIREADKIVSATSLLVDSILP 300  
Db 241 LGLHMETDDGNLKSISWSSPPLVPFPLOYQVYKSENSTVIREADKIVSATSLLVDSILP 300  
QY 301 GSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYWMNLAEKIPQSQYDVVSDHVSKVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYWMNLAEKIPQSQYDVVSDHVSKVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVININISCEITDGLTKMTCRMSTSTIOSLAESTLOLRYHRSLSYCSIDPSIH 480  
Db 421 RYAEIYVIDVININISCEITDGLTKMTCRMSTSTIOSLAESTLOLRYHRSLSYCSIDPSIH 480  
QY 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSPICVLPDSVVKPLPP 540  
Db 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSPICVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQMKMYEYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQMKMYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCRRLDGLGYSNMNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNY 660  
Db 601 PDLCAVYAVQVRCRRLDGLGYSNMNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNY 660  
QY 661 TLLMKPLMKNDLSVQRYVINHHHTSCNGTWSERVEDVGNHTKFTFLMTQEAHTVTVALAINSI 720  
Db 661 TLLMKPLMKNDLSVQRYVINHHHTSCNGTWSERVEDVGNHTKFTFLMTQEAHTVTVALAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKMLRISSSVKKYIYHDFPIEIKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKKYIYHDFPIEIKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDEVNPNKCSWAQGLNFQKPEFHEHLEFI 900  
Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDEVNPNKCSWAQGLNFQKPEFHEHLEFI 900  
QY 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLLEKGSVCISDQFN 960  
QY 961 SVNFEAEGETEVTYEDESQRPVKYATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFEAEGETEVTYEDESQRPVKYATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020

DB 961 SVNFSEAGTEVTEYDESDQRPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
DB 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

## RESULT 13

US-09-671-049-7  
; Sequence 7, Application US/09671049  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; WELCHER, ANDREW A.  
; FLETCHER, FREDERICK A.  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/671,049  
; FILING DATE: 27-Sep-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,414  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessia, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382-A  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1216 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-671-049-7

Query Match 100.0%; Score 6254; DB 20; Length 1216;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYVITAFNLSTPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
DB 1 MICQFCVLLHMEFIYVITAFNLSTPITPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAPEKNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSNLVF 120  
DB 61 NGHYETAPEKNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSNLVF 120  
QY 121 QOIDANWNIQWLKGLDLFLICYVESLFLKNLFRNINYNKVHLLVLPPEVLEDSPLVPQKGS 180  
DB 121 QOIDANWNIQWLKGLDLFLICYVESLFLKNLFRNINYNKVHLLVLPPEVLEDSPLVPQKGS 180

QY 181 FQMVHNCNVHECCCLVPTAKLNDTLMLCKITSGGYIFQSPLMVQPINWKPDP 240  
DB 181 FQMVHNCNVHECCCLVPTAKLNDTLMLCKITSGGYIFQSPLMVQPINWKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVYSENSTYVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVYSENSTYVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPISWDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCYKKENKI 360  
DB 301 GSSYEVQVRGKRLDGPISWDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCYKKENKI 360  
QY 361 VPSKEIWMNMNLAEKIPQSDYDVSDHVSQVTFNLTNPKRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIWMNMNLAEKIPQSDYDVSDHVSQVTFNLTNPKRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCDIPSIH 480  
DB 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCDIPSIH 480  
QY 481 PISEPKDCYLOSDGFYECTIQPIFLLSGYTMWIRINHSLSGLDSPPTCYLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDGFYECTIQPIFLLSGYTMWIRINHSLSGLDSPPTCYLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKIWEKVPFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKIWEKVPFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSMWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYSMWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSERVEDVGNHFKFTFLTEQAHVTVLAINSI 720  
DB 661 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSERVEDVGNHFKFTFLTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPWMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANENLTFSPWMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GETKWLRISSSVKYYIHDHFLPIEKYQFSLYPIEMEGVGKPKIINSFTODDIEKHOSDA 840  
DB 781 GETKWLRISSSVKYYIHDHFLPIEKYQFSLYPIEMEGVGKPKIINSFTODDIEKHOSDA 840  
QY 841 GLYIVIPVITISSILLLGTLISHQRMKLLFEMEDVPPNPKNSWAQGLNFQKPETFEHLFI 900  
DB 841 GLYIVIPVITISSILLLGTLISHQRMKLLFEMEDVPPNPKNSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVVSILSTDLKSGVCSISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVVSILSTDLKSGVCSISDQFN 960  
QY 961 SVNFSEAGTEVTEYDESDQRPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAGTEVTEYDESDQRPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
DB 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFEVNNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

## RESULT 14

US-09-948-933-284  
; Sequence 284, Application US/09948933  
; GENERAL INFORMATION:

```

: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
: TITLE OF INVENTION: DETECTION AND USES THEREOF
: FILE REFERENCE: CL000787
: CURRENT APPLICATION NUMBER: US/09/948,933
: CURRENT FILING DATE: 2001-09-10
: PRIOR APPLICATION NUMBER: 60/231,399
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 6404
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 284
: LENGTH: 1167
: TYPE: PRT
: ORGANISM: Human
US-09-948-933-284

Query Match          99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHMEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS 62
QY 61 NGHYETAVERPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120
Db 63 NGHYETAVERPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGRTFVSTVNSLVE 122
QY 121 QOIDANMNIOQWLKGDCLKFICYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS 180
Db 123 QOIDANMNIOQWLKGDCLKFICYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS 182
QY 181 FQMVHNCVSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMVKPDP 240
Db 183 FQMVHNCVSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFRSPLMSVQPINMVKPDP 242
QY 241 LGLHMETDDGNLKLISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDLSILP 300
Db 243 LGLHMETDDGNLKLISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDLSILP 302
QY 301 GSSYEQVGRKRLDGPGLMSDWSPTAVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
Db 303 GSSYEQVGRKRLDGPGLMSDWSPTAVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNNINISCEITDGYLTKMTCRWSSTIQLAESTLQLRHSSSLYCSDIPSIIH 480
Db 423 RYAEIYVIDVNNINISCEITDGYLTKMTCRWSSTIQLAESTLQLRHSSSLYCSDIPSIIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLISGYTMIRINHSLSGLSDSPTCVLPDSVVKPLPP 542
QY 541 SSYKAEITINIGLKLISWEKPVFPENNLQFOIRYGLSGKEVQMKMEYVYDAKSKSVSLPV 600
Db 543 SSYKAEITINIGLKLISWEKPVFPENNLQFOIRYGLSGKEVQMKMEYVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCRRLDGLGYSWMSNPAITVVMIDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCRRLDGLGYSWMSNPAITVVMIDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLMTQAHVTVLAINSI 720
Db 663 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLMTQAHVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSISAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 723 GASVANFNLTFSWPMKVNIVQSISAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 782
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QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSETODDIEKHOSDA 840
Db 783 GEIKWLRISSVKKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSETODDIEKHOSDA 842
QY 841 GLYIVIVPVISSILLGLTLLISHQRMKLFMEDVDPNPKNCSWAQGLNFOKPETFEHLFI 900
Db 843 GLYIVIVPVISSILLGLTLLISHQRMKLFMEDVDPNPKNCSWAQGLNFOKPETFEHLFI 902
QY 901 KHTASVTCGPIILEPETISEDISVDTSWKNKDEMPPTTVVSLSTDLKGSVCISDQFN 960
Db 903 KHTASVTCGPIILEPETISEDISVDTSWKNKDEMPPTTVVSLSTDLKGSVCISDQFN 962
QY 961 SVNFESEAEGTEVYEDESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 963 SVNFESEAEGTEVYEDESQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1022
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELCLKLEGNFEENNDKSIYYL 1080
Db 1023 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELCLKLEGNFEENNDKSIYYL 1082
QY 1081 GVTSIKKRESGVLLTDKSRVSCPAPACLETDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140
Db 1083 GVTSIKKRESGVLLTDKSRVSCPAPACLETDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1142
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

RESULT 15
US-09-948-947-87
: Sequence 87, Application US/09948947
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL000786
: CURRENT APPLICATION NUMBER: US/09/948,947
: CURRENT FILING DATE: 2001-09-10
: PRIOR APPLICATION NUMBER: 60/231,397
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 2172
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 87
: LENGTH: 1167
: TYPE: PRT
: ORGANISM: Human
US-09-948-947-87

Query Match          99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHMEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLLPAGLSKNTSNS 62
QY 61 NGHYETAVERPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120
Db 63 NGHYETAVERPKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGRTFVSTVNSLVE 122
QY 121 QOIDANMNIOQWLKGDCLKFICYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS 180
Db 123 QOIDANMNIOQWLKGDCLKFICYVESLFEKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS 182
QY 181 FQMVHNCVSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMVKPDP 240
Db 183 FQMVHNCVSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFRSPLMSVQPINMVKPDP 242
QY 241 LGLHMETDDGNLKLISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDLSILP 300
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|||||
Db 243 LGLHMEITDDGNLKLISWSSPLVPEPLQYQVKYSENSTVIREADKIVSATSLVDLILP 302
QY 301 GSSYEVOVRGKRDLDPGIMSDWSTPRVFTTQDVIYPPKILTSVGSNVSFHCITYKKENKI 360
Db 303 GSSYEVOVRGKRDLDPGIMSDWSTPRVFTTQDVIYPPKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIWMWMLAEKIPQSQYDVSDHVKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIWMWMLAEKIPQSQYDVSDHVKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVININISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480
Db 423 RYAEIYVIDVININISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLKLISWEKPVPEPENNLOQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLKLISWEKPVPEPENNLOQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVOVRCKRDLGLGYWSNMSNPAYTVMDIKYPMRGPEFWRIINGDTMKREKNV 660
Db 603 PDLCAVYAVOVRCKRDLGLGYWSNMSNPAYTVMDIKYPMRGPEFWRIINGDTMKREKNV 662
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHVTVLAINSI 720
Db 663 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTSEDEVGNHTKFTFLWTEQAHVTVLAINSI 722
QY 721 GASVANENLTFSWPMKKNVIVOSLSAYPLNSCVIYSWILSPSDYKLMYFIIEWKNLNED 780
Db 723 GASVANENLTFSWPMKKNVIVOSLSAYPLNSCVIYSWILSPSDYKLMYFIIEWKNLNED 782
QY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKKYYIHDHFPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVPNPKNCWAQGLNFQKPETFEHLFI 900
Db 843 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVPNPKNCWAQGLNFQKPETFEHLFI 902
QY 901 KHTASVTCGPIILLEPETISEDISVDTSMKNKDEMPPTVYSLSTTDLEKGSVCISDQFN 960
Db 903 KHTASVTCGPIILLEPETISEDISVDTSMKNKDEMPPTVYSLSTTDLEKGSVCISDQFN 962
QY 961 SYNFESEAGTEVTYEDESQROPFVKYATLISNSKPSSETGEEOGLINSSVTKCFSSKNSPL 1020
Db 963 SYNFESEAGTEVTYEDESQROPFVKYATLISNSKPSSETGEEOGLINSSVTKCFSSKNSPL 1022
QY 1021 KDSFSNSSWEIEAQAEFIISDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDDKKSIIYYL 1080
Db 1023 KDSFSNSSWEIEAQAEFIISDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDDKKSIIYYL 1082
QY 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINIGTSSSKKTFAS 1140
Db 1083 GYTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINIGTSSSKKTFAS 1142
QY 1141 YMPQFQTCSTQTHKIMENKMDLTY 1165
Db 1143 YMPQFQTCSTQTHKIMENKMDLTY 1167
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Search completed: May 18, 2002, 06:59:12  
Job time: 680 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 06:50:31 ; Search time 54.75 Seconds  
(without alignments)  
562.412 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 6254  
Sequence: 1 MICQKFCVLLHMEFYVIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 107366 seqs, 26430961 residues

Total number of hits satisfying chosen parameters: 107366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	6.1	1158	5 US-09-935-868-26	Sequence 26, Appl
2	376	6.0	1168	5 US-09-935-868-24	Sequence 24, Appl
3	345.5	5.5	918	5 US-09-853-180-4	Sequence 4, Appl
4	309.5	4.9	859	5 US-09-935-868-7	Sequence 7, Appl
5	308.5	4.9	951	5 US-09-935-868-9	Sequence 9, Appl
6	220.5	3.5	862	5 US-09-853-180-5	Sequence 5, Appl
7	218.5	3.5	582	6 US-10-119-480-92	Sequence 92, Appl
8	191.5	3.1	332	5 US-09-935-868-10	Sequence 10, Appl
9	172.5	2.8	1450	1 PCT-US02-09052-7	Sequence 7, Appl
10	172.5	2.8	1461	1 PCT-US02-09671-1148	Sequence 1148, Ap
11	170.5	2.7	1461	1 PCT-US02-10824-189	Sequence 189, App
12	170.5	2.7	1461	1 PCT-US02-09671-1147	Sequence 1147, Ap
13	170.5	2.7	1461	1 PCT-US02-09671-1149	Sequence 1149, Ap
14	170.5	2.7	1461	1 PCT-US02-09671-1150	Sequence 1150, Ap
15	163	2.6	629	5 US-09-853-180-2	Sequence 2, Appl
16	154.5	2.5	2328	1 PCT-US02-10824-196	Sequence 196, App
17	152	2.4	782	5 US-09-935-868-48	Sequence 48, Appl
18	152	2.4	782	5 US-09-935-868-52	Sequence 52, Appl
19	149.5	2.4	780	5 US-09-935-868-34	Sequence 34, Appl
20	149.5	2.4	780	5 US-09-935-868-38	Sequence 38, Appl
21	149.5	2.4	780	5 US-09-935-868-42	Sequence 42, Appl
22	146	2.3	793	5 US-09-935-868-32	Sequence 32, Appl
23	146	2.3	3063	1 PCT-US02-08253-257	Sequence 257, App
24	145.5	2.3	1433	5 US-09-695-293-40	Sequence 40, Appl
25	142.5	2.3	1236	1 PCT-US02-09671-865	Sequence 865, App
26	142.5	2.3	1236	1 PCT-US02-09671-873	Sequence 873, App

27	142.5	2.3	1308	1 PCT-US02-09671-864	Sequence 864, App
28	142.5	2.3	1308	1 PCT-US02-09671-874	Sequence 874, App
29	141	2.3	778	5 US-09-935-868-50	Sequence 50, Appl
30	140	2.2	778	5 US-09-935-868-46	Sequence 46, Appl
31	134.5	2.2	776	5 US-09-935-868-40	Sequence 40, Appl
32	134.5	2.2	1180	1 PCT-US02-09671-863	Sequence 863, App
33	134.5	2.2	1180	1 PCT-US02-09671-870	Sequence 870, App
34	134.5	2.2	1180	1 PCT-US02-09671-871	Sequence 871, App
35	133.5	2.1	776	5 US-09-935-868-36	Sequence 36, Appl
36	133.5	2.1	776	5 US-09-935-868-44	Sequence 44, Appl
37	132.5	2.1	1192	1 PCT-US02-09671-866	Sequence 866, App
38	132.5	2.1	1192	1 PCT-US02-09671-867	Sequence 867, App
39	132.5	2.1	1192	1 PCT-US02-09671-868	Sequence 868, App
40	131.5	2.1	1299	1 PCT-US02-09671-862	Sequence 862, App
41	131.5	2.1	1299	1 PCT-US02-09671-869	Sequence 869, App
42	131.5	2.1	1299	1 PCT-US02-09671-872	Sequence 872, App
43	129	2.1	784	5 US-09-935-868-30	Sequence 30, Appl
44	128.5	2.1	1465	1 PCT-US02-07825-219	Sequence 219, App
45	128.5	2.1	1465	6 US-10-097-340-219	Sequence 219, App

ALIGNMENTS

RESULT 1  
US-09-935-868-26  
; Sequence 26, Application US/09935868  
; GENERAL INFORMATION:  
; APPLICANT: Regeneron Pharmaceuticals, Inc  
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
; FILE REFERENCE: REG 203D  
; CURRENT APPLICATION NUMBER: US/09/935,868  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 1158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-935-868-26

Query Match	6.1%; Score 384; DB 5; Length 1158;
Best Local Similarity	19.8%; Pred. No. 1.3e-18;
Matches	214; Conservative 180; Mismatches 44; Indels 244; Gaps 53;
QY	196 CLVPTAKLNDTL-MCLKTSQGVIFQSLMSVQPINVAKDPLGLHMET--DDGN 252
Db	176 CQAVPEGDSSFYIVSMCVASSVSKF--SKTQTFQGGCGLDPPANITVAVARNPRN 233
QY	253 LKISNSPP-----LVFPLOYQVYSENST-VIREADKIVASLLVDSILPGSSY 304
Db	234 LSVTQDDPHSWNSFFYRLRFELRYAERSKFTTWMVKDLQ-----HCVIHDAMSGLRH 288
QY	305 EVOYAGKRLDGPQIWSDS-----TP-----RVFTQDVI-----YFPKI-LTS 343
Db	289 VVQLAQBEEFGQGEWSEWSPAMCTPWTESRSPRAENEVSTPMELLPCGYSPESPVQ 348
QY	344 VGSNVSEHCYKK--ENKIVPSKEIWMNLAEKIPQSOYDVVSDHVSQVTFENLNETK 400
Db	349 LHSNPTAVCVLKEKCMDFHVNANYIWKTN-HFTIPKEQYTIINRPASSVTFDI---- 403
QY	401 PRGRFTYDAVCCNEHECHRYAEIVDV-----NINISC-EVDGYLTKMTQWST 451
Db	404 -----ASLNIQTCNITLFGQLQEVNYGITITISGLPPEKPKNLSCTVNEG--KKMRCEWDG 457
QY	452 STIGSLAESTLQRYHRSSLYCSDIPSIHPISPKDCYLOSDGFEYECI--FOPIFLSGY 509
Db	458 G-----RETHLETFNLTLSKSEWAT-----HKFA--DCKAKRDIPTSCVDYSTVYFVN-I 503
QY	510 TMMIRINHSLSLDSPTCVLPDVSVKPLPSSVKAETITN-----ICLLKISWEKP----- 561

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Query Match	6.0%;	Score 376;	DB 5;	Length 1168;
Best Local Similarity	19.6%;	Pred. No. 4.7e-18;		
Matches 213;	Conservative 177;	Mismatches 445;	Indels 254;	Gaps 51;
QY 196	CLVPEVPTAKLNDTLL-MCLKITSQVIFQSPPLMSVQPINMVKRPDPLGLHMEIT--DDGN	252		

Db	176	COLAVPEGDSSFYIVSMCVASSVSGKF--SKTQTFOGCGILQDPDPANITVTAVARNPRW	233
Qy	253	LKISWSSPP-----LVFPPLQYOVKYSNSTT-VIREADKIVSATSLVDSILPGSSY	304
Db	234	LSVTWQOPHSWNSSFYRLRFELRRAERSKFTTMTWVKDLOH-----HCVIDHAWSGLRH	288
Qy	305	EVQVRGRRLDGPICWSDMSTPRVFTTQDVIYFPP-----KILTSVG	345
Db	289	VVOLRAQEEFGQGESEMSPEANGTPTESRSPRAENEVSPTMTGAPSGAQLLELDPGC	348
Qy	346	-----SNVSFHCITYK--ENKIVPSKEIYMMMLAEKIPQOYDVVSDHYSK	390
Db	349	YISPESPVQOLHSNFTAVCVLKEKCMDYFHVNANYIWKTN-HFTIPKEQYTIINRTASS	407
Qy	391	VTFENINETKPRGKFTYDAVYCCNEHECHHRYAELVIDY-----NINISC-ETDGY	441
Db	408	VTFETDI-----ASLNIQLTGMLITFGQLEQNVGITITISGLPPEKPKNLSCIVNEG-	458
Qy	442	LTKMTCRWSTSTIOSLAESTLOLRHRSLLYCSDIPSIHPISEPKDCYLOSDFYECI--	499
Db	459	-KKMRCEWDGG-----RETHLETNETLKSEWAT----HKFA--DCKAKRDTPTSCYVD	504
Qy	500	FOPIFILSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPSSVKAETITN---IGLTK	555
Db	505	YSTVYEVN-IEVWVEAENALGKYVSDHINEDPVYKVKPNPHNLS--VINSEELSLTK	560
Qy	556	ISWEKP-----VEPENNLQFOIRYGLSGKEVQWKMVEYDASKSVSLPVPDL-CAYYA	608
Db	561	LTWINPSTIKSVIILKYNIOYRTKAST-----WSQIPREDTASTRSSFTVQDLKPFTEYV	615
Qy	609	VQVRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEFWIRINGDTMKKEKNVTLLMKPLM	668
Db	616	FRIKMKEDGKGYSWDSWSEASGITIEDR-PSKAPSEFWYKIDPSHTQGYRTVQLVWKTLP	674
Qy	669	KNDSLCSVQRYVINHHTSCNGIMSEDEVGNH---TKFTFLMTEQAHVTVLAINSIGASV	724
Db	675	PFEANGKILDYEVT-----LTRMKSHLQNTYVATKTLVNLINDRYLATLTVRNLVGRSD	729
Qy	725	ANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKIMYFIEMKNLNEDGE--	782
Db	730	AAVLTTPACDFQATHPVMDLKAFP-KDNMLMVEWTTPRESVK--KYILEMVCVLSDKAPCI	786
Qy	783	IKWLRISSSVKKYYIHDHFIPIEKQFSLYPIEMEGVGKPKIINSFTQODDIEKHQSDAGL	842
Db	787	TDMQOEGDGTVHRTYLRGNLAESKCYLITVTPYADGPGSPESIKAY---LKQAPPSKG-	841
Qy	843	YVIVPVIYISSILLGLTLLISHQRMKK-----LFMEDVPRPNKCSWAQGLN-FQKP--	892
Db	842	-----PTV-----RTKKVGKNEAVLEMDQLPYDVQNGCFIRNYTIFIRITII	881
Qy	893	--ETPEHLFIKHT---ASVTCGPILLEPETISEDISVDTSMKKNKDEMMPTTVVSLSTT	946
Db	882	GNETAVNVDSHTEYTLSSLTSPDLYM---VRMAAYTDEGGKDGPEFTFTT--PKFAOG	935
Qy	947	DLEKGS-----VCISDQF-----NSVNFSEAEGTEVTEDESQRQPEVK	985
Db	936	EIESGDDKHTHCPCPAPELLGDSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVK	995
Qy	986	YATLL-----SNSKPS-----TGEQGLINSSVTKCFSSKN--SPLKD	1022
Db	996	FNNYVDGVEVHNAKTKPREEOYNSTYRVSVLTVLHQDLNNGKEYKCKVSNKALPAPIEK	1055
Qy	1023	SFSNSWIEIAQAFILSDQHPINISPLHTFS--EGL---DELLKLEGNFPEENN---1072	
Db	1056	TISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVEMESNGQPENNYKTT	1115
Qy	1073	---DKSIYYLGVTSIKKRESGVLLTDKSR---VSCFPAPCLFTDIRVLQDSC-S	1121
Db	1116	PVVIDSDGSEFLL-----YSKLTVDKSRMOQGNVFSK-----SYMHEALHN	1155
Qy	1122	HFVENNINL	1130

QY	1075	PRVLDSDGSSFFL	YKRLTVDKSRWQGGNVFSC	SVMHGALHN	1155
Db	1116	PRVLDSDGSSFFL	YKRLTVDKSRWQGGNVFSC	SVMHGALHN	1155
QY	1122	HEVENNINL	1130		



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OY 846 VPIIISILLGLTLLISHQRMK-----LFWEDVPNPKNCWSAQLN-FQKP-----E 893
Db 523 -PTV-----RTKKVGKNEAVLEWDLPVDQNGEIRNYTIFRTIIGNE 565
OY 894 TFEHLFIKHT---ASVTCGPLLEPETISEDISVDTSMKNDMMPTVSLSTDL 949
Db 566 TAVAVDSHTEYLLSLTSDLYM---VRMAAYTDEGCKDGEFTFTT--PKAAGEIE 619
OY 950 KGSVCISDQF-----NSVNSEAEGETEVTYEDESQRPV 984
Db 620 SGEKSCDKHTHTPCPAPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 679
OY 985 KYATLI-----SNSKPSE-----TGEEOGLINSSVTCKCFSSKN---SPLK 1021
Db 680 KEMVYVDGVEVHNAKTKPREDOYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 739
OY 1022 DSEFNSSWEIEAQAFFILSDQHNIISPHLTPS--EGL--DELLKLEGNPEENN--- 1072
Db 740 KTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKT 799
OY 1073 -----DKSIYVIGVTSIKKRESGVLLTDKSR-----VSCDFPAPCLFTDIRVLQDSC- 1120
Db 800 TPVLDSDGSFLL-----YSKLTVDKSRMGOQGVNFSC-----SYMHEALH 839
OY 1121 SHEVENNINL 1130
Db 840 NHTYQKSLSL 849
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RESULT 5
US-09-935-868-9
; Sequence 9, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-868-9
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Query Match 4.9%; Score 308.5; DB 5; Length 951;  
Best Local Similarity 22.4%; Pred. No. 1.7e-13;  
Matches 117; Conservative 92; Mismatches 241; Indels 73; Gaps 22;

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OY 337 PPKILTSVGSNVSFHCITYKK---ENKIVPSKEIYVMMNLAEKIPQSQYDVVSDHVSQYTF 393
Db 33 PESBVQVLSNFTAVCVLKEKCMDFHVNANYIWMKTN-HFTLPKEQYTIINRTASSVTF 91
OY 394 FNLNETKPRGKFTYDAVAYCCNEHECHHRYAELVIDY-----NINISC-ETDGYLTK 444
Db 92 TDI-----ASLNIQITCNILTFGQLEQNVYGITIISGLPEKPKNLSCIVNEG--KK 141
OY 445 MTCRMSTSTIOSLAESTIOLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECT--FQP 502
Db 142 MRCEWDG-----RETHLETFNFTLKSEWAT-----HKFA---DCKAKRDTPTSCTVDYST 188
OY 503 IFLSGYTMIRINHSLSLSDSPTCVLPDSVVKPLPPSSVKAETITN---IGLKLISW 558
Db 189 VYEVN-IEVWEAENALGKVTSDHINEDPVYKVKPNPHNL---VINSEELSSILKLTW 244
OY 559 EKP-----VFPENNLQFQIRYGLSGKEVQWKMEYVDKSKSVSLPVPDL--CAVAVQV 611
Db 245 TNSIKSVIILKYNIOYRTKAST-----WSQIPPEDTASTRSSFTVQDLKPFTEYVFR 299
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OY 612 RCKRLDGLGWSNMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNVTLMLKPLMKND 671
Db 300 RCMKEDGKGYMSDWSSEASGITYEER-PSKAPSFWYKIDPSHTQGYRTVQLVWKTLPFE 358
OY 672 SLCSVQRYVINHHTSCNGTWSQVGNH---TKFTFLMTEQAHVTVLAINSIGASVANE 727
Db 359 ANGKILDEVT-----LTRWKSHLQNTVNAATKLTVNLTNDRIYLAITLVRLNVGKSDAV 413
OY 728 NLTFSPMSKVNIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNEDGE--IKW 785
Db 414 LTIPLACDQATHPVMDLKAFP-KDNMLVEMWTTPRESVK--KYLLECVLSDKAPCITDW 470
OY 786 LRISSVAKYIYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSE 828
Db 471 QQEDGTVHRTYLRGNLAESKCYLITVTPYADGPGSPESIKAY 513
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RESULT 6
US-09-853-180-5
; Sequence 5, Application US/09853180
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christl L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/09/853,180
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-853-180-5
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Query Match 3.5%; Score 220.5; DB 5; Length 862;  
Best Local Similarity 19.8%; Pred. No. 2e-07;  
Matches 182; Conservative 129; Mismatches 322; Indels 285; Gaps 49;

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Db 32 DVITYPPSHVIL-LGSTVNITCSLKRQGCFFHYSRRNKLILYK-----FD 74
OY 383 -VVS DH-----VSKVTFFNLNETKPRGKFTYDAVAYCCNEHECHHRYAELV---IDVIN 433
Db 75 RIRNFHGHSLNSQVTLPLGTLTFVCKLA-----CINSDEIQGAEIFVGAPEQPN 129
OY 434 ISCTDGYLTMTCRWSTSTIQL-AESTIOLRYHRSSLY---CSDIPSIHPISEPKDC- 488
Db 130 LSCIQGEGGTACTWGRGRDTHLYTEYTLQLSGPKNLTWQCKDI-----YCD 179
OY 489 YLQSDGFYECIFQPIFLLSGYTMIRINHSLSLSDSPTCVLPDSVVKPLPPSSVKAETI- 547
Db 180 YLD-----FGINLTPESPESNETAKYAVNSLSSSSSLPSTFTFLDIVRPLPPWDIRIKFQ 235
OY 548 TINIGLKLISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPVPDLCAVY 607
Db 236 KASVSRCTLYWRDEGLVLLN---RLRYRPSNSRL-WNMVNVYAKAKGRHDLDLKPF--TEY 290
OY 608 AVQVCKRLDGLGWSNMSNPAYTVMDIKVPMRGP---EEFWRIINGDTMKK-----EK 658
Db 291 EFOISKLHLKGSWSDWSES-----LRAQTPEEPTGMLDVW-----YMKRHIDYSRQ 339
OY 659 NVTLLMKPLMKNDLSQVQRYVINHHTSCNG-TWSEVDGNTHTKFTFLMTEQAH-TVTVLA 716
Db 340 QISLFWKNLSVSEARGKILHYQVTLQELLTGKAMTONITGHTSWTTVIVIRGTGMVAVSA 399
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QY 717 INSIGASVANENLTFSWMSKVNI-----QSLSAYPLNSSCVIVSWITSPSD-Y 765
    | | : |
Db 400 ANSKGSSLP-----TRINIMNLCEAGLLAPROVSANSEGMDNITLVTWQPPKDPDS 449
    : : : |
QY 766 KLMFYIEWKNLNEDGE---IKWL-----ISSVKKYYIHD-----799
    : : | | : | | | | : : |
Db 450 AVQETVEWERELHPGGDYOVLNWLRSRPYNVSALISENIKSYICYEIRVALSBDGCC 509
    : : | | : | : | | : : |
QY 800 -----HFPIEKYQFSL--YPIF--MEGYKP 822
    : | : : | | : |
Db 510 SSILGSKHKAPLSCPHINAITEEGSILISWNISPQEQMGCLLHYRIYWKERDSNSQP 569
    : : | |
QY 823 KI-----INS-----FTQDIKEH-----QSDAGLYVIYPV 848
    : : | | | | | |
Db 570 QUCEIPYRVSONSHPI NSLOPRVTYVLMTALTAAGESHHGNEREFCLQGKANMMAFVAP 629
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QY 849 IISSILLGLTLISHQRMKLF-----W--EDVPNPKNCSWAQGLNFQKPEP--- 894
    | : : : | : : | : : | : : | : : |
Db 630 SICIALIMWG-IFSTHYFOOKFVLLAALRPQWCSEIREIDPANSTCAKKYPIAEKTQLP 688
    : | | | | | | | | : : |
QY 895 FEHLFIKHTASVTCGPLLEPETISEDISVDT-----SWKNKDEMPTTVSVLLST 945
    : | | | | | | | | : : |
Db 689 LDRLLIDWPT-----PEDREPLVISEVLHQVTPVFRHPPCCSNMWPOREK-----731
    : | | | | | | | | : : |
QY 946 TDLEKGSVCISDQFNSVNFS-----EAEGTEVT--YE-----DESQRPFVKYATLI 990
    : : | : | : : | : : | : : |
Db 732 -GIQGHQAASEKDMMHSASSPPPRALOAESRQLVDLYKYLESGSDPKPENPACPWTVLP 790
    : : | : | : | : | : | : |
QY 991 SNSKPSSETGEEOGLINSSVTKCFSSKNSPLKDSFSNSSMEIEAQ---AFFILSDQHNI 1046
    : | : | : | : | : | : | : |
Db 791 AGDLPT----HDGYLPASNIDD-LPSHEAPLADGLE---ELEPOHISLSVFSSSLHP-- 839
    : | : | : | : | : | : |
QY 1047 ISPHLTFSEG---LDEL 1060
    | | | | | | | |
Db 840 ----LTFSCGDKLTLDDQL 853

```

```

RESULT      7
US-10-119-480-92
: Sequence 92, Application US/10119480
: GENERAL INFORMATION:
:   APPLICANT: Baker, Kevin P.
:   APPLICANT: Desnoyers, Luc Gerritsen, Mary
:   APPLICANT: Goddard, Audrey
:   APPLICANT: Godowski, Paul J.
:   APPLICANT: Grimaldi, J. Christopher
:   APPLICANT: Gurney, Austin L.
:   APPLICANT: Smith, Victoria
:   APPLICANT: Stephan, Jean-Philippe F.
:   APPLICANT: Watanabe, Colin L.
:   APPLICANT: Wood, William I.
:   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
:   TITLE OF INVENTION: ACIDS ENCODING THE SAME
:   FILE REFERENCE: P3530P1C1
:   CURRENT APPLICATION NUMBER: US/10/119,480
:   CURRENT FILING DATE: 2002-04-09
:   NUMBER OF SEQ ID NOS: 246
:   Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 92
:   LENGTH: 582
:   TYPE: PRT
:   ORGANISM: Homo Sapien
US-10-119-480-92

```

```

Query Match          3.5%; Score 218.5; DB 6; Length 582;
Best Local Similarity 20.4%; Pred. No. 1.6e-07;
Matches 118; Conservative 100; Mismatches 243; Indels 117; Gaps 28;

QY 433 NISCETDGYLTMTCRWSTSTIQSLAESTLQRLRYHRSSLY--CSDIPSIHPISPKDCYL 490
      |||| 1 :|| || 1 :|:: 1 :|: 1
Db 59 NISC-VYYRRKNLTCTWSPGKEKSYQYTVKRTYAFGEKHNDCTNSS----- 105

```

[illegible]

```

RESULT      8
US-09-935-868-10
; Sequence 10, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-10

```

```

Query Match          3.18; Score 191.5; DB 5; Length 332;
Best Local Similarity 23.2%; Pred. No: 5.5e-06;
Matches 77; Conservative 56; Mismatches 140; Indels 59; Gaps

QY      337 PPKILTSVGSNVSPFHCITYKK--ENKIIVPSKEIIVMMMLAEKIPQSÖYDVVDSDHVSKYTF 393
        | : : ||| : | : : | : ||| | : ||| : |||
Db       33 PESPVQLHSNFTAVCVLKEKCMDFHVANANYIVWKTN-HETIPKEQYTIINRTASSVT 91

QY      394 FNLNETPRCKEFTYDAVCCNEHECHHRYAELVIDY-----NINISC-ETDGYLT/K 444
        : : : : || : : ||| : : ||| : : |||
Db       92 TDI-----ASLNIOQLTCNILTEGQLEQNYGITIIISGLPPEKPNLSCIYNES--KK 141

QY      445 MTRCWSTSTIQSLAESTLÖLRHYRHRSSLYCSDIPSIHPISEPKDCITQSDGFYECT--FQP 502
        | | | : : ||| : : ||| : : ||| : : |||
Db      142 MRCEWDGG----RETHLETNETFLKSEWAT----HKFA---DCKAKRDPTPGCTVDYST 188

```



```

QY 503 IFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVKKPLPSSSVKAEITIN----IGLLKISW 558
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 189 YFEVN-IEVWVEAENALGKVTSDHINPDPYVKKPNPPHNLS---VINSEETSSILKLTW 244
      .
QY 559 EKP-----VEPENNLQFOIRYGLSGKEYQWKMEYVYDAKSKSVSLPVPDL--CAVYAVQV 611
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 TNPSIKSVIILKYNIOYRTKDAST-----WSQIPPEDTASTRSSFTYQDLKPFTEYVERI 299
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 612 RCKRLDGLGYWSNMSNPATYVVMIDIKVPMRGP 643
      || : || |||| : || : : : : : : : : : : : : : : : : : : : : :
Db 300 RCKMEDGKGYWSDWSEASGITYEDR-PSKAP 330
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 9

```

PCT-US02-09052-7
: Sequence 7, Application PC/TUS0209052
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: YUE, Henry
: APPLICANT: XU, Yuming
: APPLICANT: THANGAVELU, Kavitha
: APPLICANT: WARREN, Bridget A.
: APPLICANT: TANG, Y. Tom
: APPLICANT: DUGGAN, Brendan M.
: APPLICANT: TRAN, Uyen K.
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: HONCHELL, Cynthia D.
: APPLICANT: BURFORD, Neil
: APPLICANT: FORSYTHE, Ian J.
: APPLICANT: YANG, Junming
: APPLICANT: MASON, Patricia M.
: TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
: FILE REFERENCE: PF-0925 PCT
: CURRENT APPLICATION NUMBER: PCT/US02/09052
: PRIOR FILING DATE: 2002-03-12
: PRIOR APPLICATION NUMBER: 60/275,249; 60/316,810; 60/323,977; 60/348,447;
: 60/343,880
: PRIOR FILING DATE: 2001-03-12; 2001-08-31; 2001-09-21; 2001-10-26;
: 2001-11-02
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PERL Program
: SEQ ID NO 7
: LENGTH: 1450
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 7500191CD1
PCT-US02-09052-7

```

Query Match	2.8%;	Score 172.5;	DB 1;	Length 1450;
Best Local Similarity	19.6%;	Pred. No. 0.00093;		
Matches 218;	Conservative 151;	Mismatches 407;	Indels 339;	Gaps 54;

```

QY 48 LIPAGL-----SKNTSNSNGHYE--TAVE-----PKNS----SG 76
    ||| |         ||: | |: |         | | | | |
Db 103 LIPDGSLEISNVVSHKHKNKPDDEGYQCVATVESLGTIISRTAKLIVAGLPRETSQPEPSS 162
QY 77 THFSNLKSTTFHC-----CFRSEDNRNCSLCADNI--EGKTFVSIVNSLVEFQOID 124
    : |         : | | | | | | : | |
Db 163 VYAGN--NALNCEVNADLVPEVRWEQNRQPLLLDDRVIKLPSCGMLVISNAT----- 212
QY 125 ANMNIQCWLKGDKLFICYVESLEFRNFRNYKYKVHLLYVL--PEVLED-----SPLVP 176
    : || | | : | | | | | | | | | | |
Db 213 -----EGDGLYRCVAVES---GSPPKYSDEVELKVLDPFEVISDLVFLKQSPPLVR 260
QY 177 QKGSFQMVHNCNSVHECCCECLVVPVPTAK-----LNDTLMLCKITSGGVIIFQSPIMSV 229
    | : | | | | : | | | | | | | | |
Db 261 VIGQDVLLPCVASG-----LPPTTKMKMKEALDTESSERLYVLLAGS-----SL 305
QY 230 QPINMVKPDPPLGLHMEITDGNLKIISWSSPPLVPFLQYQVKYSSENSTTV--IREADKIY 288
    : : : : | | : | | | | | : : | | : : | |

```

Db	306	EISDVTEDD--AGTYFCIADNGNETIEAQA----	ELTVQAQPEFLKOPTINIAHESMDIV	359
QY	289	SATSLIVDSILPGSSYEVOVRGKRLDGPGIWDSTPRV--	FTTQDVI--YFP-----	337
Db	360	-----	FECEVTGK-----PTPTVKWVKNGDMVIPSDEYFKTYKEH	393
QY	338	-PKILTSVGSNVSFH-CIYKKEKNIVPSKEIYWMNNLAE-----	KIPQSDVAVSDHVS	389
Db	394	NLOVGLVKSDEGFYQCI--AENDVGNAGAGOLILIEHAPAT	TGPLPSAPRDVAVSLVS	451
QY	390	KVTFENNETKPRGKFTYDAVYCCNEHECHHRYAELIYIDVINIS	CETDGIYTKMTCRM	449
Db	452	-TRFKLTWRTP-----	ASDPHGDNLTYSVFYTKEGIAREVENTSHPGEMOV--	498
QY	450	STSTIOSLAESTLQLRHYRHSLSLYCSDIPSIHDPSEPKDCYLOS	DGFYECIEQPIFLLSGY	509
Db	499	---TIQNIMPATVYI-----	-----F	511
QY	510	TMWIRINHSLSLDSPTCYLPDSVYKPLRBPSSVKAETTINIGL	KISWEKPYEPENNIO	569
Db	512	RYMAQNKHGSSESSAPLRVETQPEVQLPGPAPNLRA--	YAASPTSIYTWETPVSNGEIQ	570
QY	570	-FOIRGLSGKEVQWKMEYVYDAKSKSVSLPYDLCAYVAVOVRC	RJDLGLGYMSNMSNP	628
Db	571	NKLYIYMEKGTDE---QDVIDSSHSTYTINGLKKYTEYSFRVAV	YNKHGPGV---STP	622
QY	629	AYTVYMDIKVPMRGPEFWRIINGDTMKKEKNVTLMLKPLMKNDSL	CSVQRYVINNH-TSC	687
Db	623	DVAVPTLSDVPSAPQNLSTL---EVRNKSIMIHWO	PPAPATONGITGKIKRYKASR	678
QY	688	NGTWEDEVGNHTKFTFL-----WTEQAHVTYVLAINSIGASVANFL	-TFSWPMKSVNI	740
Db	679	KSPVETLVYSGTQLSOLIEGLDRGETEYNEFRVAA	LTINGTGPATDWLSAETFESDDETRV	738
QY	741	VQ---SLSAVPLNSSCVIVSWILSPSD-----	YKLMYFI-----IEMKNLNE	780
Db	739	PEYVPSLHVRPLVTS-IVVSW--TPPENQNTIVRGYALGYGIGS	PHAQTIKVDYK-----	790
QY	781	GEIKMLRISSVKKYIHDHFIPIEKYQFSLYPIEMEGVGKPKIINS	FTODIEKHQSDA	840
Db	791	-----QRYTIENTDPSSHVYTLKAFNNVGE	GIPLYESAVTTRPHTD--TSEV	836
QY	841	GLVYI-----	VPVITISSILLLCTLLISHQRMKKLTWEDVPRNPKCSMAQG	886
Db	837	DLEVINAPYTPVPDPTPMPMPVGVQASIL-----	SHDTI-RITWADNSLPKH-----	882
QY	887	LNFQKPETFEHLFIKHTASVTCGPLLEPETISEDISVDT	SWKNKDEMPPTVAVSLSTT	946
Db	883	---OKITDSRYTYTRW-----	KTNIPANTKYKNANATLSLYATGLKPN	923
QY	947	DLEKGSVCISDQFNSVNFs-EAEGTEVYEDESORQPFVKYATLIS	NSKPSFT-----	998
Db	924	TLVEFSYVWTKGRRSSTWSMTAHGT--TFELVPTSPP--	KDVTVVSKEGKPKTIIIVNQP	979
QY	999	-GEEOLLINSSVTKCFSSKNSPLKDSFNSSSWEIE	1032	
Db	980	PSFANGKITGYIIITYSTDVNAEIH-----	WVIE 1008	

RESULT 10  
PCT-US02-09671-1148  
; Sequence 1148, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: ZYCOS Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801

PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1148  
LENGTH: 1461  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-09671-1148

Query Match 2.8%; Score 172.5; DB 1; Length 1461;  
Best Local Similarity 19.6%; Pred. No. 0.00094;  
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;

48 LLPAGL-----SKNTSNGHYE--TAVE-----PKFNS---SG 76  
103 LLPDGLFISNVVSHKHNKPDGYYQCVATVESLGTIISRTAKLIVAGLPRFTSQPESS 162  
77 THFSNLKSTFHC-----CFRSEODRNCSLCADNI-----EGKTFVSTVNSLVFOQID 124  
163 VYAGN--NAILNCEVNADLVFVFWEQNRQPLLDRLVYIKLPSGMLVISNAT----- 212  
125 ANWNIOCWKLKDLKLFICYESLFKNLFRNYKXHLVYL-PEVLED-----SPLVP 176  
213 -----EGDGLYRCVYES--GPPKYSDEVELKVPDPEVTSIDLVLKQPSPLVR 260  
177 QKGSFQMVHNCNVHCECECLVVPPTAK-----LNDTLMLCKITSGVIFQSPILMSV 229  
261 VIGQDVLPVAVASG-----LPTPTIKMKNEALDTESSESLVLAGG-----SL 305  
230 QPINMVKPDPPLGLHMEITDDGNLKSMSPLVPFPLQYQVYSENSTTV-IREADKIV 288  
306 EISDVTEDD--AGTYFCIADNGNETIEQA---ELTVQAQPEFLKQPTNIYAHESMDIV 359  
289 SATSLLVDSILPGSSYEQVGRKRLDGPGLMSDWTSPRV--FTTQDVI---YFP----- 337  
360 -----FCEVYTGK-----PPTPVKWKNGDMVIPSDFYKIVKEH 393  
338 -PKILTSVGSNVSEH-CIYKKNKIIVPSKEIWMNLA-----KIPSOYDVVSDHVS 389  
394 NLOVLGLVKSDEGTYQCI--AENDVGNQAQAOLILLEHAPATTGPLPSAPRDVVASIVS 451  
390 KYTFENLNETKPRGKFTYDAVYCCNEHECHRYAELVYIDVININISCECTGYLTKMTCRW 449  
452 -TRFIKLTWRTP-----ASDPHGDNLTVSVFYTKEGTAREVENTSHPGEMQV-- 498  
450 STSTIQSLAESTLQLRHRSLSLYCSDIPSIHPISEPKCYLQSDGFYECIFQPIFLSGY 509  
499 ---TIGNLMPATVYI-----F 511  
510 TMTIRINHSLSLSPPTCYLPDSVYKPLPPSSVKAETITNIGLLKISWEKPVFENNLO 569  
512 RYMAQNKHSGESSAPLRVETQPEVQLPGPAPNLRA-YAASPTISITVETPVSGNGEIQ 570  
570 -FOIRYGLSGKEVQWKMEYDAKSKSVSLPVPDLCAVYAVQYRCKRLDGLGYSWMSNP 628  
571 NYKLYYMEKGTDE---QVDVSSHSTYTINGLKKYTESFRVVAYNKHGPGV---STP 622  
629 AITVYMDIKVPMRGPFWRIINGDTMKKEKNVTLWKPLMKNDLSLQSVQRYVINHH-TSC 687  
623 DVAVRTLSDVPSAAPONLSL---EVRNSKSIIMHQPAPATQNGQITGYKIRYRKASR 678  
688 NGTWESEDVGNHTKFTFL-----WTEQAHTVTVLAINSIGASVANFNL-TFSWPMKSVNI 740  
679 KSDVTEIVSGTQLSOLIEGLDRGTEYNFRVAALTITNGTPATDMLSAETFEESDLDETFRV 738  
741 VQ---SLSAVPLNSSCVIYVNLISPSD-----YKLMYFI-----IEWKNLNEED 780

739 PEVPSLHVRPLVTS-IVVSW--TPPENONIVRGYALGIGSPHAOTIKVDYK----- 790  
781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMGVGKPKINSFTQDDIEKHQSDA 840  
791 -----QRYTIENTDPSHHVITLKAFFNNVGEJTLYESAVTRPHD--TSEV 836  
841 GLVYI-----VPYIISSSILLAGTILISHORMKLPWEDVNPKNCSNAOG 886  
837 DLFVINAFTVPDPPTMPMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882  
887 LNFQKPETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSMKNKDEMPPTVVSLSLSTT 946  
883 ---OKITDSRYITVRM-----KTNIPANTKYKNANATTLSLYLVYGLKPN 923  
947 DLEKGSVCISDOFNSVNF--EAEGETEVTYEDESQROPFVKYATLISNSKPSSET----- 998  
924 TLXFSVMVTKGRSSSTWSMTAHTG--TFELVPTSP--KDYIVVSKEGKPKTIIVNQOP 979  
999 -GEEGLINSSVTKCFSSKNSPLKDSFNSMSWEIE 1032  
980 PSEANGKITGYITYSTVDVNAEIHID-----WVIE 1008

RESULT 11  
PCT-US02-10824-189  
Sequence 189, Application PC/TUS0210824  
GENERAL INFORMATION:  
APPLICANT: Origene Technologies  
TITLE OF INVENTION: Prostate Cancer Expression Profiles  
FILE REFERENCE: 9U 206 PCT  
CURRENT APPLICATION NUMBER: PCT/US02/10824  
CURRENT FILING DATE: 2002-04-08  
PRIOR APPLICATION NUMBER: US 60/281,732  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: US 60/281,731  
PRIOR FILING DATE: 2001-04-06  
NUMBER OF SEQ ID NOS: 211  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 189  
LENGTH: 1461  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-10824-189

Query Match 2.7%; Score 170.5; DB 1; Length 1461;  
Best Local Similarity 19.6%; Pred. No. 0.0013;  
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;

48 LLPAGL-----SKNTSNGHYE--TAVE-----PKFNS---SG 76  
103 LLPDGLFISNVVSHKHNKPDGYYQCVATVESLGTIISRTAKLIVAGLPRFTSQPESS 162  
77 THFSNLKSTFHC-----CFRSEODRNCSLCADNI-----EGKTFVSTVNSLVFOQID 124  
163 VYAGN--GAILNCEVNADLVFVFWEQNRQPLLDRLVYIKLPSGMLVISNAT----- 212  
125 ANWNIOCWKLKDLKLFICYESLFKNLFRNYKXHLVYL-PEVLED-----SPLVP 176  
213 -----EGDGLYRCVYES--GPPKYSDEVELKVPDPEVTSIDLVLKQPSPLVR 260  
177 QKGSFQMVHNCNVHCECECLVVPPTAK-----LNDTLMLCKITSGVIFQSPILMSV 229  
261 VIGQDVLPVAVASG-----LPTPTIKMKNEALDTESSESLVLAGG-----SL 305  
230 QPINMVKPDPPLGLHMEITDDGNLKSMSPLVPFPLQYQVYSENSTTV-IREADKIV 288  
306 EISDVTEDD--AGTYFCIADNGNETIEQA---ELTVQAQPEFLKQPTNIYAHESMDIV 359  
289 SATSLLVDSILPGSSYEQVGRKRLDGPGLMSDWTSPRV--FTTQDVI---YFP----- 337  
360 -----FCEVYTGK-----PPTPVKWKNGDMVIPSDFYKIVKEH 393

```

QY 338 -PILTSVGSNVSEH-CIYKKEKNIVPSKEIWMNNLAE-----KIPQSOYDVNSDHVS 389
Db 394 MLOVGLVKSDEGFYQCI--AENDVGNAGAQOLITLEHAPATGTPPLPSABRDVVASLVS 451
QY 390 KVTFFENLNETKPRGKFTYDAVYCCNEHCHHRYAELVIDVININISCEITDGLTKMTQCRW 449
Db 452 -TRFKLTWRTP-----ASDPHGDNLTVSVFYTKEGIAREREVENTSHGEMQV-- 498
QY 450 STSTIOSLAESTLQLRYHRSSLYCSDIPSINHPISEPKDCYLOSDFYECILOPIFLLSGY 509
Db 499 ---TIONLMPATVYI-----F 511
QY 510 TMTWIRINHSLSLSDSPTCYLPDSVYKPLPPSSVKAETITINIGLKISNEKPYFPENNLO 569
Db 512 RYMAONKHGSGESSAPLRVETQPEVQDGPAPNLRA-YAASPTSTIVTWETIPVSGNGEIO 570
QY 570 -FOIRYGLSGKEVQWKMEYVDAKSKSVSLPVPDLCAVYAVQVRCRRLDGLCYWSNWSNP 628
Db 571 NKLYTMEKGTDE---QDVVSSHSTYINGLKKYTEYSFRVVAYNKHGPGV---STP 622
QY 629 AYTVVMDIKVPMRGPETWRIINGDMKEKNVTLLKPLMKNDLSGVQRYVINHH-TSC 687
Db 623 DVAVRTLSDVPSAAPONLSL---EVNRSKSIIMHWOPAPATONGQITGYKIRYRKASR 678
QY 688 NGTWSDEVGNHTKFTFL-----WTEQAHVTVLAINSIGASVANENL-TESWPMKSVNI 740
Db 679 KSDVTEITLVSGTOLSQIEGLDRGETNFRVAALTINGTGPATDWLSAETRESDDLDETRV 738
QY 741 VQ---SLAYPLNSSCVIVSWILSPD-----YKIMYFI-----IEMKNLNE 780
Db 739 PEYPSLSLHVRPLVTS-IVVSW--TPPENQNIVRGYAIGYGISPHAGTIKYDK----- 790
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQSLYPTMEGVGKPKTIINSFTQDDIEKHQSDA 840
Db 791 -----QRYTIENTLDPSSHVYITLKAENNVEGIGIPLYESAVTTRPHD--TSEV 836
QY 841 GLVYI-----VPVLISSSTILLGLTLLISHQRMKKLFWEDEVPNPKNCWSAOG 886
Db 837 DLEVINAPYTPVPDPTPMMPRGVQASIL-----SHDTI-RITWADNSLEKH----- 882
QY 887 LNFQKPETFEHLFIKHTASVTCGPLLEPETISEDISVDTSMKKNKDEMPPTIVVSLSTT 946
Db 883 ---QKITDSRYTYVRW-----KTINIPANTKKYKNANATLSLYLTGLKPN 923
QY 947 DLEKGSVCISQFNSVNFs-EAEGTEVYEDESOROPVKYATLISNKBSET----- 998
Db 924 TLYEFSVWVTKGRRSSTWSMTAHGT--TFELVPTSP--KDVTVVSKKEGPKTIIIVNWOP 979
QY 999 -GEOGLINSSVTKCFSSSKNSPLKDSFSNSSWEIE 1032
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WVIE 1008

RESULT 12
PCT-US02-09671-1147
; Sequence 1147, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04

```

```

; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1147
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1147

```

Query Match	2.7%;	Score 170.5;	DB 1;	Length 1461;
Best Local Similarity	19.6%;	Pred. No. 0.0013;		
Matches 218;	Conservative 151;	Mismatches 407;	Indels 339;	Gaps 54;

OY	48	LLEPGL-----SKNTSNSNGHYE--TAVE-----PRNS---SG	76
Dd	103	LEPDGSLFISNVVSHKHNKPDEGYQCVATVESLGTIISRKLIVAGLPRTSQPEPS	162
OY	77	TFFSNLSKTTFHC-----CFRSEQDRNCSICADNI---EGKTFVSFNLSLVFOQID	124
Dd	163	VYAGN--GALLNCEVNADLVPFVRMEONQPILLDDRVIKLPSSGMVISNAI-----	212
OY	125	AANNIOCMUKGDCLKFCICYVESLFKNLERNNYKVHLLYL-PEVED-----SPLVP	176
Dd	213	-----EGDGLRYRCVYES--GGPKYSDEVELKVLPPDEVISDLVFLKOPSPLYR	260
OY	177	OKSFOMVHCNCSVHECCCLVPVPPIAK-----LNDTLMLCKITSGVIFQSPLMSV	229
Dd	261	VIGQDVLPVCVASG-----LPPTIKMKNEALDTESSERLVLAGG-----SL	305
OY	230	OPINWVKPDPRLGLHMETDDGNLKISWSPPPLVPPLQYOVKYSENSTTV-IREADKIY	288
Dd	306	EISDYTEDD--AGTYFCIADNGNETIEAQ----ELTVQAQPEFLKQPTNYAHESMDIV	359
OY	289	SATSLLVDILPGSSYEVOVRGRKRLDGIMSDWSTPRV--FTYQDVI-----YEP----	337
Dd	360	-----FECEVTGK-----PTPYKWVKNGDMVIPSDYEKIVKEH	393
OY	338	-PKILTSGSNVSFH-CITYKKENKIYPSKEIYWMMNLAE-----KIPSOQDYVSDHVS	389
Dd	394	NLOYGLVKSDEGEFYOCI--AENDVGNAOAGAQLILEHAPATTGPLPSABRDVVASLVS	451
OY	390	KVFEEFNINETKPRGFETYDAVYCCENHCHHRAYELVIDVINISCETDGYLTMTCRW	449
Dd	452	-TRFIKUTWRTP-----ASDPHGDNLTYSVFYTKEGIAREVENTSHGEMOV--	498
OY	450	STSTIOSLAESTLOLRHYRRSSLYCSDIPSIHPISEPKDCYLOSDFYECIJOPIFLLSGY	509
Dd	499	--TIQNLMPATVXI-----F	511
OY	510	TWMTIRINHSLGSLSDSPTCVLPDSVYKPLPPSSVKAETINIGLIKISMEXPFENNLO	569
Dd	512	RMAONKHGSGESSAPLRKETQPEYOQLGPAPNLRRA-YAASPSTIYTWETPIVSCNGEIQ	570
OY	570	-FOIRYGLSGKEVOWKMVEYIDAKSVSLLPVLDCAVYA VOVRCKRLDGLCYSMWSNP	628
Dd	571	NKRLLYMEKGTDKE---QDVDSSHSTYINGLKKEYTESFRVAANYNKHBGV---STP	622
OY	629	AVTYVMDIKVPMRGPWFRIINGDJMKEKENVTLLMKPLMKNDJLSYORXYINHH-TSC	687
Dd	623	DVAVRTLSADVSAAPONLSL---EVARNKSIMIHWOBPAPATONGOLTCYKIRYRKASR	678
OY	688	NGTWESEDVGNHTKFTEL-----WTEDAHVTYVLAINSIGASVANENL-TFSWPMKSVNI	740
Dd	679	KSDVTE TLVSGTOLSOLIEGLDRGETEYNERVALTINGCTPATDWLSAETFESDDLDETREV	738
OY	741	VO---SLSAYP LNSSCIVIVSWILSPSD-----YKIMFYI-----IEWKNLNED	780
Dd	739	PEYPSLSLHVRLPTS-IVVSW--TPPENONIVRVGAIGAIGISPHAQT IKVDYK-----	790
OY	781	CETKWLRISSVKKYYIHDHFIPLEKXQFSLYPIFMGVGPKIIINSFTQDDIDEKHOSDA	840

Db 791 -----QRYTTIENIDPSSHVITLKAENNNGEGILPYESAVTRPHTD--TSEV 836  
QY 841 GLYVI-----VPIVLISSILLGLTLLISHQRMKLEWEDVPPNPKNCNMAOG 886  
Db 837 DLEVINAPYTPVDPPTMPMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882  
QY 887 LNFQKPEFTEHLEFIKHTASVTCGPIILLEPETISEDISVDTSMKNKDEMPPTVSLSTT 946  
Db 883 ---QKITDSRYTYTRW-----KTNIPANTKYKNANATTLSTLVLTGLKPN 923  
QY 947 DLEKGSVCISDOFNSVNFSEAEGETEYTEDESQROPFVKYATLISNSKPSSET----- 998  
Db 924 TLVEFSVMVTKGRSSSTWSMTAHT--TFELVPTSP--KDVTVVSKGKPKTIIVNWQP 979  
QY 999 -GEEGLINSSVTKCFSSKNSPLKDSFSNSSWEIE 1032  
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WVIE 1008

RESULT 13  
PCT-US02-09671-1149  
; Sequence 1149, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1149  
; LENGTH: 1461  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-09671-1149

Query Match 2.7%; Score 170.5; DB 1; Length 1461;  
Best Local Similarity 19.6%; Pred. No. 0.0013;  
Matches 218; Conservative 151; Mismatches 407; Indels 339; Gaps 54;  
QY 48 LLPAGL-----SKNTSNSNGHYE--TAVE-----PKFNS-----SG 76  
Db 103 LLPDGLFISNVVSHKHNKPDDEGYIQCAVATESLGTIISRTAKLIVAGLPRFTSQPEPSS 162  
QY 77 THFSNLSKTTFHC-----CFRSEDNRNCSLCADNI---EGKTFVSTVNSLVFOQID 124  
Db 163 VYAGN--GALNCEVNADLVPEVWEQNRQPLLDRLVTKLPSCMLVISNAT----- 212  
QY 125 ANWNIOQWLKGDLLFCYVESLFRNRYNYKVHLLVYL-PEVLED-----SPLVP 176  
Db 213 -----EGDGLYRCVYES---GGPPKYSDEVELKVLDPPEVISDLVFLKQSPPLVR 260  
QY 177 QKGSFQVHCNCSVHECCCECLVPVPTAK-----LNDTLLMCLKITSGVIFQSPLMSV 229  
Db 261 VIGQDVILPCVAGS-----LPTPTIKMKNEALDTESSERLVLAGG-----SL 305  
QY 230 QPINWYKPDPLGLHMEITDDGNLKISWSSPPLVFPLOYQVAKYSENSTTV-IREADKIV 288  
Db 306 EISDVTEDD--AGTYFCIADNGNETIEAQA---ELTVQAQPEFLKOPTNITIAHESMDIV 359

QY 289 SATSLVDLSILPGSSYEVOVRGKRLDGPGLWSDWSTPRV--FTQDVI-----YFP----- 337  
Db 360 -----FECEVTGK-----PTPTVKWVKNQMDVILPSDYFKIVKEH 393  
QY 338 -PKILTSVGSNVSPH-CIYKKEKNTIVPSKEIWMNMLAE-----KIPQSOYDVVSDHVS 389  
Db 394 NLQVIGLIVKSGDEGFYQCI--AENDVNAQAQAQLIILEHAPATIGPCLPSAPRDVVASLVS 451  
QY 390 KVFERNINETKPRGKFTYDAVYCCNEHECHHRYAELVIVIDVINISCEETDGYLTKMTCRW 449  
Db 452 -TRFIKLTWRTP-----ASDPHNDLTYSVFYTKEGIAREVENTSHPGEMOV-- 498  
QY 450 STSTQSLAESTLQLRHRSLSYCSIDPSIHPISEPKDCYLQSGGFVECFQPIFLLSGY 509  
Db 499 ---TIQNLMPATVYI-----F 511  
QY 510 TMMIRINSLGLSDSPPTCVLPDGYVKPLPPSSVKAETTINIGLTKISMEKPVFPENNLO 569  
Db 512 RYMAQNKHSGESSAPLRVETQPEVQLBGPAPNLRA-YAASPTSTVTWETPVSGNGEIQ 570  
QY 570 -EQIRYGLSGKEVQWKMVEYVDARSKSVSLPVPDLCAYAVQVRCRRLDGLGWSNWSNP 628  
Db 571 NYKLIYMEKGTDK-----QDVVSSHSTYTINGLKKYTEYSFRVAVANKHGPV---STP 622  
QY 629 AYTVMIDIKVPMRGPEFWRIINGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHH-TSC 687  
Db 623 DVAVRTLSDVPSAPQNLNL---EYVNSKSIIMHWQPPAPATONQITGYKIRYRKASR 678  
QY 688 NGTWEDEVGNHTKFTFL-----WTEQAHTVTVLAINSIGASVANEML-TESWPMKSVNI 740  
Db 679 KSDVTEFLVSGTQLSOLIEGLDRGTEYNFRVAALTINGTPATDVLSAETFEESLDDETRV 738  
QY 741 VQ---SLSAYPLNSSCVIVSWILSPD-----YKLMYFI-----IEWKNLNE 780  
Db 739 PEVPSLSLHVRLVTS-IVVSW--TPPENQNTIVRGYALIGYGISPAQTIKVDYK----- 790  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSEFTQODIEKHQSDA 840  
Db 791 -----QRYTTIENIDPSSHVITLKAENNNGEGILPYESAVTRPHTD--TSEV 836  
QY 841 GLYVI-----VPIVLISSILLGLTLLISHQRMKLEWEDVPPNPKNCNMAOG 886  
Db 837 DLEVINAPYTPVDPPTMPMPVGVQASIL-----SHDTI-RITWADNSLPKH----- 882  
QY 887 LNFQKPEFTEHLEFIKHTASVTCGPIILLEPETISEDISVDTSMKNKDEMPPTVSLSTT 946  
Db 883 ---QKITDSRYTYTRW-----KTNIPANTKYKNANATTLSTLVLTGLKPN 923  
QY 947 DLEKGSVCISDOFNSVNFSEAEGETEYTEDESQROPFVKYATLISNSKPSSET----- 998  
Db 924 TLVEFSVMVTKGRSSSTWSMTAHT--TFELVPTSP--KDVTVVSKGKPKTIIVNWQP 979  
QY 999 -GEEGLINSSVTKCFSSKNSPLKDSFSNSSWEIE 1032  
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WVIE 1008

RESULT 14  
PCT-US02-09671-1150  
; Sequence 1150, Application PC/TUS0209671  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: PCT/US02/09671  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370

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; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1150
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1150

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Query Match	2.7%;	Score 170.5;	DB 1;	Length 1461;
Best Local Similarity	19.6%;	Pred. No. 0.0013;		
Matches 218;	Conservative 151;	Mismatches 407;	Indels 339;	Gaps 54;

QY	48	LTPAGL-----SKNTSNSNGHYE--TAVE-----PKFNS-----SG	76
Db	103	LTPDGLFISNVVSHKHNKPDEGYQCVATVESLGTIISRTAKLIYAGLPRFTSQPEPSS	162
QY	77	THFSNLSKTTFFHC-----CFRSEODRNCSLCADNI---EGKTFVSTVNSLVFOQID	124
Db	163	VYAGN--GAILNCEVNADLVPEFVRWEQNRQPLLDREVIKLPSGMLVISNAT-----	212
QY	125	ANWNIOCWLKGDCLKFICYVESLFKNLEFRNYKVHLLVYL-PEVLED-----SPVLP	176
Db	213	-----EGDGLYRCVYES---GGPRKXSDEVELKVLDPDEVISDLVFLKQPSPLVR	260
QY	177	QKSGFQMVHNCNSVHECCCLVPVPTAK-----LNDTLLMCLKITSGVIFQSPPLMSV	229
Db	261	VIGDQVYLPVCVASG-----LPTPTIKMKNEEALDTESSERVLVLAG-----SL	305
QY	230	QPINWVKRPDPPLGLHMEITDDGNKISMSSPPLVPFPLOYOVKXSENSTIV-IREADKIV	288
Db	306	EISDVTEDD--AGTYFCIADNGNETIEAQA---ELTVQAQPEFLKOPTNIYAHESMDIV	359
QY	289	SATSLLYDSILPGSSYEVOVRGKRLLDGPGLWSDWSTPRV--FTQDVI---YFP-----	337
Db	360	-----FECEVTGK-----PTPVKWKNGDMVIPSDFYKIVKEH	393
QY	338	-PKILTSVGSNVSFH-CIYKKENKIIVPSKEIYWMNLAE-----KIPQSQYDVVSDHVS	389
Db	394	NLOVGLVKSDEGFYQCI--AENDVGNAQAGAQLLILEHAPATGTPLPAPRQVVASLVS	451
QY	390	KVTFENLNETKPRGKFTYDAVYCCNEHECHHRYAELVYDVNINISCEITDGYLTKMTCRM	449
Db	452	-TRFIKLTWRTP-----ASDPHGDNULTYSVEYTKEGIAREVENTSHPGEMQV--	498
QY	450	STSTIQSLAESTLQLRHYRHSLSLYCSDIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGY	509
Db	499	---TIQNLMPATVYI-----F	511
QY	510	TMTIRINHSLSGLDSPPTCVLPDSVYKPLPPSSVKAETINIGLKISWEKVPFPENNLO	569
Db	512	RYMAONKHGSGESSAPLRVETOPEVQLPGPAPNLA-YAASPTISITVETWETPVSGNGEIQ	570
QY	570	-FOIRYGLSGKEVQWKMEYVYDAKSYSVLPVDPDCAVYAVOVRCRRLDGLGYSMWSNP	628
Db	571	NYKLIYMEKGTDE---QDVVSSHSTYINGLKKYTEYSFRVAVYANKHGPV---STP	622
QY	629	AYTVVMDIKVPMRGPPEFWRIINGDTMRKEKNVTLLMKPLMKNDSLCSVQRYVINHH-TSC	687
Db	623	DVAVRTLSDVPSAQPONLSL---EVRNSKSIMIHQOPAPATQNGQITGVKIRYRKASR	678
QY	688	NGTWSEDEVGNHTKFTFL-----WTEQAHTVTVLAINSIGASVANFNL-TFSWPMKSVNI	740
Db	679	KSDVTEFLVSGTQLSQJLIEGLDRGETEYNERVAALTINGTGPATDWLSAETFESEDDETRV	738
QY	741	VQ---SLSAYPLNSSCVIVSWILSPSD-----YKLMYFI-----IEMKNLNE	780
Db	739	PEYVPSLHVRFPLVTS-IVVSW--TPPENONIVVRGYAIGYIGSGPQAOTIKVDYK-----	790

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QY 781 GEIKWLRISSSVKKYYIIHDHFIPLEKQPSLYPIFMEGVGKPKIINSEFTODDIEKHOSDA 840
Db 791 -----QRYTYIENDPSSHVYITLKAFNNVGEIGIPLYESAATRPHTD--TSEV 836
QY 841 GLVYI-----VPVLISSSILLGLTLLISHQRMKKLWEDVBNPKNCSSWAG 886
Db 837 DLEVINAPYTPVPDPTPMPMPVGVQASIL-----SHDTI-RITWADNSLPKX----- 882
QY 887 LNFQKPEFEHLEFIKHTASVTCGPLLEPETISEDISVDTSMKKNKDEMPTTVSLLST 946
Db 883 ---QKTDSTRYYTVRW-----KTNIPANTKKYKNANATILSYLVTLGLKPN 923
QY 947 DLEKGSYCISDOFNSVNFs-EAEGTEVYEDESOROPFVKYATLISNSKPSSET----- 998
Db 924 TLYEFSVMYTKGRRSSTWSMTAHC--TFELVPTSP--KDVTVVSKKEGKPKTIIVNQOP 979
QY 999 -GEEOGLINSSVTKCFSSKNSPLKDSFNSSSWEIE 1032
Db 980 PSEANGKITGYIIYYSTDVNAEIH-----WVIE 1008

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RESULT 15
US-09-853-180-2
; Sequence 2, Application US/09853180
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/09/853,180
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: The 'Xaa' at location 3 stands for Gln, or His.
; NAME/KEY: misc_feature
; LOCATION: (149)..(149)
; OTHER INFORMATION: The 'Xaa' at location 149 stands for Gly, or Arg.
US-09-853-180-2

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Query Match	2.6%;	Score 163;	DB 5;	Length 629;
Best Local Similarity	19.7%;	Pred. No. 0.0013;		
Matches 144;	Conservative 101;	Mismatches 252;	Indels 234;	Gaps 36;

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OY 334 IYPPKILTSVGSNVSEPHCIYKKENKIYPSKEIYVMMNLAEKIPQSYDVVSDHVKVTF 393
      | : : | | : | : : | : : | : : : : :
Db 34 IWVEPATIFKMGMNISICYQAAIKN-CQPRKLHFYKNGIKERF--QITRINKTTARLMY 89
      | : : | : : | : : | : : | : : | : :
OY 394 FNLNETKPRGKFTYDAVYC---CNEH-----EGHHRVYALYVIDVNNISCEYTDGYLTGM 445
      | | : : | | : | : | : : | : : |
Db 90 KNFLE-----PHASMYCTAECPRKHQETILTCGKDISSGYPDPIDPEVYTCVLEYSGNM 142
      | : : | : : | : : | : : | : : |
OY 446 TCRWSTSTIOSLAESTLOLRHYRSSLYCSDIPISHIPISEPKDCYLOSOGFYECTFOPIFL 505
      | | : : | : : | : : | : : | : : |
Db 143 TCTWNAKKLTYI-----DFKYVHVAKSLE--TEEQOYLTS---SYINISTDS 185
      | : : | : : | : : | : : | : : |
OY 506 LSG---YTMWIRINHSIGSLDSPCTCVLPDSVVKPLPSSVKAKEITINIGLTK--ISWEK 560
      | | : : | : : | : : | : : | : : | : :
Db 186 LOGGKRYLWVQANALNATGMEESKQLOIHLDDIVIPSAAVISRAE-TINATVPKTIITYWDS 244
      | : : | : : | : : | : : | : : | : :
OY 561 PYFPENNLOFOIRYGLSGKEVQWKNYEYIDAK---SKSVSLPVPDLCAVYAVOVRCCKRL 616

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Db 245 QTTIE-KVSCEMRYKATNTOT-WNVKE-FDTNFTYVQOSEFYLEPNI--KYVEQVRQOE- 298
OY 617 DGLGYWNSNPNATYTVMDIKVPMRGPDEFWRILINGDTMKKEKNVTLMKPLMKNDLSLSV 676
Db 299 TGRKRYWQWSSPEFH-----KTPEYVPOY-----TSKAFQHDY-W-----NSGLTV 338
OY 677 QRYVINHHYSCNGTWSDEVGNHTKFTFLTEQAHTVTVLAINSIGASVANFNLT----- 731
Db 339 ASISTGHLTSDN---RGDIG-----LLIGMIVEFAVMLSTLSL---IGIFNRSFRGTIK 385
OY 732 -----SW-----PMKVNIVQSL---SAYPLNSSCVIVSWI-----L 760
Db 386 RRILLIPKWLIEDIPNMKNSNVAKMLQENSELMNNNSSEQVLYVDPMTIEIKEIFIPER 445
OY 761 SPSDYK-----LMYFIIEWKNLNEDEIK 784
Db 446 KPTDYKKENTGPLETRDYPQNSLFDNTTVYIPDLNTGYKPKQISNLEPGSHLSNNNEIT 505
OY 785 WLRISSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKI--INSFTQDDIEKHQSDAGL 842
Db 506 SLTL-----KRPVDSLDSGNNPRLQKHPNFA-- 531
OY 843 YVIVPYIISSTILLGTLTLLISHQRMKLEWEDVNPKNCSWAQGLNEQKPEFTEHLEFIKH 902
Db 532 FSVSVVNSLSNTIFLGELSL-----ILNGECSSPDIGNSVYEET----- 571
OY 903 TASVTCGPILEPETISEDISVDTSWKNKDEMPPTVVSLSLTIDLEKGSV-----CI 955
Db 572 -----TMLLENDSPSETIPEOT-----LLPDEFVSCLGIVNEELPSINTYFPQNIL 617
OY 956 SDQFNSVNFSE 966
Db 618 ESHFNRIISLLE 628
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Search completed: May 18, 2002, 07:00:08  
Job time: 577 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 05:18:35 ; Search time 54.58 seconds  
(without alignments)  
521.360 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 6254  
Sequence: 1 MICKRCVLLHWEFIVIT.....QTCSTQTHKIMKMDLTV 1165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6254	100.0	1165	2	US-08-599-455B-4
2	6254	100.0	1165	4	US-09-069-781B-4
3	6246	99.9	1165	4	US-09-093-814-1
4	6246	99.9	1165	4	US-08-618-957A-11
5	6172	98.7	1165	2	US-08-640-389A-11
6	4819.5	77.1	958	4	US-08-618-957A-8
7	4819.5	77.1	960	1	US-08-355-888A-8
8	4819.5	77.1	960	2	US-08-693-697-8
9	4819.5	77.1	960	2	US-08-640-389A-3
10	4819.5	77.1	960	3	US-08-693-696-8
11	4816	77.0	960	2	US-08-693-697-33
12	4814.5	77.0	960	2	US-08-588-190-3
13	4814.5	77.0	960	4	US-08-618-957A-3
14	4814	77.0	896	4	US-08-618-957A-10
15	4814	77.0	898	2	US-08-693-697-36
16	4799	76.7	906	4	US-08-618-957A-9
17	4799	76.7	908	2	US-08-588-526-3
18	4791.5	76.6	958	2	US-08-640-389A-8
19	4788	76.6	906	2	US-08-640-389A-9
20	4786	76.5	896	2	US-08-640-389A-10
21	4784.5	76.5	1162	4	US-08-803-346-1
22	4776.5	76.4	1162	4	US-08-827-962-15
23	4770.5	76.3	1162	2	US-08-599-455B-43
24	4770.5	76.3	1162	4	US-08-827-962-20
25	4770.5	76.3	1162	4	US-09-069-781B-43
26	3801	60.8	896	2	US-08-640-389A-12
27	3792	60.6	894	4	US-08-618-957A-12

28	3785	60.5	894	2	US-08-599-455B-2	Sequence 2, Appl
29	3785	60.5	894	4	US-09-069-781B-2	Sequence 2, Appl
30	3779	60.4	895	4	US-08-827-962-19	Sequence 19, Appl
31	3753	60.0	895	4	US-08-827-962-21	Sequence 21, Appl
32	3057	48.9	569	1	US-08-306-231-3	Sequence 3, Appl
33	421	6.7	77	4	US-08-803-346-64	Sequence 64, Appl
34	395	6.3	76	4	US-08-803-346-61	Sequence 61, Appl
35	377	6.0	77	4	US-08-803-346-62	Sequence 62, Appl
36	370	5.9	77	4	US-08-803-346-63	Sequence 63, Appl
37	345.5	5.5	918	2	US-08-825-558-6	Sequence 6, Appl
38	316	5.1	708	1	US-07-797-556-2	Sequence 2, Appl
39	316	5.1	708	1	US-08-308-881-2	Sequence 2, Appl
40	316	5.1	708	2	US-09-058-263-2	Sequence 2, Appl
41	316	5.1	708	2	US-09-059-099-2	Sequence 2, Appl
42	316	5.1	708	3	US-09-058-264-2	Sequence 2, Appl
43	316	5.1	708	5	PCT-US95-06530-2	Sequence 2, Appl
44	313	5.0	837	1	US-07-923-976-2	Sequence 2, Appl
45	309.5	4.9	75	4	US-08-803-346-60	Sequence 60, Appl

## ALIGNMENTS

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RESULT 1
US-08-599-455B-4
; Sequence 4, Application US/08599455B
; Patent No. 5972621
;
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
;
; TELETYPE: 200154
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown

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MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-599-455B-4

Query Match 100.0%; Score 6254; DB 2; length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTIPWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSYPTIPWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANNIOQWLKGLKLFICYVESLFKNLFRNRYKVVHLLYVPEVLEDSPLVPQKGS 180  
DB 121 QOIDANNIOQWLKGLKLFICYVESLFKNLFRNRYKVVHLLYVPEVLEDSPLVPQKGS 180  
QY 181 FOMVHCNCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMVKPDP 240  
DB 181 FOMVHCNCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKISWSSPLVPFLQYQVKSSENSTVIREADKIVATSLSLVDSILP 300  
DB 241 LGLHMETDDGNLKISWSSPLVPFLQYQVKSSENSTVIREADKIVATSLSLVDSILP 300  
QY 301 GSSYEVOYRGKRLDGPQIMSDWSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVOYRGKRLDGPQIMSDWSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYIDVNNINISCEITDGYLTAKTCRWSSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
DB 421 RYAEIYIDVNNINISCEITDGYLTAKTCRWSSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
DB 481 PISEPKDCYLQSDGYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISWEKRVFPENNLOQIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKRVFPENNLOQIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCRRLDGLGYWSMNSNPATVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCRRLDGLGYWSMNSNPATVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHHNSCNGTWSSEVGNHTKFTFLWTEQAHVTVLAINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINHHNSCNGTWSSEVGNHTKFTFLWTEQAHVTVLAINSI 720  
QY 721 GASVANFNLFWSMPSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
DB 721 GASVANFNLFWSMPSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPTEKYQFSLYPIFMEGVGKRIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYIHDHFIPTEKYQFSLYPIFMEGVGKRIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLLFWMEDVPPNPKNCMAOGLNFQKPEFTEHLEFI 900  
DB 841 GLYIVPVIISSSILLGLTLLISHQRMKLLFWMEDVPPNPKNCMAOGLNFQKPEFTEHLEFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTTVVSLSTTDLEKGSVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTTVVSLSTTDLEKGSVCISDQFN 960

QY 961 SVNFSEAEGETEYTYEDESQROPFVKYATLLISNSKPSSETGEEQGLNSSVTYKCFSSKNSPL 1020  
DB 961 SVNFSEAEGETEYTYEDESQROPFVKYATLLISNSKPSSETGEEQGLNSSVTYKCFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEQAQAFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNCKSIYYL 1080  
DB 1021 KDSFSSNSWEIEQAQAFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNCKSIYYL 1080  
QY 1081 GVTSSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
DB 1081 GVTSSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQCTSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQCTSTQTHKIMENKMDLTV 1165

RESULT 2  
US-09-069-781B-4  
Sequence 4, Application US/09069781B

Patent No. 6287782

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,781B

FILING DATE: 29-APRIL-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: US 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: US 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: US 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: US 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: US 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: US 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: US 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: US 08/562,663

FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/082001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1165 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 US-09-069-781B-4

Query Match 100.0%; Score 6254; DB 4; Length 1165;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIQCWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQGS 180
Db 121 QOIDANWNIQCWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQGS 180
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
Db 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMETDDGNLKLISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
Db 241 LGLHMETDDGNLKLISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RYAEIYVIVNININISCEIDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCS DIPSIH 480
Db 421 RYAEIYVIVNININISCEIDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCS DIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSLSGLDSPPTCVLPDSVVKPLRP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSLSGLDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLLKISWEKPEPPENNLQFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPEPPENNLQFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSEDEVGNHTKFTFLWTEQAHTVTLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSEDEVGNHTKFTFLWTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVOSLSAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNE 780
Db 721 GASVANFNLTFSWPMKVNIVOSLSAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNE 780
QY 781 GEIKMLRISSSVKRYIHDHFIPLEKYQFSLYPIFMEGVGKPKTIINSFTQDDIEKHSDA 840
Db 781 GEIKMLRISSSVKRYIHDHFIPLEKYQFSLYPIFMEGVGKPKTIINSFTQDDIEKHSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCMAQGLNFQKPEFTEHLFI 900
Db 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCMAQGLNFQKPEFTEHLFI 900

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QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPPTVVSLLSTDLKGSVCISDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPPTVVSLLSTDLKGSVCISDQFN 960
QY 961 SVNFSEAEGETVTEYDESDQROPVVKYATLISNSKPSFETGEEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETVTEYDESDQROPVVKYATLISNSKPSFETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSGLDELKLEGNFPEENNDKSIYLL 1080
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSGLDELKLEGNFPEENNDKSIYLL 1080
QY 1081 GVTSIKKRESGLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

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RESULT 3  
 US-09-093-814-1  
 ; Sequence 1, Application us/09093814  
 ; Patent No. 6270981  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carpenter et al.  
 ; TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS  
 ; FILE REFERENCE: REG 580-A  
 ; CURRENT APPLICATION NUMBER: US/09/093,814  
 ; CURRENT FILING DATE: 1998-06-09  
 ; PRIOR APPLICATION NUMBER: 60/049,108  
 ; PRIOR FILING DATE: 1997-06-09  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1165  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-093-814-1

Query Match 99.9%; Score 6246; DB 4; Length 1165;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIQCWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQGS 180
Db 121 QOIDANWNIQCWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQGS 180
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
Db 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMETDDGNLKLISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
Db 241 LGLHMETDDGNLKLISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTQDVYFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420

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QY 421 RYAEIYIDVININISCEITDGLTKMTCRSTSTIOSLAESTLQLRHRSLSYCDIPSIH 480  
Db 421 RYAEIYIDVININISCEITDGLTKMTCRSTSTIOSLAESTLQLRHRSLSYCDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPTCYLPDSVVKPLRP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPTCYLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV 600  
QY 601 PDLCAVYAVOYRCKRLDGLGYSNMSNDAYTVMDIKVPMRGPEFWRLINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOYRCKRLDGLGYSNMSNDAYTVMDIKVPMRGPEFWRLINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWESEVGNHTKFTFLMTEQAHVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWESEVGNHTKFTFLMTEQAHVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780  
Db 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKQPSLYPIFMEGVGKPKIINSFTQDDIEKHSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKQPSLYPIFMEGVGKPKIINSFTQDDIEKHSDA 840  
QY 841 GLYIVIPVYIISILLGLTLLISHQKMKLFWEDVNPKNCSMAOGLNFQKPEFELFI 900  
Db 841 GLYIVIPVYIISILLGLTLLISHQKMKLFWEDVNPKNCSMAOGLNFQKPEFELFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVSTSWKNKDEMPPTVSVLSTDLLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDIVSTSWKNKDEMPPTVSVLSTDLLEKGSVCISDQFN 960  
QY 961 SVNFEAEGETEYTYEDESQROPFVKATLLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFEAEGETEYTYEDESQROPFVKATLLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNDDKSIYYL 1080  
Db 1021 KDSFNSNWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNDDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPACLTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPACLTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 4  
US-08-618-957A-11  
: Sequence 11, Application US/08618957A  
: Patent No. 6355337  
: GENERAL INFORMATION:  
: APPLICANT: Snodgrass, H. Ralph  
: APPLICANT: Cioffi, Joseph  
: APPLICANT: Zupancic, Thomas Joel  
: APPLICANT: Shafer, Alan Wayne  
: TITLE OF INVENTION: METHODS FOR USING THE OBSE  
: TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
: NUMBER OF SEQUENCES: 28  
: CORRESPONDENCE ADDRESS:  
: ADDRESS: Pennie & Edmonds LLP  
: STREET: 1155 Avenue of The Americas  
: CITY: New York  
: STATE: NY  
: COUNTRY: USA

ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,957A  
FILING DATE: 20-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Polissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 008907-0033-999  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-618-957A-11

Query Match 99.9%; Score 6246; DB 4; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPPNSTYDVLPLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPPNSTYDVLPLPAGLSKNTS 60  
QY 61 NGHYETAVERKFNSSGTHFNSLSKTFHGCFRSEQDRNCSLADNIEGKTFVSTVNSLV 120  
Db 61 NGHYETAVERKFNSSGTHFNSLSKTFHGCFRSEQDRNCSLADNIEGKTFVSTVNSLV 120  
QY 121 QOIDANWNIQWLKGLDKLFICYVESLEKLNFRNRYKVVHLLVYBEVLEDSPLVPQGS 180  
Db 121 QOIDANWNIQWLKGLDKLFICYVESLEKLNFRNRYKVVHLLVYBEVLEDSPLVPQGS 180  
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPILMSVQPINMVKPDP 240  
Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMETIDGNLKLISWSSPLVPFPLOYQVYKSENSTTVIREADKIVATSLSLVDSTLP 300  
Db 241 LGLHMETIDGNLKLISWSSPLVPFPLOYQVYKSENSTTVIREADKIVATSLSLVDSTLP 300  
QY 301 GSSYEVOYRCKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOYRCKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHYSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHYSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYIDVININISCEITDGLTKMTCRSTSTIOSLAESTLQLRHRSLSYCDIPSIH 480  
Db 421 RYAEIYIDVININISCEITDGLTKMTCRSTSTIOSLAESTLQLRHRSLSYCDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPTCYLPDSVVKPLRP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPTCYLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV 600

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Db 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNNSCVIWSILSPSDYKLMYFIIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNNSCVIWSILSPSDYKLMYFIIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLSHQRMKLLFWEDEVNPNKNCWAQGLNFQKPEFHEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLSHQRMKLLFWEDEVNPNKNCWAQGLNFQKPEFHEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVVSLLSTDLEKGSVCISDQFN 960
QY 961 SVNFSEAEGETEYTESQRPVFKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAEGETEYTESQRPVFKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSEFNSSWEIEAOAFILSDQHPNITSPHLTFSEGLDELKLEGNPEENNDKRSIYYL 1080
Db 1021 KDSEFNSSWEIEAOAFILSDQHPNITSPHLTFSEGLDELKLEGNPEENNDKRSIYYL 1080
QY 1081 GVTSIKKRESGLTLDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGLTLDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

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RESULT 5
US-08-640-389A-11
; Sequence 11, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-640-389A-11

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Query Match          98.7%; Score 6172; DB 2; Length 1165;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1155; Conserved 1; Mismatches 8; Indels 2; Gaps 2;

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QY 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSICMPNPNSTYDYFLPAGLSKNTS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSICMPNPNSTYDYFLPAGLSKNTS 60
QY 61 NGHYETAVEPKFNSSGTHFNSLSKTFHCCFRSEQDRNCISLCAONTGKTFVSTVNSLVE 120
Db 61 NGHYETAVEPKFNSSGTHFNSLSKTFHCCFRSEQDRNCISLCAONTGKTFVSTVNSLVE 120
QY 121 QQIDANNIQCWLKGDLLFCYVESLEKLEFRNYKYVHLVYLPEVLEDSPLVPQKS 180
Db 121 QQIDANNIQCWLKGDLLFCYVESLEKLEFRNYKYVHLVYLPEVLEDSPLVPQKS 180
QY 121 QQIDANNIQCWLKGDLLFCYVESLEKLEFRNYKYVHLVYLPEVLEDSPLVPQKS 180
Db 121 QQIDANNIQCWLKGDLLFCYVESLEKLEFRNYKYVHLVYLPEVLEDSPLVPQKS 180
QY 181 FQMVHCNCSVHECCCLVPTAKLNDTLLMCLKITSGGVIFQSPKSVQPINMKPDP 240
Db 181 FQMVHCNCSVHECCCLVPTAKLNDTLLMCLKITSGGVIFQSPKSVQPINMKPDP 240
QY 241 LGLHMETDDGDLKISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
Db 241 LGLHMETDDGDLKISWSSPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEHCYKKEKN 360
Db 301 GSSYEYQVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEHCYKKEKN 360
QY 361 VPSKEIYMMNLAEKIPQSOYDVVSDHYSKVTFENLNETKPRGKTYDAVYCCNEHECH 420
Db 361 VPSKEIYMMNLAEKIPQSOYDVVSDHYSKVTFENLNETKPRGKTYDAVYCCNEHECH 420
QY 421 RYAEIYVIDVININISCEITDGYLTMTKTCWSTSTIOSLAESTLQLRHRSLSYCSIDPSIH 480
Db 421 RYAEIYVIDVININISCEITDGYLTMTKTCWSTSTIOSLAESTLQLRHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYIQSDGEYECIFQPIFILSGYTMIRINHSLSGLSDSPICVLPDSVVKPLPP 540
Db 481 PISEPKDCYIQSDGEYECIFQPIFILSGYTMIRINHSLSGLSDSPICVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNNSCVIWSILSPSDYKLMYFIIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNNSCVIWSILSPSDYKLMYFIIEWKNLNED 780

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QY 781 GEIKWLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNCSWAOGLNFOKPEFHEHFI 900  
Db 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNCSWAOGLNFOKPEFHEHFI 900  
QY 901 KHTASVTCGPLEPETISEDISVDTSWKNDEMPTTVSLSTDLKGSVCISDQFN 960  
Db 901 KHTASVTCGPLEPETISEDISVDTSWKNDEMPTTVSLSTDLKGSVCISDQFN 960  
QY 961 SVNFSEAEGETEYEAESQROPFVKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETEYEAESQROPFVKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPPENNDKKSIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPPENNDKKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLODSCHSFVENNINIGTSSSKTFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLODSCHSFVENNINIGTSSSKTFAS 1140  
QY 1141 YMPQFOTCSTQ-THKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIME-KMCDLTV 1165

RESULT 6  
US-08-618-957A-8  
; Sequence 8, Application US/08618957A  
; Patent No. 6355237  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. Ralph  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas Joel  
; APPLICANT: Shafer, Alan Wayne  
; TITLE OF INVENTION: METHODS FOR USING THE OBES  
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of The Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/618, 957A  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Polsant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 008907-0033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 958 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-618-957A-8

Query Match 77.18; Score 4819.5; DB 4; Length 958;  
Best Local Similarity 94.18; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPEWREKLSICMPNSTYDYFLLPAGLSKNTS 60  
Db 1 MICQKFCVLLHMEFIYVITAFNLSTPTPEWREKLSICMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAPEKPNSSGTHFSNLSKTFHCCFRSEQDRNCSLACADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAPEKPNSSGTHFSNLSKATFHCCFRSEQDRNCSLACADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANWNIOGWLKGDCLKLFICYVESLFKNLFRNRYKVHLLYVLEVEDSPLVPQKS 180  
Db 121 QQIDANWNIOGWLKGDCLKLFICYVESLFKNLFRNRYKVHLLYVLEVEDSPLVPQKS 180  
QY 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFOSPLMSVQPINMVKPDP 240  
Db 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFOSPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDGNLKISWSSPPLVPFPLOYKYSENSTTVIREADKIVSATSLVDLSILP 300  
Db 241 LGLHMETDGNLKISWSSPPLVPFPLOYKYSENSTTVIREADKIVSATSLVDLSILP 300  
QY 301 GSSYEVQVRGRKLDGPGIWSDWSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVQVRGRKLDGPGIWSDWSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNINISCETDGYLTQKTCRSTQSLAESTLQLRHRSLSYCSIDPSIH 480  
Db 421 RYAEIYVIDVNNINISCETDGYLTQKTCRSTQSLAESTLQLRHRSLSYCSIDPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLSGTYMMIRINHSLSGLSDSPPTCYLLPDSVVKPLP 540  
Db 481 PISEPKDCYLOSDFEYECIFQPIFLSGTYMMIRINHSLSGLSDSPPTCYLLPDSVVKPLP 540  
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQIRYGLSGKEVQWKNEYDYDAKSYSVLPV 600  
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOQIRYGLSGKEVQWKNEYDYDAKSYSVLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYWSNWSNPAITYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGYWSNWSNPAITYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLWKPLMKNDLSLQVQRYVINNHTSCNGTSEEDVGNHTKFTFLMTEQAHTVTVLAINSI 720  
Db 661 TLLWKPLMKNDLSLQVQRYVINNHTSCNGTSEEDVGNHTKFTFLMTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAAYPLNSSCVIVSWILSPSDYKLMFYIEMKNLNE 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAAYPLNSSCVIVSWILSPSDYKLMFYIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNCSWAOGLNFOK-----PE 893  
Db 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVYPNPKNCSWAOGLNFOKLEGSMPYK 900  
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSWKNKDE 933  
Db 901 SHHHSLSSTQGHKHGCRPGPRLHRTKTRDLSLVYLLTLPPLSLYDPAKSPSVRNTQE 958

RESULT 7  
US-08-355-888A-8  
; Sequence 8, Application US/08355888A  
; Patent No. 5763211  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/355,888A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 7225-078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 960 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-355-888A-8

Query Match 77.18; Score 4819.5; DB 1; Length 960;  
Best Local Similarity 94.18; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSICMPNSTYDYFLPAGLSKNTS 60  
DB 3 MICQKFCVLLHWEFIYVITAFNLSTPITPWREKLSICMPNSTYDYFLPAGLSKNTS 62  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSCADNIEGKTFVSTVNSLVF 120  
DB 63 NGHYETAVERPKFNSSGTHFSNLSKATFHCCFRSEQDRNCSCADNIEGRTFVSTVNSLVF 122  
QY 121 QQIDANMNIQCWLKGLDKLFLCYVESLFEKNLFRNRYNRYKVLHLLVLPVLEDSPLVPQKS 180  
DB 123 QQIDANMNIQCWLKGLDKLFLCYVESLFEKNLFRNRYNRYKVLHLLVLPVLEDSPLVPQKS 182  
QY 181 FQWVHCNCSVHECCCLVPVPYPAKLNLTLLMCLKITSQGVTFQSPPLMSVQPINMVKPDP 240  
DB 183 FQWVHCNCSVHECCCLVPVPYPAKLNLTLLMCLKITSQGVTFQSPPLMSVQPINMVKPDP 242  
QY 241 LGLHMEITDDGNLKSWSPLVFPLOYOVKYSNSTVIVREADKIVATSLSLVDSILP 300  
DB 243 LGLHMEITDDGNLKSWSPLVFPLOYOVKYSNSTVIVREADKIVATSLSLVDSILP 302  
QY 301 GSSYEYQVRGKRLDGPGLMSDMSIPRVFTTQDVIYFPFKILTSVGSNVSFHCITYKKENKI 360  
DB 303 GSSYEYQVRGKRLDGPGLMSDMSIPRVFTTQDVIYFPFKILTSVGSNVSFHCITYKKENKI 362

QY 361 VPSKEIYWMNLAEKIPQSQYDVYSDHVSQVTFEFLNETKPRGKFTYDAYVCCNEHECH 420  
DB 363 VPSKEIYWMNLAEKIPQSQYDVYSDHVSQVTFEFLNETKPRGKFTYDAYVCCNEHECH 422  
QY 421 RYAEIYVIDVININISCEITDGLTKMTCRWSTSTIOSLAESTIQLRYHRSSLYCSDIPSIH 480  
DB 423 RYAEIYVIDVININISCEITDGLTKMTCRWSTSTIOSLAESTIQLRYHRSSLYCSDIPSIH 482  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPP 540  
DB 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPP 542  
QY 541 SSVKAEITINIGLKSISWEKPEPENNLQFQIRYGLSGKEVQKMEYVDKAKSVSLPV 600  
DB 543 SSVKAEITINIGLKSISWEKPEPENNLQFQIRYGLSGKEVQKMEYVDKAKSVSLPV 602  
QY 601 PDLCAVYAVQVRCKRLDGLGYMSNMSNPAYTVMDIKVPMRGPREFWRLINGDTMKKEKNV 660  
DB 603 PDLCAVYAVQVRCKRLDGLGYMSNMSNPAYTVMDIKVPMRGPREFWRLINGDTMKKEKNV 662  
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSQEDVGNHTKFTFLMTEQAHVTYLAINSI 720  
DB 663 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSQEDVGNHTKFTFLMTEQAHVTYLAINSI 722  
QY 721 GASVANFNLTFSWPMKVNIVOSISAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780  
DB 723 GASVANFNLTFSWPMKVNIVOSISAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 782  
QY 781 GEIKWLRISSSVKKYIYHDFPIEKYQFSLYPIFMEGVGKPKIIN3FTODDIEKHQSDA 840  
DB 783 GEIKWLRISSSVKKYIYHDFPIEKYQFSLYPIFMEGVGKPKIIN3FTODDIEKHQSDA 842  
QY 841 GLVYIVPYIISSTILLGLTLLSHQRMKLLWEDVDPNPKNCSNAQGLNFOK-----PE 893  
DB 843 GLVYIVPYIISSTILLGLTLLSHQRMKLLWEDVDPNPKNCSNAQGLNFOK-----PE 902  
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDLSVDTSWKNKDE 933  
DB 903 SHHSLISSTQGHKHGCRPQGPLHRTKTRDLCSLVYLLTLPPLLSYDPAKSPSVRNTOE 960

RESULT 8  
US-08-693-697-8  
; Sequence 8, Application US/08693697  
; Patent No. 5869610  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/693,697  
; FILING DATE: 05-AUG-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0037-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-693-697-8

Query Match 77.1%; Score 4819.5; DB 2; Length 960;  
Best Local Similarity 94.1%; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

OY 1 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
DB 3 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 62  
OY 61 NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 63 NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 122  
OY 121 QQIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 180  
DB 123 QQIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 182  
OY 181 FQMVHNCVHCECECLVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKPDP 240  
DB 183 FQMVHNCVHCECECLVPPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKPDP 242  
OY 241 LGLHMETDDGNLKLISWSSPLVPFPLOYOVKYSNSTVIREADKIVATSLLVDSILP 300  
DB 243 LGLHMETDDGNLKLISWSSPLVPFPLOYOVKYSNSTVIREADKIVATSLLVDSILP 302  
OY 301 GSSYEVOVRGKRLDGPGLMSDWSPTFTQDVLYFPKILTSVGSNVSFHCYKKEKNI 360  
DB 303 GSSYEVOVRGKRLDGPGLMSDWSPTFTQDVLYFPKILTSVGSNVSFHCYKKEKNI 362  
OY 361 VPSKEIVWMNLAEKIPQSOQYDVSDVHSKVTFEFLNETKPRGFTYDAVYCCNEHECH 420  
DB 363 VPSKEIVWMNLAEKIPQSOQYDVSDVHSKVTFEFLNETKPRGFTYDAVYCCNEHECH 422  
OY 421 RYAEIYVDVNNINISCEIDGLTKMTCRMSTSTIOSLAESTLOLRHSSSLYCSDIPSIH 480  
DB 423 RYAEIYVDVNNINISCEIDGLTKMTCRMSTSTIOSLAESTLOLRHSSSLYCSDIPSIH 482  
OY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLRP 540  
DB 483 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLRP 542  
OY 541 SSVKAEITINIGLKLISWEKVPFPENNLQOIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600  
DB 543 SSVKAEITINIGLKLISWEKVPFPENNLQOIRYGLSGKEVQMKMEVYDAKSKSVSLPV 602  
OY 601 PDLCAVYAVQVRCKRLDGLGYWSMNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 660  
DB 603 PDLCAVYAVQVRCKRLDGLGYWSMNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 662  
OY 661 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSSEVDGNHTKFTFLMTQAHVTVLAINSI 720  
DB 663 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSSEVDGNHTKFTFLMTQAHVTVLAINSI 722  
OY 721 GASVAFNLFESWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKIMFYIEMKNLNE 780  
DB 723 GASVAFNLFESWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKIMFYIEMKNLNE 782  
OY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 783 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842

DB 783 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842  
OY 841 GLYIVAPVLISSSILLGLTLLISHQRMKLLFWEDVNPKNCSNAOGLNFQK-----PE 893  
DB 843 GLYIVAPVLISSSILLGLTLLISHQRMKLLFWEDVNPKNCSNAOGLNFQKLEGSMPVK 902  
OY 894 TFEHLFIKHT-ASVTCG-----LLEPETISEDIVSDTSWKNDKOE 933  
DB 903 SHHSLISSYQGHKHCGRPGPLHRRTRDLSLVYLLTLPPLSYDPAKSPSVRNTQE 960

RESULT 9

US-08-640-389A-3  
Sequence 3, Application US/08640389A  
Patent No. 5912123

GENERAL INFORMATION:  
APPLICANT: Snodgrass, H. R.

APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas J.

APPLICANT: Shafer, Alan W.

TITLE OF INVENTION: DETECTION OF THE LEPTIN  
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR  
TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/640,389A  
FILING DATE: 29-Apr-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0032

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-640-389A-3

Query Match 77.1%; Score 4819.5; DB 2; Length 960;  
Best Local Similarity 94.1%; Pred. No. 0;  
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

OY 1 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
DB 3 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 62  
OY 61 NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 63 NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 122  
OY 121 QQIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 180  
DB 123 QQIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 182



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QY 181 FQWVHNCNSVHECCCECLVPEVPTAKLNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDP 240
Db 183 FQWVHNCNSVHECCCECLVPEVPTAKLNDTLLMCLKITSGGVIFRSPILMSVQPINMVKPDP 242
QY 241 LGLHMEITDDGNLKISWSSPPLVPEPLQYQVKYSENSTFVIREADKIVATSLSLVDSTLP 300
Db 243 LGLHMEITDDGNLKISWSSPPLVPEPLQYQVKYSENSTFVIREADKIVATSLSLVDSTLP 302
QY 301 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCYKKENKI 360
Db 303 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCYKKENKI 362
QY 361 VPSKEIWMNMNLAEKIPQSQYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECH 420
Db 363 VPSKEIWMNMNLAEKIPQSQYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECH 422
QY 421 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLTKISWEKPVFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLTKISWEKPVFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRITNGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRITNGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTWSDEDVGNHTKFTFLWTEQAHVTYVLAINSI 720
Db 663 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTWSDEDVGNHTKFTFLWTEQAHVTYVLAINSI 722
QY 721 GASVANENLTFSPWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 723 GASVANENLTFSPWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSTODDIEKHQSDA 840
Db 783 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSTODDIEKHQSDA 842
QY 841 GLYVIVPVITISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQK-----PE 893
Db 843 GLYVIVPVITISSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKLEGSMEFK 902
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDIVDTSWKNKDE 933
Db 903 SHHSLISSTQGHKHCGRPOGPHKRTDCLCSLYLLTLPPLLSYDPAKSESVANTQOE 960

RESULT 10
US-08-693-696-8
; Sequence 8, Application US/08693696
; Patent No. 6005080
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693, 696
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/355, 888
: FILING DATE: 14-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7225-078
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 960 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-693-696-8

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Db 603 PDLCAVYAVQVCKRLDGLGYSWMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 662  
QY 661 TLLWKPLMKNDSLCSVQRYVINNHTSCNGTSEDEVGNHTKFTFLTEQAHTVTVAINSI 720  
Db 663 TLLWKPLMKNDSLCSVQRYVINNHTSCNGTSEDEVGNHTKFTFLTEQAHTVTVAINSI 722  
QY 721 GASVANFNLFSPMPSKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780  
Db 723 GASVANFNLFSPMPSKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 782  
QY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 783 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 842  
QY 841 GLYIVPVYIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCMAOGLNFQK-----PE 893  
Db 843 GLYIVPVYIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCMAOGLNFQKLEGSMEFVK 902  
QY 894 TFEHLFIKHT-ASVTCGP-----LLEPETISEDISVDTSMKNKDE 933  
Db 903 SHHSLISSTQGHKHCGRPOGPLHRTKTRDCLSLVYLLTLPLESLYDPAKSPSVRNTQE 960

RESULT 11

US-08-693-697-33  
; Sequence 33, Application US/08693697  
; Patent No. 5869610  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: HU-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/693,697  
; FILING DATE: 05-AUG-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0037-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 908 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-693-697-33

Query Match 77.0%; Score 4816; DB 2; Length 908;  
Best Local Similarity 99.1%; Pred. No. 0;

Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;  
QY 1 MICQKFCVALLHMEFIYVITAFNLSTYPTIPWRFKLSGCMPPNSTYDYFLLPAGLSKNTS 60  
Db 3 MICQKFCVALLHMEFIYVITAFNLSTYPTIPWRFKLSGCMPPNSTYDYFLLPAGLSKNTS 62  
QY 61 NGHYETAVERKFNSSGTHFSLNLSKTFTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLV 120  
Db 63 NGHYETAVERKFNSSGTHFSLNLSKTFTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLV 122  
QY 121 QOIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKS 180  
Db 123 QOIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYKVHLLYLPEVLEDSPLVPQKS 182  
QY 181 FOMVHCNCSYHECCCECLVPVPTAKLNDTLLMCLKITSGGVIPOSPIMSVOPINMKPDP 240  
Db 183 FOMVHCNCSYHECCCECLVPVPTAKLNDTLLMCLKITSGGVIPOSPIMSVOPINMKPDP 242  
QY 241 LGLHMEITDDGNLKSWSPPPLVPPLQYQVYSENSTVIREADKIVSATSLLVDSILP 300  
Db 243 LGLHMEITDDGNLKSWSPPPLVPPLQYQVYSENSTVIREADKIVSATSLLVDSILP 302  
QY 301 GSSYEVQVGRKRLDGPISWDSMTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360  
Db 303 GSSYEVQVGRKRLDGPISWDSMTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 362  
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGAFITYDAVYCCNEHECH 420  
Db 363 VPSKEIYWMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGAFITYDAVYCCNEHECH 422  
QY 421 RYAEIYVDVININISCEITDGLTKMTCRSTSTIQSLAESTIQLRHRSLSYCSIDPSIH 480  
Db 423 RYAEIYVDVININISCEITDGLTKMTCRSTSTIQSLAESTIQLRHRSLSYCSIDPSIH 482  
QY 481 PISEPKDYLQSDGFYECIFQPIFLSGYTMIRINHSIGSLDSPICVLPDSVVKPLPP 540  
Db 483 PISEPKDYLQSDGFYECIFQPIFLSGYTMIRINHSIGSLDSPICVLPDSVVKPLPP 542  
QY 541 SSVKAETINIGLLKISWEKVPFENNLOQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 543 SSVKAETINIGLLKISWEKVPFENNLOQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 602  
QY 601 PDLCAVYAVQVCKRLDGLGYSWMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 603 PDLCAVYAVQVCKRLDGLGYSWMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 662  
QY 661 TLLWKPLMKNDSLCSVQRYVINNHTSCNGTSEDEVGNHTKFTFLTEQAHTVTVAINSI 720  
Db 663 TLLWKPLMKNDSLCSVQRYVINNHTSCNGTSEDEVGNHTKFTFLTEQAHTVTVAINSI 722  
QY 721 GASVANFNLFSPMPSKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780  
Db 723 GASVANFNLFSPMPSKVNIVQSLAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 782  
QY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 783 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 842  
QY 841 GLYIVPVYIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCMAOGLNFQK-----PETEHL 898  
Db 843 GLYIVPVYIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCMAOGLNFQKMPGTGTELL 902

RESULT 12

US-08-588-190-3  
; Sequence 3, Application US/08588190  
; Patent No. 5856098  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. Ralph  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas Joel  
; APPLICANT: Shafer, Alan Wayne  
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR

```

1  TITLE OF INVENTION:  VARIANT AND METHODS FOR REGULATING OBESITY
2  NUMBER OF SEQUENCES:  4
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Pennile & Edmonds LLP
5  STREET:  1155 Avenue of The Americas
6  CITY:  New York
7  STATE:  NY
8  COUNTRY:  USA
9  ZIP:  10036-2811
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Diskette
12 COMPUTER:  IBM Compatible
13 OPERATING SYSTEM:  DOS
14 SOFTWARE:  FastSeq Version 2.0
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  US/08/588,190
17 FILING DATE:  18-JAN-1996
18 CLASSIFICATION:  435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:
21 FILING DATE:
22 ATTORNEY/AGENT INFORMATION:
23 NAME:  Poissant, Brian M.
24 REGISTRATION NUMBER:  28,462
25 REFERENCE/DOCKET NUMBER:  008907-0029-999
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE:  650-493-4935
28 TELEFAX:  650-493-5556
29 TELEX:  66141 PENNIE
30 INFORMATION FOR SEQ ID NO:  3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH:  960 amino acids
33 TYPE:  amino acid
34 STRANDEDNESS:  single
35 TOPOLOGY:  linear
36 MOLECULE TYPE:  protein
37
38 US-08-588-190-3

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TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
us-08-618-957A-3

Query Match 77.0%; Score 4814.5; DB 4; Length 960;  
Best Local Similarity 93.9%; Pred. No. 0;  
Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRKLSKMPNSTYDYFLLPAGLSKNTSNS 60  
DB 3 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRKLSKMPNSTYDYFLLPAGLSKNTSNS 62  
QY 61 NGHYETAVERKFNSSGTHFSNLKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 63 NGHYETAVERKFNSSGTHFSNLKATPHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 122  
QY 121 QOIDANMNIOCWLGDKLFLICYVESLEKFLFRNYNYKVHLLVLPVLEDSPLVPQKGS 180  
DB 123 QOIDANMNIOCWLGDKLFLICYVESLEKFLFRNYNYKVHLLVLPVLEDSPLVPQKGS 182  
QY 181 FQMVHNCVSVECCCLVPPVPTAKLNDTLLMCLKITSGGVIFQSPFMSVQPINMVKPDP 240  
DB 183 FQMVHNCVSVECCCLVPPVPTAKLNDTLLMCLKITSGGVIFRSPFMSVQPINMVKPDP 242  
QY 241 LGLHMEITDDGNLKLISWSSPPLVPEPIQYQVYKSENSTVIREADKIVSATSLVDILP 300  
DB 243 LGLHMEITDDGNLKLISWSSPPLVPEPIQYQVYKSENSTVIREADKIVSATSLVDILP 302  
QY 301 GSSYEYQVRGKRLDGPIMSDWSTPRTQDVITYEPKILTSVGSNVSFHCITYKKENKI 360  
DB 303 GSSYEYQVRGKRLDGPIMSDWSTPRTQDVITYEPKILTSVGSNVSFHCITYKKENKI 362  
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVKYTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 363 VPSKEIYVMMNLAEKIPQSQYDVVSDHVKYTFENLNETKPRGKFTYDAVYCCNEHECHH 422  
QY 421 RYAEIYIDVYNINISCESTDGYLTMTKCRMSTSTIQSLAESTLQLRHRSLSYCSDDIPSIH 480  
DB 423 RYAEIYIDVYNINISCESTDGYLTMTKCRMSTSTIQSLAESTLQLRHRSLSYCSDDIPSIH 482  
QY 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPICVLPDSVVKPLRP 540  
DB 483 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPICVLPDSVVKPLRP 542  
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 600  
DB 543 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 602  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 603 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662  
QY 661 TLLMKPLMKNDLSGVORYVINHHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 663 TLLMKPLMKNDLSGVORYVINHHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 722  
QY 721 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFYIIEWKNLNE 780  
DB 723 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFYIIEWKNLNE 782  
QY 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 783 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842  
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK-----PE 893

DB 843 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKLEGSMEVK 902  
QY 894 TFEHLFIKHT-ASYTGP-----LLEPETISED1SYDTSWKNKDE 933  
DB 903 SHHSLISSTQGRHCGRPQGPLHRKTRDLSLVYLLTLPPLLSYDPAKSPSVRNTQE 960

RESULT 14  
US-08-618-957A-10  
Sequence 10, Application us/08618957A  
Patent No. 6355237

GENERAL INFORMATION:  
APPLICANT: Snodgrass, H. Ralph  
APPLICANT: Cloeff, Joseph  
APPLICANT: Zupancic, Thomas Joel  
APPLICANT: Shafer, Alan Wayne  
TITLE OF INVENTION: METHODS FOR USING THE OBESE  
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of The Americas  
CITY: New York  
STATE: NY

COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618, 957A  
FILING DATE: 20-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 008907-0033-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 896 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-618-957A-10

Query Match 77.0%; Score 4814; DB 4; Length 896;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRKLSKMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRKLSKMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERKFNSSGTHFSNLKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAVERKFNSSGTHFSNLKATPHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120  
QY 121 QOIDANMNIOCWLGDKLFLICYVESLEKFLFRNYNYKVHLLVLPVLEDSPLVPQKGS 180  
DB 121 QOIDANMNIOCWLGDKLFLICYVESLEKFLFRNYNYKVHLLVLPVLEDSPLVPQKGS 180

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QY 181 FQWVHCNCSVHECCCLVVPVPAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKRDP 240
Db 181 FQWVHCNCSVHECCCLVVPVPAKLNDTLLMCLKITSQGVIFRSPLMSVQPINMVKRDP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKSSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKSSENSTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLMSDMSSTPRVFTTQDVIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEVOVRGKRLDGPGLMSDMSSTPRVFTTQDVIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIH 480
Db 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTSEDEVGNHRTFTFLMTEQAHVTYVLAINSI 720
Db 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTSEDEVGNHRTFTFLMTEQAHVTYVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
QY 841 GLTYIVPVISSSILLGLTLLSHORMKLFWEDEVNPNKNCWAQGLNFOK 891
Db 841 GLTYIVPVISSSILLGLTLLSHORMKLFWEDEVNPNKNCWAQGLNFOK 891

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```

RESULT 15
US-08-693-697-36
; Sequence 36, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1 219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-36

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Query Match 77.0%; Score 4814; DB 2: length 898;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICRRCVLLHMEFIYVITAFNLSTYPTPWRFKLSQMPNSTYDYFLPAGLSKNTS 60
Db 3 MICRRCVLLHMEFIYVITAFNLSTYPTPWRFKLSQMPNSTYDYFLPAGLSKNTS 62
QY 61 NGHYETAPEPKFNSSGTHFSNLKTFHCCERSEODRNCSLCADNIEGKTFVSTVNSLV 120
Db 63 NGHYETAPEPKFNSSGTHFSNLKTFHCCERSEODRNCSLCADNIEGKTFVSTVNSLV 122
QY 121 QQIDANMNIQWLKGLKLFICYVESLFFKNLFRNRYNKVHLVLPVLEDSPLVPQGS 180
Db 123 QQIDANMNIQWLKGLKLFICYVESLFFKNLFRNRYNKVHLVLPVLEDSPLVPQGS 182
QY 181 FQWVHCNCSVHECCCLVVPVPAKLNDTLLMCLKITSQGVIFRSPLMSVQPINMVKRDP 240
Db 183 FQWVHCNCSVHECCCLVVPVPAKLNDTLLMCLKITSQGVIFRSPLMSVQPINMVKRDP 242
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKSSENSTVIREADKIVSATSLLVDSILP 300
Db 243 LGLHMEITDDGNLKISWSSPPLVPFPLOYQVKSSENSTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVRGKRLDGPGLMSDMSSTPRVFTTQDVIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 303 GSSYEVOVRGKRLDGPGLMSDMSSTPRVFTTQDVIFPPKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSOQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIH 480
Db 423 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTSEDEVGNHRTFTFLMTEQAHVTYVLAINSI 720

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DB 663 TLLMKPLMKNDLSCSVQRYVINHTSCNGTWSERVEDVGNHTKFTFLWTEQAHTVTVLAINSI 722  
QY 721 GASVANFNLTFSWPMKVNIVQSLSAFPLNSSCVIYVSWILSPSDYKLMYFIIWKLNED 780  
DB 723 GASVANFNLTFSWPMKVNIVQSLSAFPLNSSCVIYVSWILSPSDYKLMYFIIWKLNED 782  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHOSDA 840  
DB 783 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHOSDA 842  
QY 841 GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVPNPKNCSWAOGINFQK 891  
DB 843 GLYVIVPVIISSILLGLTLLISHQRMKLFMEDVPNPKNCSWAOGINFQK 893

Search completed: May 18, 2002, 06:53:57  
Job time: 5722 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:00:11 ; Search time 24.69 Seconds  
(without alignments)  
4533.984 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVVLHWEFIYIT.....QTGSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	3.6	805	2 S68441	leptin receptor, s
2	42	3.6	892	2 S68439	leptin receptor, s
3	42	3.6	894	2 S68437	leptin receptor, s
4	42	3.6	900	2 S68440	leptin receptor, s
5	42	3.6	1162	2 S68438	leptin receptor, s
6	42	3.6	1162	2 PC4184	leptin receptor, O
7	41	3.5	895	2 S74225	leptin receptor, i
8	8	0.7	124	2 T38142	hypothetical prote
9	8	0.7	222	2 B97118	hypothetical prote
10	8	0.7	236	2 S75373	probable DNA-(apur
11	8	0.7	425	2 F83990	lactose transport
12	8	0.7	459	2 F83602	hypothetical prote
13	8	0.7	498	2 JQ2353	glycoprotein E pre
14	8	0.7	608	2 S09790	hypothetical prote
15	8	0.7	864	2 T48474	hypothetical prote
16	8	0.7	937	2 G87640	TonB-dependent rec
17	8	0.7	1270	2 T21269	hypothetical prote
18	8	0.7	1291	2 T21267	hypothetical prote
19	8	0.7	1318	2 T21266	hypothetical prote
20	8	0.7	1327	2 T21268	hypothetical prote
21	7	0.6	64	2 H82849	hypothetical prote
22	7	0.6	72	2 S34404	ribosomal protein
23	7	0.6	87	2 T44104	hypothetical prote
24	7	0.6	94	2 AD1704	class I heat-shock
25	7	0.6	94	2 AE1333	class I heat-shock
26	7	0.6	101	4 S59321	hypothetical prote
27	7	0.6	104	2 AC1159	hypothetical prote
28	7	0.6	104	2 AC1518	hypothetical prote
29	7	0.6	123	2 AC2259	hypothetical prote

30	7	0.6	127	2 AE1445	hypothetical prote
31	7	0.6	127	2 A11362	hypothetical prote
32	7	0.6	134	2 D70518	probable membrane
33	7	0.6	141	2 C82889	hypothetical prote
34	7	0.6	144	2 C70937	hypothetical prote
35	7	0.6	146	1 R5BSL5	ribosomal protein
36	7	0.6	152	2 AH1193	hypothetical prote
37	7	0.6	154	2 E87029	hypothetical prote
38	7	0.6	181	2 C84592	hypothetical prote
39	7	0.6	185	1 YQECPP	fibrillar protein p
40	7	0.6	187	1 YQECKS	KS71A fibrillar pro
41	7	0.6	187	1 C43597	pilin type F7-1 pr
42	7	0.6	188	1 YQECF2	F7-2 fibrillar prot
43	7	0.6	190	2 A41863	cysteine synthase
44	7	0.6	191	2 A43597	pilin type F9 prec
45	7	0.6	197	1 C71022	hypothetical prote
46	7	0.6	211	2 C90031	hypothetical prote
47	7	0.6	219	2 S75541	hypothetical prote
48	7	0.6	220	1 A35996	metalloprotease
49	7	0.6	231	1 C69798	probable membrane
50	7	0.6	231	2 H72234	uridylylate kinase
51	7	0.6	233	2 T01205	sulfate transport
52	7	0.6	235	2 S48924	hypothetical prote
53	7	0.6	237	2 S63389	hypothetical prote
54	7	0.6	240	2 C83428	probable amidotran
55	7	0.6	243	2 G81736	conserved hypotet
56	7	0.6	245	2 F71474	probable muramidase
57	7	0.6	252	2 F70711	probable membrane
58	7	0.6	253	2 E89130	protein F52E1.2 [1
59	7	0.6	254	2 T51562	hypothetical prote
60	7	0.6	257	2 B69012	probable membrane
61	7	0.6	258	2 T32939	hypothetical prote
62	7	0.6	259	2 C75410	methionine aminope
63	7	0.6	264	2 PQ0478	pistil extensin-11
64	7	0.6	275	2 A96552	unknown protein, 9
65	7	0.6	277	2 B72226	hypothetical prote
66	7	0.6	282	2 T24693	hypothetical prote
67	7	0.6	283	2 S65961	mann protein - Par
68	7	0.6	291	1 NCBPT5	phosphodiesterase
69	7	0.6	293	2 G64050	N-acetylneuraminat
70	7	0.6	293	2 E90186	conserved hypotet
71	7	0.6	295	2 B86320	3-phosphoserine ph
72	7	0.6	295	2 T51362	phosphoserine phos
73	7	0.6	295	2 T20629	hypothetical prote
74	7	0.6	305	2 T06763	hypothetical prote
75	7	0.6	309	2 E97175	cysteine synthase/

ALIGNMENTS

RESULT 1  
S68441  
leptin receptor, splice form Ob-Re - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-2000 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68441  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, R.M.; Darvishzadeh, J.G.; Lee, J.I.;  
Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68441  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-805 <LEE>  
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493  
A:Experimental source: splice form Re; tissue hypothalamus  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Comment: For alternative splice forms, see PIR:S68438, PIR:S68439, PIR:  
C:Genetics:  
A:Gene: Ob-Re  
C:Keywords: alternative splicing; appetite.

Query Match 3.6%; Score 42; DB 2; Length 805;  
Best Local Similarity 100.0%; Pred. No. 2.9e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 2

S68439  
leptin receptor, splice form Ob-Rc - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-2000 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68439; S68441  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68439  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 664-892 <LEE1>  
A:Cross-references: EMBL:U49108; NID:g1195488; PIDN:AAC52422.1; PID:g1195489  
A:Experimental source: splice form Rc; tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
A:Accession: S68441  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-796, 'GMCTVLFMD' <LEE2>  
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493  
A:Experimental source: splice form Re; tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
A:Note: this sequence from splice form Re is included to produce a complete sequence  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439  
C:Genetics:  
A:Gene: Ob-Rc  
C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 892;  
Best Local Similarity 100.0%; Pred. No. 2.9e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 3

S68437  
leptin receptor, splice form Ob-Ra - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-2000 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68437  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68437  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-894 <LEE>  
A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485  
A:Experimental source: splice form Ra; tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439  
C:Genetics:  
A:Gene: Ob-Ra  
C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 894;  
Best Local Similarity 100.0%; Pred. No. 2.9e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 4

S68440  
leptin receptor, splice form Ob-Rd - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Dec-2000  
C:Accession: S68440  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68440  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-900 <LEE>  
A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491  
A:Experimental source: tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439  
C:Genetics:  
A:Gene: Ob-Rd  
C:Keywords: alternative splicing; appetite; transmembrane protein  
F:840-860/Domain: transmembrane #status predicted <TMM>

Query Match 3.6%; Score 42; DB 2; Length 900;  
Best Local Similarity 100.0%; Pred. No. 2.9e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 5

S68438  
leptin receptor, splice form Ob-Rb - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1998 #sequence\_revision 31-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: S68438; S68441  
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996  
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997  
A:Accession: S68438  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 664-1162 <LEE1>  
A:Cross-references: EMBL:U49107; NID:g1195486; PIDN:AAC52421.1; PID:g1195487  
A:Experimental source: splice form Rb; tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
A:Note: only a part of the translation is shown  
A:Accession: S68441  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-796, 'GMCTVLFMD' <LEE2>  
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493  
A:Experimental source: splice form Re; tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439  
C:Genetics:  
A:Gene: Ob-Rb  
C:Keywords: alternative splicing; appetite

Query Match 3.6%; Score 42; DB 2; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 3.6e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 6  
leptin receptor, Ob-Rb - rat  
PC4184  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: JC4895; JC4896; JC4897; PC4184; JC4797  
R:Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Tamura  
Biochem. Biophys. Res. Commun. 225, 75-83, 1996  
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identificat  
A:Reference number: JC4895; MUID:96332408  
A:Accession: JC4895  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1162 <TA3>  
A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAAL2831.1; PID:d1013515; PID:g15264  
A:Accession: JC4896  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-889, 'RADTL' <TA2>  
A:Cross-references: DDBJ:D85557  
A:Accession: JC4897  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-796, 'G', 1157-1158, 'TVLLN' <TA3>  
A:Cross-references: DDBJ:D85559  
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.  
Biochem. Biophys. Res. Commun. 224, 597-604, 1996  
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R) cDN  
A:Reference number: PC4184; MUID:96295531  
A:Accession: PC4184  
A:Molecule type: mRNA  
A:Residues: 840-1162 <IID>  
A:Cross-references: DDBJ:D84550  
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.  
Biochem. Biophys. Res. Commun. 222, 19-26, 1996  
A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker fatt  
A:Reference number: JC4797; MUID:96212906  
A:Accession: JC4797  
A:Molecule type: mRNA  
A:Residues: 1-889, 'RADTL' <IT2>  
A:Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAAL2230.1; PID:g1374708  
A:Experimental source: adipose cell  
C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa) r  
C:Genetics:  
A:Gene: fa  
C:Keywords: appetite; transmembrane protein  
F:840-860/Domain: transmembrane #status predicted <TMM>  
F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 3.6%; Score 42; DB 2; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 3.6e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 7  
leptin receptor, isoform Ob-Rf - rat  
S74225  
C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 05-Nov-1999  
C:Accession: S74225  
R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.  
FEBS Lett. 392, 87-90, 1996  
A:Title: A novel leptin receptor isoform in rat.  
A:Reference number: S74225; MUID:96368027  
A:Accession: S74225  
A:Molecule type: mRNA  
A:Residues: 1-895 <WAN>  
A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AB03088.1; PID:g1395213  
A:Experimental source: strain Sprague-Dawley; tissue type brain  
C:Genetics:  
A:Gene: rob-R  
C:Keywords: appetite; transmembrane protein  
F:840-860/Domain: transmembrane #status predicted <TMM>

Query Match 3.5%; Score 41; DB 2; Length 895;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 501 QPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 499 QPIFLSGYTMWIRINHSLSGSLDSPPTCVLPDSVVKPLPPS 539

RESULT 8  
T38142  
hypothetical protein SPAC22A12.02c - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C:Accession: T38142  
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21774  
A:Accession: T38142  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-124 <PEA>  
A:Cross-references: EMBL:Z99295; PIDN:CAB16572.1; GSPDB:GN00066; SPDB:SPAC22A12.02c  
A:Experimental source: strain 972h-; cosmid c22A12  
C:Genetics:  
A:Gene: SPDB:SPAC22A12.02c  
A:Map position: 1  
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22A12.02c

Query Match 0.7%; Score 8; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AGISKNTS 58  
|||||  
Db 45 AGISKNTS 52

RESULT 9  
B97118  
hypothetical protein CAC1767 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: B97118  
R:Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97118  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-222 <KUR>  
A:Cross-references: GB:AF001437; PIDN:AAK79733.1; PID:g15024737; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:  
A:Gene: CAC1767

Query Match 0.7%; Score 8; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 KNLFRRNYN 156  
|||||  
DB 4 KNLFRRNYN 11

## RESULT 10

S75373  
probable DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Sulfolobus solfataricus  
N:Alternate names: endonuclease III; protein c04006  
C:Species: Sulfolobus solfataricus  
C>Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 20-Jun-2000  
C:Accession: S75373  
R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.  
Mol. Microbiol. 22, 175-191, 1996  
A:Title: Organizational characteristics and information content of an archaeal genome: 1  
A:Reference number: S73076; MUID:97055432  
A:Accession: S75373  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <SEN>  
A:Cross-references: EMBL:Y08257; NID:g1707772; PID:g1707778  
A:Experimental source: strain P2  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996  
C:Superfamily: apurinic/apyrimidinic endonuclease III  
C:Keywords: 4Fe-4S; carbon-oxygen lyase; metalloprotein  
F:204,211,214,219/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 0.7%; Score 8; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1058 DELLKLEG 1065  
|||||  
DB 122 DELLKLEG 129

## RESULT 11

F83990  
lactose transport system (lactose-binding protein) BH2726 [imported] - Bacillus halodurans  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: F83990  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: F83990  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-425 <STO>  
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06445.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH2726

Query Match 0.7%; Score 8; DB 2; Length 425;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 854 ILLGTLL 861  
|||||  
DB 8 ILLGTLL 15

## RESULT 12

F83602  
hypothetical protein PA0344 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F83602  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337  
A:Accession: F83602  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-459 <STO>  
A:Cross-references: GB:AE004472; GB:AE004091; NID:g9946188; PIDN:AG03733.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0344  
C:Superfamily: Neisseria meningitidis hypothetical protein NMB1644

Query Match 0.7%; Score 8; DB 2; Length 459;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 838 SDAGLYVI 845  
|||||  
DB 116 SDAGLYVI 123

## RESULT 13

JQ2353  
glycoprotein E precursor - turkey herpesvirus  
N:Alternate names: ORF 8 protein  
C:Species: turkey herpesvirus  
C>Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 07-May-1999  
C:Accession: JQ2353  
R:Zelnik, V.; Darteil, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ro  
J. Gen. Virol. 74, 2151-2162, 1993  
A:Title: The complete sequence and gene organization of the short unique region of he  
A:Reference number: JQ2346; MUID:94014999  
A:Accession: JQ2353  
A:Molecule type: DNA  
A:Residues: 1-498 <ZEL>  
C:Keywords: glycoprotein; transmembrane protein  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-498/Product: glycoprotein E #status predicted <MAT>  
F:396-412/Domain: transmembrane #status predicted <TM>  
F:44,60,133,148,370/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 0.7%; Score 8; DB 2; Length 498;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 DAGLYVIV 846  
|||||  
DB 318 DAGLYVIV 325

## RESULT 14

S09790  
hypothetical protein UL27 - human cytomegalovirus (strain AD169)  
C:Species: human cytomegalovirus, human herpesvirus 5  
A:Note: host Homo sapiens (man)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 08-Oct-1999  
C:Accession: S09790  
R:Chae, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T  
M.; Barrell, B.G.  
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990



A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
A:Reference number: S09749; MUID:90269039  
A:Accession: S09790  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-608 <CHE>  
A:Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35426.1; PID:g59632  
A:Note: this sequence was submitted to the EMBL Data Library, December 1989

Query Match 0.7%; Score 8; DB 2; Length 608;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 DYFLPAG 52  
|||||||  
Db 369 DYFLPAG 376

RESULT 15  
T48474  
hypothetical protein T1E3.140 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T48474  
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De  
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24491  
A:Accession: T48474  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-864 <BEV>  
A:Cross-references: EMBL:AL162972  
A:Experimental source: cultivar Columbia; BAC clone T1E3  
C:Genetics:  
A:Map position: 5  
A:Introns: 612/2; 626/3; 677/1; 696/3; 770/3  
A:Note: T1E3.140

Query Match 0.7%; Score 8; DB 2; Length 864;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 RSSLYCSD 475  
|||||||  
Db 640 RSSLYCSD 647

RESULT 16  
G87640  
TonB-dependent receptor [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C:Accession: G87640  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: G87640  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-937 <STO>  
A:Cross-references: GB:AE005673; NID:g13424831; PIDN:AAK25123.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC3161

Query Match 0.7%; Score 8; DB 2; Length 937;  
Best Local Similarity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 626 SNPATTV 633  
|||||||  
Db 724 SNPATTV 731

RESULT 17  
T21269  
hypothetical protein F22E10.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T21269  
R:Gardner, A.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19398  
A:Accession: T21269  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1270 <WIL>  
A:Cross-references: EMBL:Z67882; PIDN:CAA91802.1; GSPDB:GN00028; CESP:F22E10.4  
A:Experimental source: clone F22E10  
C:Genetics:  
A:Gene: CESP:F22E10.4  
A:Map position: X  
A:Introns: 69/2; 120/2; 162/3; 207/2; 264/3; 680/2; 828/3; 923/3; 972/2; 1131/3; 1204  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 0.7%; Score 8; DB 2; Length 1270;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 IREADKIV 288  
|||||||  
Db 623 IREADKIV 630

RESULT 18  
T21267  
hypothetical protein F22E10.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T21267  
R:Gardner, A.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19398  
A:Accession: T21267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1291 <WIL>  
A:Cross-references: EMBL:Z67882; PIDN:CAA91800.1; GSPDB:GN00028; CESP:F22E10.2  
A:Experimental source: clone F22E10  
C:Genetics:  
A:Gene: CESP:F22E10.2  
A:Map position: X  
A:Introns: 19/3; 63/2; 81/3; 114/2; 156/3; 201/2; 258/3; 354/1; 642/2; 724/1; 791/3;  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

Query Match 0.7%; Score 8; DB 2; Length 1291;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 IREADKIV 288  
|||||||  
Db 584 IREADKIV 591

RESULT 19  
T21266  
hypothetical protein F22E10.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C/Accession: T21266  
R/Gardner, A.  
submitted to the EMBL Data Library, November 1995  
A/Reference number: Z19398  
A/Accession: T21266  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1318 <WIL>  
A/Cross-references: EMBL:Z67882; PIDN:CAA91799.1; GSPDB:GN00028; CESP:F22E10.1  
A/Experimental source: clone F22E10  
C/Genetics:  
A/Gene: CESP:F22E10.1  
A/Map position: X  
A/Introns: 26/3; 81/3; 114/2; 156/3; 201/2; 258/3; 300/2; 396/3; 676/2; 818/3; 939/3; 10  
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match                    0.7%; Score 8; DB 2; Length 1318;  
Best Local Similarity    100.0%; Pred. No. 43;  
Matches    8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY    281 IREADKIV 288  
      |||||  
Db    617 IREADKIV 624

RESULT 20  
T21268  
hypothetical protein F22E10.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C/Accession: T21268  
R/Gardner, A.  
submitted to the EMBL Data Library, November 1995  
A/Reference number: Z19398  
A/Accession: T21268  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1327 <WIL>  
A/Cross-references: EMBL:Z67882; PIDN:CAA91801.1; GSPDB:GN00028; CESP:F22E10.3  
A/Experimental source: clone F22E10  
C/Genetics:  
A/Gene: CESP:F22E10.3  
A/Map position: X  
A/Introns: 23/3; 93/3; 213/2; 270/3; 686/2; 827/3; 1261/3  
C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match                    0.7%; Score 8; DB 2; Length 1327;  
Best Local Similarity    100.0%; Pred. No. 44;  
Matches    8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY    281 IREADKIV 288  
      |||||  
Db    629 IREADKIV 636

RESULT 21  
H82849  
hypothetical protein XF0098 [imported] - Xylella fastidiosa (strain 9a5c)  
C/Species: Xylella fastidiosa  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C/Accession: H82849  
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A/Reference number: A82515; MUID:20365717  
A/Note: for a complete list of authors see reference number A59328 below  
A/Accession: H82849  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-64 <SIM>

A/Cross-references: GB:AF003863; GB:AE003849; MID:g9104863; PIDN:AAF82911.1; GSPDB:GN  
A/Experimental source: strain 9a5c  
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A/Reference number: A59328  
A/Contents: annotation  
C/Genetics:  
A/Gene: XF0098

Query Match                    0.6%; Score 7; DB 2; Length 64;  
Best Local Similarity    100.0%; Pred. No. 33;  
Matches    7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY    372 LAEKIPO 378  
      |||||  
Db    29 LAEKIPO 35

RESULT 22  
S34404  
ribosomal protein L15 - Bacillus licheniformis (fragment)  
C/Species: Bacillus licheniformis  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C/Accession: S34404  
R/Tschauder, S.; Driessen, A.J.M.; Frendl, R.  
Mol. Gen. Genet. 235, 147-152, 1992  
A/Title: Cloning and molecular characterization of the secY genes from Bacillus liche  
A/Reference number: S30115; MUID:93062802  
A/Accession: S34404  
A/Molecule type: DNA  
A/Residues: 1-72 <TSC>  
A/Cross-references: EMBL:X70087  
C/Genetics:  
A/Gene: rpl15  
C/Superfamily: Escherichia coli ribosomal protein L15  
C/Keywords: protein biosynthesis; ribosome

Query Match                    0.6%; Score 7; DB 2; Length 72;  
Best Local Similarity    100.0%; Pred. No. 37;  
Matches    7; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY    967 AEGTEVT 973  
      |||||  
Db    12 AEGTEVT 18

RESULT 23  
T44104  
hypothetical protein [imported] - Staphylococcus aureus (fragment)  
C/Species: Staphylococcus aureus  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 11-May-2000  
C/Accession: T44104  
R/Ito, T.; Katayama, Y.; Hiramatsu, K.  
Antimicrob. Agents Chemother. 43, 1449-1458, 1999  
A/Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-m  
A/Reference number: Z22733; MUID:99278010  
A/Accession: T44104  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-87 <ITO>  
A/Cross-references: EMBL:D86934; PIDN:BAA82206.1

A:Experimental source: strain N315

Query Match 0.6%; Score 7; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1109 LFTDIRV 1115  
|||||||  
DB 8 LFTDIRV 14

RESULT 24

AD1704

class I heat-shock protein (chaperonin) GROES [imported] - Listeria innocua (strain Cl1p11262)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD1704  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1704  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-94 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97404.1; PID:g16414688; GSPDB:GN00178  
A:Experimental source: strain Cl1p11262  
A:Genetics: groES  
A:Gene: groES

Query Match 0.6%; Score 7; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 969 GTEVTYPE 975  
|||||||  
DB 71 GTEVTYPE 77

RESULT 25

AE1333

class I heat-shock protein (chaperonin) GROES [imported] - Listeria monocytogenes (strain C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AE1333  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1333  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-94 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAD00147.1; PID:g16411539; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
A:Genetics: groES  
A:Gene: groES

Query Match 0.6%; Score 7; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 969 GTEVTYPE 975  
|||||||  
DB 71 GTEVTYPE 77

RESULT 26

S59321

hypothetical protein L3125 (L3123 internal orf) - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 29-Nov-1995 #sequence\_revision 05-Sep-1996 #text\_change 20-Oct-2000  
C:Accession: S59321  
R:Delius, H.  
submitted to the EMBL Data Library, June 1995  
A:Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CK11, PDC5, SLS  
A:Reference number: S59313  
A:Accession: S59321  
A:Status: conceptual translation of pseudogene  
A:Molecule type: DNA  
A:Residues: 1-101 <DEL>  
A:Cross-references: EMBL:X91258; NID:g995686; PIDN:CAA62344.1; PID:g995695  
A:Experimental source: strain S288C  
C:Comment: There is no evidence that this sequence is expressed.  
C:Genetics:  
A:Map position: 12R  
C:Keywords: pseudogene

Query Match 0.6%; Score 7; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 KGDLKLF 140  
|||||||  
DB 53 KGDLKLF 59

RESULT 27

AC1159

hypothetical protein lmo0675 [imported] - Listeria monocytogenes (strain EGD-e)  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AC1159  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1159  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-104 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98753.1; PID:g16410064; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
A:Genetics: lmo0675  
A:Gene: lmo0675

Query Match 0.6%; Score 7; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 859 TLLISHQ 865  
|||||||  
DB 47 TLLISHQ 53

RESULT 28

AC1518

hypothetical protein lin0683 [imported] - Listeria innocua (strain Cl1p11262)  
C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AC1518  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AC1518  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-104 <GLA>  
 A:Cross-references: GB:AL592022; PIDN:CAC95915.1; PID:g16413135; GSPDB:GN00178  
 A:Experimental source: strain Clp11262  
 C:Genetics:  
 A:Gene: lln0683

Query Match 0.6%; Score 7; DB 2; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 859 TLLISHQ 865  
 |||||  
 Db 47 TLLISHQ 53

RESULT 29  
 AC2259  
 hypothetical protein all3626 [imported] - *Anabaena* sp. (strain PCC 7120)  
 C:Species: *Anabaena* sp.  
 A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120  
 C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 11-Jan-2002  
 C:Accession: AC2259  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AC2259  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-123 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BA875325.1; PID:g17132759; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all3626

Query Match 0.6%; Score 7; DB 2; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1014 SSKNSPL 1020  
 |||||  
 Db 16 SSKNSPL 22

RESULT 30  
 AE1445  
 hypothetical protein lln0100 [imported] - *Listeria innocua* (strain Clp11262)  
 C:Species: *Listeria innocua*  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AE1445  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AE1445  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-127 <GLA>  
 A:Cross-references: GB:AL592022; PIDN:CAC95333.1; PID:g16412520; GSPDB:GN00178  
 A:Experimental source: strain Clp11262  
 C:Genetics:  
 A:Gene: lln0100

Query Match 0.6%; Score 7; DB 2; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDELKTL 1063  
 |||||  
 Db 27 LDELKTL 33

RESULT 31  
 A11362  
 hypothetical protein lmo2305 [imported] - *Listeria monocytogenes* (strain EGD-e)  
 C:Species: *Listeria monocytogenes*  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: A11362  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: A11362  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-127 <GLA>  
 A:Cross-references: GB:NC\_003210; PIDN:CAD00383.1; PID:g16411775; GSPDB:GN00177  
 A:Experimental source: strain EGD-e  
 C:Genetics:  
 A:Gene: lmo2305

Query Match 0.6%; Score 7; DB 2; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDELKTL 1063  
 |||||  
 Db 27 LDELKTL 33

RESULT 32  
 D70518  
 probable membrane protein - *Mycobacterium tuberculosis* (strain H37RV)  
 C:Species: *Mycobacterium tuberculosis*  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 02-Sep-2000  
 C:Accession: D70518  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
 A:Reference number: A70500; MUID:9829587  
 A:Accession: D70518  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-134 <COL>  
 A:Cross-references: GB:Z97193; GB:AL123456; NID:g3261816; PIDN:CAB10033.1; PID:e32486  
 A:Experimental source: strain H37RV  
 C:Genetics:

A:Gene: RV1903  
C:Superfamily: hypothetical protein yvld

Query Match 0.6%; Score 7; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 755 IVSWILS 761  
|||||  
Db 115 IVSWILS 121

## RESULT 33

C82889

hypothetical protein U0445 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C:Accession: C82889

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

Submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mlr

A:Reference number: A82870

A:Accession: C82889

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-141 &lt;GLA&gt;

A:Cross-references: GB:AE002141; GB:AF222894; NID:g6899434; PIDN:AAF30857.1; GSPDB:GN001

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: U0445

A:Genetic code: SGC3

Query Match 0.6%; Score 7; DB 2; Length 141;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 FPIPKY 807  
|||||  
Db 49 FPIPKY 55

## RESULT 34

C70937

hypothetical protein RV2185c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C:Accession: C70937

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987

A:Accession: C70937

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-144 &lt;COL&gt;

A:Cross-references: GB:AL021957; GB:AL123456; NID:g3242293; PIDN:CAA17489.1; PID:g291110

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2185c

C:Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c

Query Match 0.6%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GTEVTE 975  
|||||

Db 103 GTEVTE 109

## RESULT 35

R5BSL5

ribosomal protein L15 - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000

C:Accession: S12682; JS0491; S08628; A69696

R:Yoshikawa, H.; Doi, R.H.

Nucleic Acids Res. 18, 1647, 1990

A:Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.

A:Reference number: S12680; MUID:90221911

A:Accession: S12682

A:Molecule type: DNA

A:Residues: 1-146 &lt;YOS&gt;

A:Cross-references: EMBL:M31102; NID:g1184272; PIDN:BA059117.1; PID:g143577

R:Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.

J. Biochem. 107, 603-607, 1990

A:Title: Cloning and characterization of a Bacillus subtilis gene homologous to E. co

A:Reference number: JS0490; MUID:90292990

A:Accession: JS0491

A:Molecule type: DNA

A:Residues: 1-146 &lt;NAK&gt;

A:Cross-references: DDBJ:D00619; NID:g216336; PIDN:BA00494.1; PID:g216338

R:Sub, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.

Mol. Microbiol. 4, 305-314, 1990

A:Title: Isolation of a secY homologue from Bacillus subtilis: evidence for a common

A:Reference number: S08628; MUID:90251170

A:Accession: S08628

A:Molecule type: DNA

A:Residues: 94-146 &lt;SUH&gt;

A:Cross-references: EMBL:X51329; NID:g40132; PIDN:CA035711.1; PID:g40133

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A:Reference number: A69580; MUID:98044033

A:Accession: A69696

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-146 &lt;KUN&gt;

A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11911.1; PID:g26324

A:Experimental source: strain 168

C:Genetics:

A:Gene: rplO

C:Superfamily: Escherichia coli ribosomal protein L15

C:Keywords: protein biosynthesis; ribosome

Query Match 0.6%; Score 7; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 AEGTEVT 973  
|||||  
Db 86 AEGTEVT 92

## RESULT 36

AH1193

hypothetical protein lmo0952 [imported] - Listeria monocytogenes (strain EGD-e)



C:Species: *Listeria monocytogenes*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AH1193  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Eshti, H.; Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simoes, N.; Tlerraz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1193  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-152 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC99030.1; PID:g16410354; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0952

Query Match 0.6%; Score 7; DB 2; Length 152;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VVSLST 945  
|||||  
DB 116 VVSLST 122

RESULT 37  
E87029

hypothetical protein [imported] - *Mycobacterium leprae*

C:Species: *Mycobacterium leprae*  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C:Accession: E87029  
R:Coile, S.T.; Elglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, M.A.; Rutherford, K.M.; Nature 409, 1007-1011, 2001  
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq, A.; Title: Massive gene decay in the leprosy bacillus.  
A:Reference number: A86909; MUID:21128732; PMID:11234002  
A:Accession: E87029  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-154 <STO>  
A:Cross-references: GB:AL450380; NID:g13093011; PIDN:CAC31344.1; GSPDB:GN00147  
C:Genetics:  
A:Gene: ML0963

Query Match 0.6%; Score 7; DB 2; Length 154;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 943 LSTDL 949  
|||||  
DB 39 LSTDL 45

RESULT 38  
C84592

hypothetical protein At2g20700 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: C84592  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A:Reference number: A84420; MUID:20083487

A:Accession: C84592  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-181 <STO>  
A:Cross-references: GB:AE002093; NID:g4454478; PIDN:AAD20925.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g20700  
A:Map position: 2  
C:Superfamily: *Arabidopsis thaliana* probable GPI-anchored protein F26K10.160

Query Match 0.6%; Score 7; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 502 PIFLLSG 508  
|||||  
DB 13 PIFLLSG 19

RESULT 39  
YQECPP

fimbrial protein papa precursor - *Escherichia coli*

N:Alternate names: pap pil1  
C:Species: *Escherichia coli*  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 16-Jul-1999  
C:Accession: A23221; S25216; A05229; S16395  
R:Bagu, M.; Normark, S.; Hardy, J.; O'Hanley, P.; Lark, D.; Olsson, O.; Schoolnik, G.; J. Bacteriol. 157, 330-333, 1984  
A:Title: Nucleotide sequence of the papa gene encoding the pap pilus subunit of human  
A:Reference number: A91794; MUID:84087728  
A:Accession: A23221  
A:Molecule type: DNA  
A:Residues: 1-185 <BAG>  
A:Cross-references: GB:X03391; GB:K01176; GB:X03392; NID:g42309; PIDN:CAA27126.1; PID R;Miklund, B.I.; Tennent, J.M.; Garcia, E.; Hamers, A.; Bagu, M.; Lindberg, F.; Gaas Mol. Microbiol. 6, 2225-2242, 1992  
A:Title: Horizontal gene transfer of the *Escherichia coli* pap and prs pil operons as  
A:Reference number: S25205; MUID:93023852  
A:Accession: S25216  
A:Molecule type: DNA  
A:Residues: 1-185 <MA2>  
A:Cross-references: EMBL:X61239; NID:g42290; PIDN:CAA43562.1; PID:g42293  
A:Experimental source: strain J96  
C:Genetics:  
A:Gene: papa  
C:Superfamily: F7-2 fimbrial protein  
C:Keywords: fimbria  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-185/Product: fimbrial protein papa #status predicted <MAT>

Query Match 0.6%; Score 7; DB 1; Length 185;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
|||||  
DB 177 VANFNLT 183

RESULT 40  
YQECKS

KS71A fimbrial protein precursor - *Escherichia coli*

N:Alternate names: KS71A pilin  
C:Species: *Escherichia coli*  
C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 16-Jul-1999  
C:Accession: A23117  
R:Rhen, M.; van Die, I.; Rhen, V.; Bergmans, H.; Eur. J. Biochem. 151, 573-577, 1985  
A:Title: Comparison of the nucleotide sequences of the genes encoding the KS71A and F  
A:Reference number: A23117; MUID:85285072  
A:Accession: A23117

A:Molecule type: DNA  
A:Residues: 1-187 <RHE>  
A:Cross-references: GB:X02921; NID:g141880; PIDN:CAA26678.1; PID:g141881  
C:Superfamily: F7-2 fimbrial protein  
C:Keywords: fimbria  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-187/Product: KS71A fimbrial protein #status predicted <MAT>

Query Match 0.6%; Score 7; DB 1; Length 187;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
|||||  
Db 179 VANFNLT 185

## RESULT 41

pilin type F7-1 precursor - Escherichia coli  
C:Species: Escherichia coli  
C>Date: 12-Jan-1993 #sequence\_revision 12-Jan-1993 #text\_change 26-Aug-1999  
C:Accession: C43597  
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.D.  
Infect. Immun. 59, 3849-3858, 1991  
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strains:  
A:Reference number: A43597; MUID:92040048  
A:Accession: C43597  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-187 <DEN>  
A:Cross-references: GB:M68061; NID:g147072; PIDN:AAA24279.1; PID:g147073  
C:Superfamily: F7-2 fimbrial protein

Query Match 0.6%; Score 7; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
|||||  
Db 179 VANFNLT 185

## RESULT 42

YOECP2  
F7-2 fimbrial protein precursor - Escherichia coli  
N:Alternate names: F7-2 pilin  
C:Species: Escherichia coli

C>Date: 28-Feb-1986 #sequence\_revision 28-Feb-1986 #text\_change 16-Jul-1999  
C:Accession: A03496; B43597  
R:Van Die, I.; Bergmans, H.  
Gene 32, 83-90, 1984  
A:Title: Nucleotide sequence of the gene encoding the F7-2 fimbrial subunit of a uropath

A:Reference number: A03496; MUID:85155489  
A:Accession: A03496  
A:Molecule type: DNA  
A:Residues: 1-188 <VAN>

A:Cross-references: GB:M12861; NID:g145963; PIDN:AAA23778.1; PID:g145964  
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.D.  
Infect. Immun. 59, 3849-3858, 1991  
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strains:  
A:Reference number: A43597; MUID:92040048  
A:Accession: B43597  
A:Molecule type: DNA  
A:Residues: 1-188 <DEN>

A:Cross-references: GB:M68060; NID:g147070; PIDN:AAA24278.1; PID:g147071  
C:Genetics:  
A:Gene: pAPA  
C:Function:

A:Description: one of the fimbrial proteins involved in mannose-resistant hemagglutination  
ubunits into fimbriae, or regulation of phase variation

C:Superfamily: F7-2 fimbrial protein  
C:Keywords: fimbria; mannose-resistant hemagglutination  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-188/Product: F7-2 fimbrial protein #status predicted <MAT>

Query Match 0.6%; Score 7; DB 1; Length 188;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
|||||  
Db 180 VANFNLT 186

## RESULT 43

A41863  
cysteine synthase (EC 4.2.99.8) cysM [similarity] - Pseudomonas syringae (fragment)  
N:Alternate names: O-acetylserine (thiol)-lyase B  
C:Species: Pseudomonas syringae  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-May-2000  
C:Accession: A41863  
R:Hrabak, E.M.; Willis, D.K.  
J. Bacteriol. 174, 3011-3020, 1992  
A:Title: The lemA gene required for pathogenicity of Pseudomonas syringae pv. syringa  
A:Reference number: A41863; MUID:92234961  
A:Accession: A41863  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-190 <HRA>  
A:Cross-references: GB:M80477; NID:g151327; PIDN:AAA25876.1; PID:g151328  
A:Experimental source: pv. syringae  
A>Note: sequence extracted from NCBI backbone (NCBIN:97411, NCBI:P.97414)  
C:Genetics:  
A:Gene: cysM  
C:Superfamily: threonine dehydratase  
C:Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate  
F:66/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 0.6%; Score 7; DB 2; Length 190;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1060 LKLEGN 1066  
|||||  
Db 53 LKLEGN 59

## RESULT 44

A43597  
pilin type F9 precursor - Escherichia coli  
C:Species: Escherichia coli  
C>Date: 12-Jan-1993 #sequence\_revision 12-Jan-1993 #text\_change 26-Aug-1999  
C:Accession: A43597  
R:Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P.  
Infect. Immun. 59, 3849-3858, 1991  
A:Title: DNA sequences of three pAPA genes from uropathogenic Escherichia coli strain  
A:Reference number: A43597; MUID:92040048  
A:Accession: A43597  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <DEN>

A:Cross-references: GB:M68059; NID:g147068; PIDN:AAA24277.1; PID:g147069  
C:Superfamily: F7-2 fimbrial protein

Query Match 0.6%; Score 7; DB 2; Length 191;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
|||||

DB 183 VANFNLT 189

RESULT 45  
C71022

hypothetical protein PH1472 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: C71022

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137

A:Accession: C71022

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <RAW>

A:Cross-references: GB:AP000006; NID:g1236133; PIDN:BAA30579.1; PID:g3257896

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1472

C:Superfamily: Archaeoglobus probable DNA-polymerase

Query Match

Best Local Similarity 0.6%; Score 7; DB 1; Length 197;  
Pred. No. 90;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1057 LDELTKL 1063

|||||

DB 70 LDELTKL 76

RESULT 46  
C90031

hypothetical protein SA2111 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C:Accession: C90031

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani, H.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C90031

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-211 <RAW>

A:Cross-references: GB:BA000018; PID:g13702120; PIDN:BAB43412.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA2111

Query Match

Best Local Similarity 0.6%; Score 7; DB 2; Length 211;  
Pred. No. 96;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 541 SSVKAEI 547

|||||

DB 104 SSVKAEI 110

RESULT 47  
S75541

hypothetical protein s11218 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C:Accession: S75541

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys  
s.

A:Reference number: S74322; MUID:97061201

A:Accession: S75541

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-219 <RAW>

A:Cross-references: EMBL:D90911; GB:AB001339; NID:g1653033; PIDN:BAA18102.1; PID:g165

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: ycf39

C:Superfamily: hypothetical protein YMR090w

Query Match

Best Local Similarity 0.6%; Score 7; DB 2; Length 219;  
Pred. No. 99;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 912 LLEPETI 918

|||||

DB 52 LLEPETI 58

RESULT 48  
A35996

metalloproteinase inhibitor 2 precursor - bovine

N:Alternate names: collagenase inhibitor; tissue inhibitor of metalloproteinases (TIM

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Nov-1990 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999

C:Accession: A35996; A34468; A25322; S28151

R:Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.

Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990

A:Title: cDNA cloning and expression of a metalloproteinase inhibitor related to class

A:Reference number: A35996; MUID:90207285

A:Accession: A35996

A:Molecule type: mRNA

A:Residues: 1-220 <BOO>

A:Cross-references: GB:M32303; NID:g163341; PIDN:AAA30636.1; PID:g163342

A:Experimental source: aortic endothelial cDNA library

R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.

J. Biol. Chem. 264, 17445-17453, 1989

A:Title: Purification and characterization of two related but distinct metalloprotein

A:Reference number: A34468; MUID:9008914

A:Accession: A34468

A:Molecule type: protein

A:Residues: 27-71 <DEC>

A:Experimental source: culture medium of aortic endothelial cells

R:Murray, J.B.; Allison, K.; Sudhalter, J.; Langer, R.

J. Biol. Chem. 261, 4154-4159, 1986

A:Title: Purification and partial amino acid sequence of a bovine cartilage-derived c

A:Reference number: A25322; MUID:86140235

A:Accession: A25322

A:Molecule type: protein

A:Residues: 27-41, 'C', 43-55, 'EX', 58-59, 'X', 61-66, 'XS', 69-71 <MUR>

A:Experimental source: cartilage

R:DeClerck, Y.A.; Yean, T.D.; Lee, Y.; Tomich, J.M.; Langley, K.E.

Biochem. J. 289, 65-69, 1993

A:Title: Characterization of the functional domain of tissue inhibitor of metalloprot

A:Reference number: S28151; MUID:93143691

A:Contents: annotation; functional domain

C:Function:

A:Description: regulation of extracellular matrix remodeling by inhibition of matrix

possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potential

C:Superfamily: metalloproteinase inhibitor

C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitoge

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>

F:27-98, 29-127, 39-152, 154-201, 159-164, 172-193/Disulfide bonds: #status predicted

Query Match 0.6%; Score 7; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 855 LLGLTLL 861  
|||||||  
Db 15 LLGLTLL 21

## RESULT 49

C69798  
probable membrane protein yetF - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: C69798  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033  
A:Accession: C69798  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-231 <KUN>  
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12533.1; PID:g2633027  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yetF  
C:Superfamily: probable membrane protein ycap

Query Match 0.6%; Score 7; DB 1; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 SKSVSLP 599  
|||||||  
Db 164 SKSVSLP 170

## RESULT 50

H72234  
uridylylate kinase - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: H72234  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316  
A:Accession: H72234  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-231 <ARN>  
A:Cross-references: GB:AE001804; GB:AE000512; NID:g4982160; PIDN:AAD36671.1; PID:g498217  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM1604  
C:Superfamily: uridine 5'-monophosphate kinase

Query Match 0.6%; Score 7; DB 2; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1049 PHLTFSE 1055  
|||||||  
Db 174 PHLTFSE 180

Search completed: May 18, 2002, 07:04:33  
Job time: 262 sec





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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:04:17 ; Search time 15.27 Seconds  
(without alignments)  
2954.046 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVVLHWEFTYVIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	91.3	1165	1 LEPR_HUMAN	P48357 homo sapien
2	42	3.6	1162	1 LEPR_MOUSE	P48356 mus musculu
3	42	3.6	1162	1 LEPR_RAT	Q62959 rattus norv
4	8	0.7	608	1 UL27_HCMVA	P16763 human cytom
5	8	0.7	4036	1 RRPL_DUGBV	Q66431 dugbe virus
6	7	0.6	72	1 RL15_BACLI	P35138 bacillus li
7	7	0.6	146	1 RL15_BACSU	P19946 bacillus su
8	7	0.6	169	1 CYSM_PSESY	P48028 pseudomonas
9	7	0.6	185	1 PAPA_ECOLI	P04127 escherichia
10	7	0.6	187	1 FMK1_ECOLI	P04740 escherichia
11	7	0.6	188	1 FME2_ECOLI	P02972 escherichia
12	7	0.6	220	1 TIM2_BOVIN	P16368 bos taurus
13	7	0.6	231	1 PYRH_THEMA	Q9x1u0 thermotoga
14	7	0.6	235	1 YHE4_YEAST	P38727 saccharomyc
15	7	0.6	237	1 BIOD_YEAST	P53630 saccharomyc
16	7	0.6	252	1 YE91_MYCTU	P71772 mycobacteri
17	7	0.6	283	1 MAUN_PARDE	Q51660 paracoccus
18	7	0.6	290	1 EX05_BPT5	P06229 bacteriophag
19	7	0.6	293	1 NPL_HAEIN	P44539 haemophilus
20	7	0.6	310	1 YCJY_ECOLI	P76049 escherichia
21	7	0.6	311	1 PP11_YEAST	P20604 saccharomyc
22	7	0.6	329	1 YG54_ARCFU	O28619 archaeoglob
23	7	0.6	335	1 KCC1_SCHPO	O9p712 schizosacch
24	7	0.6	336	1 LEU3_MYCBO	P94929 mycobacteri
25	7	0.6	336	1 LEU3_MYCTU	P95313 mycobacteri
26	7	0.6	349	1 GGH_SOYBN	P93164 glycine max
27	7	0.6	349	1 SOHB_ECOLI	P24213 escherichia
28	7	0.6	353	1 SOHB_HAEIN	P45315 haemophilus
29	7	0.6	363	1 CHSB_PHANI	P48396 pharbitis n
30	7	0.6	373	1 RCL1_HUMAN	O9y2p8 homo sapien
31	7	0.6	373	1 RCL1_MOUSE	O9jft0 mus musculu
32	7	0.6	379	1 Y801_METJA	O58211 methanococc
33	7	0.6	384	1 PURT_BACSU	P39771 bacillus su

34	7	0.6	386	1 RPA2_METVA	P14247 methanococc
35	7	0.6	396	1 CHSB_IPOPU	P48398 ipomoea pur
36	7	0.6	420	1 YM57_YEAST	Q03694 saccharomyc
37	7	0.6	426	1 EXLP_TOBAC	Q03211 nicotiana t
38	7	0.6	454	1 TBB2_PHYPO	P12458 physarum po
39	7	0.6	455	1 TBB_DICDI	P32256 dictyosteli
40	7	0.6	503	1 ZNT1_MOUSE	Q60738 mus musculu
41	7	0.6	507	1 G6PD_CHLMU	O9pxk8 chlamydia m
42	7	0.6	507	1 ZNT1_RAT	Q62720 rattus norv
43	7	0.6	508	1 SPA2_STAUA	P38507 staphylococ
44	7	0.6	524	1 SPA1_STAUA	P02976 staphylococ
45	7	0.6	539	1 IL2B_MOUSE	P16297 mus musculu
46	7	0.6	555	1 C166_CARAU	Q90304 carassius a
47	7	0.6	564	1 C166_BRARE	O90460 brachydanio
48	7	0.6	569	1 IL1R_HUMAN	P14778 homo sapien
49	7	0.6	574	1 ERG1_HUMAN	O14534 homo sapien
50	7	0.6	583	1 GTB1_MOUSE	O08582 mus musculu
51	7	0.6	584	1 GTB1_HUMAN	O00178 homo sapien
52	7	0.6	609	1 COPA_PSESM	P12374 pseudomonas
53	7	0.6	609	1 GP11_YEAST	P53306 saccharomyc
54	7	0.6	616	1 YAWG_SCHPO	Q10190 schizosacch
55	7	0.6	622	1 PPCC_CHICK	P05153 gallus gall
56	7	0.6	632	1 PTMA_BUCAI	P57635 buchnera ap
57	7	0.6	644	1 YGM4_YEAST	P53129 saccharomyc
58	7	0.6	652	1 ILV3_BRANA	P27819 brassica na
59	7	0.6	655	1 ILV1_BRANA	P27818 brassica na
60	7	0.6	662	1 SUT2_STYHA	P53392 stylosanthe
61	7	0.6	665	1 DUSX_HUMAN	Q9by84 homo sapien
62	7	0.6	666	1 YJB0_YEAST	P47077 saccharomyc
63	7	0.6	667	1 SUT1_STYHA	P53391 stylosanthe
64	7	0.6	670	1 ILVB_ARATH	P17597 arabidopsis
65	7	0.6	678	1 FLHA_AQUAE	O67265 aquilex aeo
66	7	0.6	760	1 CO2_MOUSE	P21180 mus musculu
67	7	0.6	769	1 PIGR_MOUSE	P15083 rattus norv
68	7	0.6	776	1 CHS1_CANAL	P23316 candida alb
69	7	0.6	788	1 CADA_HUMAN	Q9y6n8 homo sapien
70	7	0.6	789	1 CADA_CHICK	P79995 gallus gall
71	7	0.6	831	1 PRA1_SYNY3	P74397 synechocyst
72	7	0.6	848	1 ENV_HV1JR	P20871 human immun
73	7	0.6	881	1 YEBT_HAEIN	P44288 haemophilus
74	7	0.6	950	1 CDA3_HUMAN	O9y5h8 homo sapien
75	7	0.6	960	1 VP41_LYCES	P93231 lycopersico

ALIGNMENTS

RESULT	ID	LEPR_HUMAN	STANDARD;	PRT; 1165 AA.
1	AC	P48357;		
DT	DT	01-FEB-1996 (Rel. 33, Created)		
DT	DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	DE	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).		
GN	GN	LEPR OR OBR.		
OS	OS	Homo sapiens (Human).		
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	OX	NCBI_Taxid=9606;		
RN	RN	[1]		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	TISSUE=Brain;		
RX	RX	MEDLINE=96128129; PubMed=8548812;		
RA	RA	Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,		
RA	RA	Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,		
RA	RA	Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,		
RA	RA	Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;		
RT	RT	*Identification and expression cloning of a leptin receptor, OB-R.;		
RL	RL	Cell 83:1263-1271(1995).		
RP	RP	[2]		
RA	RA	SEQUENCE FROM N.A.		
RA	RA	Thompson D.B., Ossowski V., Sutherland J., Apel W.,		

RA Biesterfeldt J.;  
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP VARIANT ARG-223.  
RX MEDLINE=96270489; PubMed=8666155;  
RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;  
RT "The hypothalamic leptin receptor in humans: identification of  
RT incidental sequence polymorphisms and absence of the db/db mouse and  
RT fa/fa rat mutations.";  
RL Diabetes 45:992-994(1996).  
RN [4]  
RP VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.  
RX MEDLINE=97289527; PubMed=9144432;  
RA Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,  
RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;  
RT "Amino acid variants in the human leptin receptor: lack of association  
RT to juvenile onset obesity.";  
RL Biochem. Biophys. Res. Commun. 233:248-252(1997).  
RN [5]  
RP VARIANTS ARG-109; ARG-223 AND ASN-656.  
RX MEDLINE=97431549; PubMed=9287054;  
RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,  
RA Sothorn M., Udall J.N., Kahle B., Leibel R.L.;  
RT "Exonic and intronic sequence variation in the human leptin receptor  
RT gene (LEPR).";  
RL Diabetes 46:1509-1511(1997).  
RN [6]  
RP VARIANTS ARG-109 AND ARG-223.  
RX MEDLINE=97301763; PubMed=9158141;  
RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;  
RT "Structure and sequence variation at the human leptin receptor gene in  
RT lean and obese Pima Indians.";  
RL Hum. Mol. Genet. 6:675-679(1997).  
RN [7]  
RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.  
RX MEDLINE=99075638; PubMed=9860295;  
RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,  
RA Stegried W., Mayer H., Hebebrand J., Grzeschik K.-H.;  
RT "Transmission disequilibrium and sequence variants at the leptin  
RT receptor gene in extremely obese German children and adolescents.";  
RL Hum. Genet. 103:540-546(1998).  
RN [8]  
RP VARIANTS ARG-109; ARG-223 AND ASN-656.  
RX MEDLINE=97318795; PubMed=9175732;  
RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,  
RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;  
RT "Leptin receptor gene variation and obesity: lack of association in a  
RT white British male population.";  
RL Hum. Mol. Genet. 6:869-876(1997).  
CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC  
DR EMBL; U43168; AAA93015.1; -;  
DR EMBL; U59263; AAB09673.1; -;  
DR EMBL; U59248; AAB09673.1; JOINED.  
DR EMBL; U59249; AAB09673.1; JOINED.  
DR EMBL; U59250; AAB09673.1; JOINED.  
DR EMBL; U59252; AAB09673.1; JOINED.  
DR EMBL; U59253; AAB09673.1; JOINED.  
DR EMBL; U59254; AAB09673.1; JOINED.  
DR EMBL; U59255; AAB09673.1; JOINED.  
DR EMBL; U59256; AAB09673.1; JOINED.  
DR EMBL; U59257; AAB09673.1; JOINED.

DR EMBL; U59258; AAB09673.1; JOINED.  
DR EMBL; U59259; AAB09673.1; JOINED.  
DR EMBL; U59260; AAB09673.1; JOINED.  
DR EMBL; U59261; AAB09673.1; JOINED.  
DR EMBL; U59262; AAB09673.1; JOINED.  
DR HSSP; P40189; 1BQU.  
DR MIM; 601007; -;  
DR InterPro; IPR002996; CRA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Polymorphism.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 1165 LEPTIN RECEPTOR.  
FT DOMAIN 22 841 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 842 862 POTENTIAL.  
FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 537 623 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 738 823 FIBRONECTIN TYPE-III 3.  
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 688 688 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 728 728 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 204 204 /FTId=VAR\_002703.  
FT VARIANT 223 223 K -> R.  
FT VARIANT 223 223 /FTId=VAR\_002704.  
FT VARIANT 656 656 Q -> R.  
FT VARIANT 656 656 /FTId=VAR\_002705.  
FT VARIANT 675 675 K -> N.  
FT VARIANT 675 675 /FTId=VAR\_002706.  
FT VARIANT 675 675 S -> T.  
SQ SEQUENCE 1165 AA; 132449 MW; 8FF21D9AF5125808 CRC64;  
Query Match 91.3%; Score 1064; DB 1; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTTPWREKLSGMPNSTDYFLLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPTTPWREKLSGMPNSTDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERKNSGTHFSNLSKTFHCCFRSEQDRNCSLCAQNIKGTFTVSTVNSLV 120  
Db 61 NGHYETAVERKNSGTHFSNLSKTFHCCFRSEQDRNCSLCAQNIKGTFTVSTVNSLV 120  
QY 121 QQIDANWNIQCKLKGDLKLFICYVESLFKNLFRNRYNKKVHLVYLPVLEDSPLVPQKS 180  
Db 121 QQIDANWNIQCKLKGDLKLFICYVESLFKNLFRNRYNKKVHLVYLPVLEDSPLVPQKS 180  
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDLLMCLKITSGGVIFQSPLSVQPINMVKPDP 240

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DB 181 FQWVHCNCSYHECCECLVPVPTAKLNDLLMCLKITSGGVTFQSPLMVQPINWVKPDP 240
OY 241 LGLHMETDDGNKISWSSPPLVPEPLQYQVYSENSTTVIREADKIVATSLLVDSTLP 300
DB 241 LGLHMETDDGNKISWSSPPLVPEPLQYQVYSENSTTVIREADKIVATSLLVDSTLP 300
OY 301 GSSYEVQVRKRLDGPGLWSDWSTPRVFTTQDVITYFPKILTSVGSNVSFHCYKKENKI 360
DB 301 GSSYEVQVRKRLDGPGLWSDWSTPRVFTTQDVITYFPKILTSVGSNVSFHCYKKENKI 360
OY 361 VPSKEIVMMNLAEKIPQSYQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSYQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
OY 421 RYAEIYVIDVMINISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLLYCS DIPSIH 480
DB 421 RYAEIYVIDVMINISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLLYCS DIPSIH 480
OY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
OY 541 SSVKAEITTINGILKISWEKVPFPENNIOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
DB 541 SSVKAEITTINGILKISWEKVPFPENNIOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
OY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660
OY 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTSEDVGNHTKFTFLWTEQAHVTYLAINSI 720
DB 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTSEDVGNHTKFTFLWTEQAHVTYLAINSI 720
OY 721 GASVANFNLTSPMPSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFLIEWKNLNE 780
DB 721 GASVANFNLTSPMPSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFLIEWKNLNE 780
OY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
OY 841 GLYVIVPVISSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQKRETFEHLFI 900
DB 841 GLYVIVPVISSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQKRETFEHLFI 900
OY 901 KHTASVTCGPILEPRTISEDISVDTSMKNDEMPTTVVSLSTTDLEKGSVCISDQFN 960
DB 901 KHTASVTCGPILEPRTISEDISVDTSMKNDEMPTTVVSLSTTDLEKGSVCISDQFN 960
OY 961 SVNFSEAEGETEYVEDESQROPEVKYATILISNKPSETGEEQGLINSSVTRCFSSKNSPL 1020
DB 961 SVNFSEAEGETEYVEDESQROPEVKYATILISNKPSETGEEQGLINSSVTRCFSSKNSPL 1020
OY 1021 KDSFNSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYYL 1080
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNFPEENNDKKSIIYYL 1080
OY 1081 GVTSIKKRESGVLTDKSRVSCPFPAPCLFTDIRVLQDSCHSFVENNINILGTSKKTFFAS 1140
DB 1081 GVTSIKKRESGVLTDKSRVSCPFPAPCLFTDIRVLQDSCHSFVENNINILGTSKKTFFAS 1140
OY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

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RESULT 2
LEPR_MOUSE STANDARD: PRT: 1162 AA.
AC P48356; O35686; Q61215; Q64309; O54986;
DT 01-FEB-1996 (Rel. 33, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219
DE receptor).
GN LEP-R OR OB-R OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT A).
RC TISSUE=Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R.";
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db
RT mice.";
RL Cell 84:491-495(1996).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS A TO E).
RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;
RX MEDLINE=96231997; PubMed=8628397;
RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
RA Lee J.I., Friedman J.M.;
RT "Abnormal splicing of the leptin receptor in diabetic mice.";
RL Nature 379:632-635(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT C).
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
RA Mikhail A., Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
RN [5]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN-NEW ZEALAND OBESSE / NZO; TISSUE=Hypothalamus;
RX MEDLINE=97462708; PubMed=9322935;
RA Igel M., Becker W., Herberg L., Joost H.G.;
RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
RT in the New Zealand obese mouse.";
RL Endocrinology 138:4234-4239(1997).
RN [6]
RP SEQUENCE FROM N.A. (VARIANTS A AND B).
RC STRAIN-FVB/N; TISSUE=Spleen;
RX MEDLINE=96270520; PubMed=8692797;
RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
RA Skoda R.C.;
RT "Defective STAT signaling by the leptin receptor in diabetic mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
RN [7]
RP SEQUENCE FROM N.A. (VARIANT E).
RC STRAIN=129/J;
RX MEDLINE=98008913; PubMed=9344648;
RA Chua S.C., Koutras I.K., Han L., Liu S.M., Kay J., Young S.J.,
RA Chung W.K., Leibel R.L.;
RT "Fine structure of the murine leptin receptor gene: splice site
RT suppression is required to form two alternatively spliced
RT transcripts.";
RL Genomics 45:264-270(1997).

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RA Mori K., Tamura N., Hosoda K., Nakao K.;  
 RT "Molecular cloning of rat leptin receptor isoform complementary  
 RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)  
 RT rats.";  
 RL Biochem. Biophys. Res. Commun. 225:75-83(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (VARIANT B).  
 RA Carlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,  
 RA Carlsson B.;  
 RT "Cloning of the rat leptin receptor.";  
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RL [5]  
 RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).  
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;  
 RX MEDLINE-96212906; PubMed-8630068;  
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;  
 RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from  
 RT Zucker fatty (fa/fa) rat.";  
 RL Biochem. Biophys. Res. Commun. 222:19-26(1996).  
 RN [6]  
 RP SEQUENCE OF 1-123 FROM N.A.  
 RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;  
 RT "Analysis of rat leptin receptor gene.";  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 694-878 FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;  
 RA Ma Z.;  
 RT "Identification of a leptin receptor in islet.";  
 RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).  
 RC STRAIN-SPRAGUE-DAWLEY;  
 RA Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S.,  
 RA Bell G.I.;  
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RL [9]  
 RP VARIANT FA PRO-269.  
 RX MEDLINE-96314329; PubMed-8690163;  
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,  
 RA Kershaw E.E., Chung W.K., Power-Rehove L., Chua M., Tartaglia L.A.,  
 RA Leibel R.L.;  
 RT "Phenotype of fatty due to Gln269pro mutation in the leptin receptor  
 RT (lepr).";  
 RL Diabetes 45:1141-1143(1996).  
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).  
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN  
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT  
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E  
 CC WHICH COULD BE SECRETED.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF  
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING  
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE  
 CC TISSUE.  
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U52966; AAC52587.1; -  
 DR EMBL; D84550; BAA12697.1; -  
 DR EMBL; D84551; BAA12698.1; -  
 DR EMBL; D85557; BAA12830.1; -  
 DR EMBL; D85558; BAA12831.1; -

DR EMBL; D85559; BAA12832.1; -  
 DR EMBL; U60151; AAB06616.1; -  
 DR EMBL; D84125; BAA12230.1; -  
 DR EMBL; D84126; BAA12231.1; -  
 DR EMBL; AB011006; BAA24899.1; -  
 DR EMBL; U67207; AAB40654.1; -  
 DR EMBL; AF007818; AAB63201.1; -  
 DR InterPro; IPR002996; CRI1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
 DR Pfam; PF00041; fn3; 2.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Polymorphism; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT DOMAIN 22 1162  
 FT TRANSMEM 840 839  
 FT DOMAIN 861 1162  
 FT DOMAIN 236 318  
 FT DOMAIN 535 621  
 FT DOMAIN 736 821  
 FT CARBOHYD 55 55  
 FT CARBOHYD 56 56  
 FT CARBOHYD 73 73  
 FT CARBOHYD 98 98  
 FT CARBOHYD 187 187  
 FT CARBOHYD 275 275  
 FT CARBOHYD 345 345  
 FT CARBOHYD 356 356  
 FT CARBOHYD 431 431  
 FT CARBOHYD 514 514  
 FT CARBOHYD 622 622  
 FT CARBOHYD 657 657  
 FT CARBOHYD 668 668  
 FT CARBOHYD 686 686  
 FT CARBOHYD 695 695  
 FT CARBOHYD 698 698  
 FT CARBOHYD 726 726  
 FT CARBOHYD 890 894  
 FT VARSPPLIC 895 1162  
 FT VARSPPLIC 893 1162  
 FT VARSPPLIC 797 805  
 FT VARSPPLIC 806 1162  
 FT VARIANT 269 269  
 FT CONFLICT 2 2  
 FT CONFLICT 12 12  
 FT CONFLICT 34 34  
 FT CONFLICT 751 752  
 FT CONFLICT 846 846  
 SQ SEQUENCE 1162 AA; 130832 MW; BAYAC2CA2D2E62AF CRC64;  
 Query Match 3.6%; Score 42; DB 1; Length 1162;  
 Best local similarity 100.0%; Pred.No. 3.1e-35;  
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 500 FQPIFLSGYTMWRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
 DB 498 FQPIFLSGYTMWRINHSGLSDSPPTCVLPDSVVKPLPPS 539  
 RESULT 4  
 UL27\_HCMVA  
 ID UL27\_HCMVA STANDARD; PRT; 608 AA.  
 AC P16763;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Hypothetical protein UL27.  
 GN UL27.  
 OS Human cytomegalovirus (strain AD169).



```

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed-2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohnl R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U4, HSV-6 AND HSV-7 U5 AND HCMV UL27.
CC -----
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CC -----
DR EMBL; X17403; CAA35426.1; .
DR PIR; S09790; S09790.
KW Hypothetical protein.
SQ SEQUENCE 608 AA; 69220 MW; 81225A5D00E2980E CRC64;

Query Match 0.7%; Score 8; DB 1; Length 608;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 DYFLPAG 52
    |||||
Db 369 DYFLPAG 376

RESULT 5
RRPL_DUGBV STANDARD; PRT; 4036 AA.
ID RRPL_DUGBV
AC Q66431;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
GN L.
OS Dugbe virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Nairovirus.
OX NCBI_TaxID=11595;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ISOLATE ARD 44313;
RX MEDLINE=96332515; PubMed-8760425;
RA Marriott A.C., Nuttall P.A.;
RT "Large RNA segment of Dugbe nairovirus encodes the putative RNA
RT polymerase."
RL J. Gen. Virol. 77:1775-1780(1996).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC {RNA}(N).
CC -----
CC -1- SIMILARITY: CONTAINS 1 OTU DOMAIN.
CC -----
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CC -----
DR EMBL; U15018; AAB18834.1; .
DR InterPro; IPR003323; OTU.
DR InterPro; IPR000822; Znf-C2H2.

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DR Pfam; PF02338; OTU; 1.
DR PROSITE; PS50802; OTU; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW Transferase; Nucleotidyltransferase; RNA-directed RNA polymerase.
FT DOMAIN 29 158 OTU.
SQ SEQUENCE 4036 AA; 459382 MW; E2EDF0B4358E31BD CRC64;

Query Match 0.7%; Score 8; DB 1; Length 4036;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 GLINSSVT 1010
    |||||
Db 2685 GLINSSVT 2692

RESULT 6
RL15_BACLI STANDARD; PRT; 72 AA.
ID RL15_BACLI
AC P35138;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 50S ribosomal protein L15 (Fragment).
GN RPL0.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93062802; PubMed-1435726;
RA Tschauder S., Driessen A.J.M., Freudl R.;
RT "Cloning and molecular characterization of the secY genes from
RT Bacillus licheniformis and Staphylococcus carnosus: comparative
RT analysis of nine members of the SecY family."
RL Mol. Gen. Genet. 235:147-152(1992).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X70087; .; NOT_ANNOTATED_CDS.
DR PIR; S34404; S34404.
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 72 AA; 7441 MW; 6DC3BA681492E6C9 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 AEGTEVT 973
    |||||
Db 12 AEGTEVT 18

RESULT 7
RL15_BACSU STANDARD; PRT; 146 AA.
ID RL15_BACSU
AC P19946;
DT 01-FEB-1991 (Rel. 17, Created)

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DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L15.
GN RPL0.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP MEDLINE=90292990; PubMed=2113521;
RX MEDLINE=90292990; PubMed=2113521;
RA Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
RT "Cloning and characterization of a Bacillus subtilis gene homologous
RL to E. coli secY.";
RN J. Biochem. 107:603-607(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90221911; PubMed=2139212;
RA Yoshikawa H., Doi R.H.;
RT "Sequence of the Bacillus subtilis spectinomycin resistance gene
RL region.";
RN Nucleic Acids Res. 18:1647-1647(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
RX MEDLINE=96186897; PubMed=8635744;
RA Suh J.W., Boylan S.A., Oh S.H., Price C.W.;
RT "Genetic and transcriptional organization of the Bacillus subtilis
RT spe-alpha region.";
RL Gene 169:17-23(1996).
RN [4]
RP SEQUENCE OF 94-146 FROM N.A.
RC STRAIN=168;
RX MEDLINE=90251170; PubMed=2110998;
RA Suh J.W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,
RA Price C.W.;
RT "Isolation of a secY homologue from Bacillus subtilis: evidence for a
RT common protein export pathway in eubacteria.";
RL Mol. Microbiol. 4:305-314(1990).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; D00619; BAA00494.1; -
DR EMBL; X51329; CAA35711.1; -
DR EMBL; L47971; AAB06818.1; -
DR EMBL; M31102; AAB59117.1; -
DR EMBL; Z99104; CAB11911.1; -
DR PIR; S12682; R5BSL5.
DR Subtilist; BG10444; rplO.
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR Pfam; PF01305; Ribosomal_L15; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 146 AA; 15383 MW; 5DB07A902B266C11 CRC64;

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Query Match          0.6%; Score 7; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 967 AEGTEVT 973
   |||||
DB 86 AEGTEVT 92

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RESULT 8
CYSM_PSESY          STANDARD; PRT; 169 AA.
ID CYSM_PSESY
AC P48028;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cysteine synthase B (EC 4.2.99.8) (O-acetylserine sulphydrylase B)
DE (O-acetylserine (Thiol)-lyase B) (CSASE B) (Fragment).
GN CYSM.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234961; PubMed=1314807;
RA Hrabak E.M., Willis D.K.;
RT "The lema gene required for pathogenicity of Pseudomonas syringae pv.
RT syringae on bean is a member of a family of two-component
RT regulators.";
RL J. Bacteriol. 174:3011-3020(1992).
CC -1- CATALYTIC ACTIVITY: O3-acetyl-L-serine + H(2)S = L-cysteine +
CC acetate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
CC SYNTHASE FAMILY.
CC -----
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CC -----
DR EMBL; M80477; AAA25876.1; -
DR HSSP; P12674; 1OAS.
DR InterPro; IPR001216; Cys_synthase.
DR InterPro; IPR001926; PALP.
DR Pfam; PF00291; PALP; 1.
DR PROSITE; PS00901; CYS-SYNTHASE; 1.
KW lyase; Cysteine biosynthesis; Pyridoxal phosphate.
FT BINDING 45 45 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 18023 MW; E12781E90CA77F87 CRC64;

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Query Match          0.6%; Score 7; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1060 LKLEGN 1066
   |||||
DB 32 LKLEGN 38

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RESULT 9
PAPA_ECOLI
ID PAPA_ECOLI          STANDARD; PRT; 185 AA.
AC P04127;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PAP fimbrial major pilin protein precursor (PAP pil1).
GN PAPA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-J96;
RX MEDLINE-84087728; PubMed-6140260;
RA Baga M., Normark S., Hardy J., O'Hanley P., Lark D., Olsson O.,
RT "Nucleotide sequence of the ppa gene encoding the Pap pilus subunit
RT of human uropathogenic Escherichia coli.";
RL J. Bacteriol. 157:330-333(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-J96;
RX MEDLINE-93023852; PubMed-1357526;
RA Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M.,
RT "Horizontal gene transfer of the Escherichia coli pap and prs pili
RT operators as a mechanism for the development of tissue-specific
RT adhesive properties.";
RL Mol. Microbiol. 6:2225-2242(1992).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STRAINS OF E. COLI THAT CAUSE INFECTION OF THE HUMAN
CC URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAGES
CC CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
CC PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
CC CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
CC LINE THE URINARY TRACT.
CC -1- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
CC -----
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CC -----
DR EMBL: X03391; CAA27126.1; -
DR EMBL: X61239; CAA43562.1; -
DR PIR: A23221; YOECP.
DR InterPro: IPR000259; Fimbrial.
DR Pfam: PF00419; Fimbrial; 1.
KW Fimbria; Signal.
FT SIGNAL 1 22
FT CHAIN 23 185 PAP FIMBRIAL MAJOR PILIN PROTEIN.
FT DISULFID 44 83 PROBABLE.
SO SEQUENCE 185 AA; 18686 MW; 93DB4FFDA211C671 CRC64;

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Query Match 0.6%; Score 7; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 724 VANFNLT 730
DB 177 VANFNLT 183

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RESULT 10
FIMB1_ECOLI
ID FIMB1_ECOLI STANDARD; PRT; 187 AA.
AC P04740;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE KS71A fimbrial precursor (P-fimbrial antigen).
GN KS71A.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85285072; PubMed-2992970;
RA Rhen M., van Die I., Rhen V., Bergmans H.;
RT "Comparison of the nucleotide sequences of the genes encoding the
RT KS71A and F7(1) fimbrial antigens of uropathogenic Escherichia
RT coli.";
RL Eur. J. Biochem. 151:573-577(1985).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
CC -----
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CC -----
DR EMBL: X02921; CAA26678.1; -
DR PIR: A23117; YOECKS.
DR InterPro: IPR000259; Fimbrial.
DR Pfam: PF00419; Fimbrial; 1.
KW Fimbria; Signal; Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 187 KS71A FIMBRIALIN.
FT DISULFID 43 82 PROBABLE.
SO SEQUENCE 187 AA; 19310 MW; 799E438264C638DC CRC64;

```

```

Query Match 0.6%; Score 7; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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OY 724 VANFNLT 730
DB 179 VANFNLT 185

```

```

RESULT 11
FIM2_ECOLI
ID FIM2_ECOLI STANDARD; PRT; 188 AA.
AC P02972;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE F7-2 fimbrial protein precursor (F7-2.pilin).
GN F7-2 OR PAPA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85155489; PubMed-6152241;
RA van Die I., Bergmans H.;
RT "Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
RT a uropathogenic Escherichia coli strain.";
RL Gene 32:83-90(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92040048; PubMed-1682251;
RA Denich K., Blyn L.B., Craiu A., Braaten B.A., Hardy J., Low D.A.,
RA O'Hanley P.D.;
RT "DNA sequences of three ppa genes from uropathogenic Escherichia
RT coli strains: evidence of structural and serological conservation.";
RL Infect. Immun. 59:3849-3858(1991).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO

```

CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.  
 CC -1- DISEASE: THIS IS ONE OF THE FIMBRIAL PROTEINS INVOLVED IN  
 CC MANNANOSE-RESISTANT HEMAGGLUTINATION OF HUMAN ERYTHROCYTES.  
 CC -1- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL; M12861; AAA23778.1; -  
 DR EMBL; M68060; AAA24278.1; -  
 DR PIR; A03496; YQECF2.  
 DR PIR; B43597; B43597.  
 DR InterPro; IPR000259; Fimbrial.  
 DR Pfam; PF00419; Fimbrial; 1.  
 KW Fimbrial; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 188 F7-2 FIMBRIAL PROTEIN.  
 FT DISULFID 43 82 PROBABLE.  
 SQ SEQUENCE 188 AA; 19184 MW; 0EEF750CFD843157 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 188;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 VANFNLT 730  
 |||||  
 DB 180 VANFNLT 186

RESULT 12  
 TIM2\_BOVIN STANDARD; PRT; 220 AA.  
 AC P16368; O9TVB1;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of  
 DE metalloproteinases-2) (Collagenase inhibitor).  
 GN TIMP2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID-9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90207285; PubMed=2157214;  
 RA Boone T.C., Johnson M.J., de Clerck Y.A., Langley K.E.;  
 RT "CDNA cloning and expression of a metalloproteinase inhibitor related  
 RT to tissue inhibitor of metalloproteinases.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2800-2804(1990).  
 RN [2]  
 RP SEQUENCE OF 22-218 FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RA Balcerzak D., Quereghesser L., Dixon W.T., Baracos V.E.;  
 RT "Involvement of fibroblasts and muscle cells in the expression of an  
 RT extracellular proteolytic cascade in bovine skeletal muscle.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 27-71.  
 RC TISSUE-Cartilage;  
 RX MEDLINE=86140235; PubMed=3005321;  
 RA Murray J.B., Allison K., Sudhalter J., Langer R.;  
 RT "Purification and partial amino acid sequence of a bovine cartilage-  
 RT derived collagenase inhibitor.";  
 RL J. Biol. Chem. 261:4154-4159(1986).  
 RN [4]

RP SEQUENCE OF 27-71.  
 RX MEDLINE=9008914; PubMed=2551903;  
 RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;  
 RT "Purification and characterization of two related but distinct  
 RT metalloproteinase inhibitors secreted by bovine aortic endothelial  
 RT cells.";  
 RL J. Biol. Chem. 264:17445-17453(1989).  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO THE TIMP FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M32303; AAA30636.1; -  
 DR EMBL; AF144764; AAD30304.1; -  
 DR PIR; A25322; A25322.  
 DR PIR; A35996; A35996.  
 DR PIR; A34468; A34468.  
 DR HSSP; P16035; IBR9.  
 DR InterPro; IPR001820; TIMP.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; TIMP; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 DR KW Metalloprotease inhibitor; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.  
 FT DISULFID 27 98 BY SIMILARITY.  
 FT DISULFID 29 127 BY SIMILARITY.  
 FT DISULFID 39 152 BY SIMILARITY.  
 FT DISULFID 154 201 BY SIMILARITY.  
 FT DISULFID 159 164 BY SIMILARITY.  
 FT DISULFID 172 193 BY SIMILARITY.  
 FT CONFLICT 42 42 D -> C (IN REF. 3).  
 FT CONFLICT 56 56 D -> E (IN REF. 3).  
 FT CONFLICT 68 68 R -> S (IN REF. 3).  
 SQ SEQUENCE 220 AA; 24355 MW; 9A5438737110E7B7 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 220;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 855 LLLGTL 861  
 |||||  
 DB 15 LLLGTL 21

RESULT 13  
 PYRH\_THEMEA STANDARD; PRT; 231 AA.  
 ID PYRH\_THEMEA  
 AC Q9X1U0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase)  
 DE (UMP kinase).  
 GN PYRH OR TM1604.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogales; Thermotoga.  
 OX NCBI\_TaxID-2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MSB8 / DSM 3109;  
 RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of *Thermotoga maritima*.";  
 RL Nature 399:323-329(1999).  
 CC -1- FUNCTION: URIDINE MONOPHOSPHATE KINASE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.  
 CC -1- SIMILARITY: TO OTHER UMP KINASE; SOME, TO ASPARTOKINASES AND TO  
 CC GLUTAMATE KINASES.  
 -----  
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 -----  
 DR EMBL; AE001804; AAD36671.1; -  
 DR TIGR; TM1604; -  
 DR InterPro; IPR001048; AakInase.  
 DR Pfam; PF00696; aakInase; 1.  
 KW Transferase; Kinase; Pyrimidine biosynthesis; Complete proteome.  
 SO SEQUENCE 231 AA; 25235 MW; 4563E9E15FA0C5ED CRC64;

QY 1049 PHLTSE 1055  
 Db 174 PHLTSE 180

RESULT 14  
 YHE4\_YEAST  
 ID YHE4\_YEAST STANDARD; PRT; 235 AA.  
 AC P38727;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 27.0 kDa protein in CBP2 5'region.  
 GN YHL044W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RX MEDLINE=94378003; PubMed=8091229;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 RA Du Z., Favello A., Fulton L., Gattung S., Giesel C., Kirsten J.,  
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,  
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,  
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 RA Vaudin M.;  
 RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome  
 RT VIII.";  
 RL Science 265:2077-2082(1994).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE DUF/COS FAMILY.  
 -----  
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 -----  
 DR EMBL; U11583; AAB65056.1; -  
 DR PIR; S48924; S48924.  
 DR SGD; S0001036; YHL044W.  
 DR InterPro; IPR001142; DUF.  
 DR Pfam; PF00674; DUF; 1.  
 KW Hypothetical protein; Transmembrane.  
 FT TRANSMEM 45  
 FT TRANSMEM 73 93 POTENTIAL.  
 SO SEQUENCE 235 AA; 26972 MW; 2A789B602087D928 CRC64;

QY 989 LISNSKP 995  
 Db 6 LISNSKP 12

RESULT 15  
 BI0D\_YEAST  
 ID BI0D\_YEAST STANDARD; PRT; 237 AA.  
 AC P53630;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dethiobiotin synthetase (EC 6.3.3.3) (Dethiobiotin synthase) (DTB  
 DE synthetase) (DTBS).  
 GN BIO4 OR YNR057C OR N3506.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FL100;  
 RA Phalip V., Jeltsch J.M., Lemoine Y.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,  
 RA Moestl D.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + 7,8-diaminononanoate + CO(2) = ADP +  
 CC phosphate + dethiobiotin.  
 CC -1- COFACTOR: MAGNESIUM.  
 CC -1- PATHWAY: BIOCONVERSION OF PIMELATE INTO DETHIOBIOTIN.  
 CC -1- SIMILARITY: BELONGS TO THE DETHIOBIOTIN SYNTHETASE FAMILY.  
 -----  
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 -----  
 DR EMBL; U53467; AAB63971.1; -  
 DR EMBL; Z71672; CAA96339.1; -  
 DR SGD; S0005340; BIO4.  
 KW Biotin biosynthesis; Ligase; Magnesium; ATP-binding.  
 FT NP\_BIND 18 26 ATP (BY SIMILARITY).  
 SO SEQUENCE 237 AA; 26257 MW; F1147BF18DA40735 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 108 GKEFVST 114  
| | | | |  
DB 24 GKEFVST 30

RESULT 16  
YE91\_MYCTU

ID YE91\_MYCTU STANDARD; PRT; 252 AA.  
AC P71772;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 26.6 kDa protein Rv1491c.  
GN Rv1491c OR MT1538 OR MTCY277.13C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Rogers R.,  
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: BELONGS TO THE UPF0043 FAMILY.  
CC -----  
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CC -----  
CC  
DR EMBL; Z79701; CAB02041.1; -  
DR EMBL; AE007022; AAK45805.1; -  
DR TIGR; MT1538; -  
DR TubercuList; Rv1491c; -  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 32 52 POTENTIAL.  
FT TRANSMEM 64 84 POTENTIAL.  
FT TRANSMEM 88 108 POTENTIAL.  
FT TRANSMEM 149 169 POTENTIAL.  
FT TRANSMEM 177 197 POTENTIAL.  
FT TRANSMEM 209 229 POTENTIAL.  
SQ SEQUENCE 252 AA; 26575 MW; 3E63BE13217B8201 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 252;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 LVPVPTA 203  
| | | | |  
DB 48 LVPVPTA 54

RESULT 17  
MAUN\_PARDE

ID MAUN\_PARDE STANDARD; PRT; 283 AA.  
AC Q51660;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Methylamine utilization ferredoxin-type protein maun.  
GN MAUN.  
OS Paracoccus denitrificans.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
OC Paracoccus.  
OX NCBI\_TaxID=266;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PD 1222;  
RX MEDLINE=95324575; PubMed=7601147;  
RA van der Palen C.J., Slotboom D.J., Jongejan L., Reijnders W.N.,  
RA Harms N., Duine J.A., van Spanning R.J.;  
RT "Mutational analysis of mau genes involved in methylamine metabolism  
RT in Paracoccus denitrificans."  
RL Eur. J. Biochem. 230:860-871(1995).  
CC -1- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).  
CC -1- PATHWAY: METHYLAMINE UTILIZATION.  
CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF  
CC 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.  
CC -----  
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CC -----  
CC  
DR EMBL; U15028; AAA86469.1; -  
DR HSSP; P00195; 1CLF.  
DR InterPro: IPR001450; 4Fe4S\_ferredoxin.  
DR Pfam: PF00037; fer4; 2.  
DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 2.  
KW Electron transport; Iron-sulfur; 4Fe-4S.  
FT METAL 227 227 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).  
FT METAL 230 230 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).  
FT METAL 233 233 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).  
FT METAL 237 237 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).  
FT METAL 260 260 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
FT METAL 263 263 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
FT METAL 266 266 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
FT METAL 270 270 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
SQ SEQUENCE 283 AA; 31035 MW; FB2C87C9B8917EDE CRC64;

Query Match 0.6%; Score 7; DB 1; Length 283;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 LLLGTL 861  
| | | | |  
DB 142 LLLGTL 148

RESULT 18  
EXOS\_BPT5  
ID EXOS\_BPT5 STANDARD; PRT; 290 AA.  
AC P06229;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, last annotation update)  
DE Exodeoxyribonuclease (EC 3.1.11.3) (5' exonuclease).  
GN D15.  
OS Bacteriophage T5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=10726;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86108899; PubMed=3002857;  
RA Kallman A.V., Krutillina A.I., Kryukov V.M., Bayev A.A.;  
RT "Cloning and DNA sequence of the 5'-exonuclease gene of bacteriophage T5."  
RL FEBS Lett. 195:61-64(1986).  
RN [2]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=96273035; PubMed=8657312;  
RA Ceska T.A., Sayers J.R., Stier G., Suck D.;  
RT "A helical arch allowing single-stranded DNA to thread through T5 5'-exonuclease."  
RL Nature 382:90-93(1996).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND MUTAGENESIS.  
RX MEDLINE=99093486; PubMed=9874768;  
RA Garforth S.J., Ceska T.A., Suck D., Sayers J.R.;  
RT "Mutagenesis of conserved lysine residues in bacteriophage T5 5'-3' exonuclease suggests separate mechanisms of endo- and exonucleolytic cleavage."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:38-43(1999).  
CC -1- CATALYTIC ACTIVITY: DEGRADATION OF DOUBLE-STRANDED AND SINGLE-STRANDED DNA. IT ACTS PROGRESSIVELY IN A 5' TO 3' DIRECTION.  
CC RELEASING 5'-PHOSPHOMONONUCLEOTIDES.  
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY.  
CC -1- SIMILARITY: CONTAINS 1 5'-3' EXONUCLEASE DOMAIN.  
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CC -----  
DR EMBL: X03402; CAA27136.1; -.  
DR EMBL: AJ001191; CAA04588.1; -.  
DR PIR: A23610; NCBP75.  
DR PDB: 1EXN; 07-JUL-97.  
DR PDB: 1X01; 12-APR-99.  
DR InterPro: IPR002421; 5\_3\_exonuclease.  
DR InterPro: IPR000513; Exo\_N\_1.  
DR InterPro: IPR003584; HHH\_2.  
DR Pfam: PF01367; 5\_3\_exonuclease; 1.  
DR SMART: SM00475; 53EXOC; 1.  
DR SMART: SM00279; Hnh2; 1.  
KW Hydrolase; Nuclease; Exonuclease; 3d-structure.  
FT INIT\_MET 0  
SQ SEQUENCE 290 AA; 33316 MW; 0947BCA05BC3BBBF CRC64;

Query Match 0.6%; Score 7; DB 1; Length 290;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 STIOSLA 458  
ID STIOSLA 458  
DB 48 STIOSLA 54

RESULT 19  
NPL\_HAEIN STANDARD; PRT; 293 AA.  
AC P44539;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE Probable N-acetylneuraminatase lyase subunit (EC 4.1.3.3) (N-acetylneuraminic acid aldolase) (N-acetylneuraminatase pyruvate lyase)  
GN DE (Nalase).  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty R.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."  
RL Science 269:496-512(1995).  
CC -1- CATALYTIC ACTIVITY: N-acetylneuraminatase - N-acetyl-D-mannosamine + pyruvate.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE DHDPs FAMILY.  
CC -----  
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CC -----  
DR EMBL: U32700; AAC21814.1; -.  
DR HSSP: P06995; INAL.  
DR TIGR: HI0142; -.  
DR InterPro: IPR002220; DHDPs.  
DR Pfam: PF00701; DHDPs; 1.  
DR PRINTS: PR00146; DHPICNTBASE.  
DR ProDom: PD001859; DHDPs; 1.  
DR PROSITE: PS00665; DHDPs\_1; 1.  
DR PROSITE: PS00666; DHDPs\_2; 1.  
KW lyase; Complete proteome.  
FT ACT\_SITE 164  
SQ SEQUENCE 293 AA; 32564 MW; ACA755D0A5D93D33 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 293;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 ELLKLEG 1065  
ID ELLKLEG 1065  
DB 256 ELLKLEG 262

RESULT 20  
YCYJ\_ECOLI STANDARD; PRT; 310 AA.  
ID YCYJ\_ECOLI  
AC P76049; P77483; P76844;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE Hypothetical protein ycjY.  
GN YCYJ OR B1327.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.

```

OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Maki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA Oshima T., Saito N., Sempel G., Seki Y., Sivasundaram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -1- SIMILARITY: TO P.AERUGINOSA HYPOTHETICAL 40.7 kDa PROTEIN IN OPDE
3'REGION (AC Q01609).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000230; AAC74409.1; -
DR EMBL; D90770; BAA14909.1; -
DR EMBL; D90771; BAA14920.1; -
DR EMBL; D90772; BAA14930.1; -
DR EcoGene; EG13922; ycjY.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 259 259 S -> R (IN REF. 2).
SQ SEQUENCE 310 AA; 34117 MW; 20291A71BD367B70 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 VYFPPK 339
|1111111
Db 25 VYFPPK 31

RESULT 21
PPI1_YEAST STANDARD; PRT; 311 AA.
ID PPI1_YEAST
AC P20604;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Serine/threonine protein phosphatase PPI-1 (EC 3.1.3.16).
GN PPH1 OR SIT4 OR YDL047W OR D2693.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89136000; PubMed=2537149;
RA Arndt K.T., Styles C.A., Fink G.R.;

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RT "A suppressor of a HIS4 transcriptional defect encodes a protein with
RT homology to the catalytic subunit of protein phosphatases.";
RL Cell 56:527-537(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RA Paulin L., Saren A.M., Laamanen P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=91172202; PubMed=1848673;
RA Sutton A., Immanuel D., Arndt K.T.;
RT "The Sit4 protein phosphatase functions in late G1 for progression
RT into S phase.";
RL Mol. Cell. Biol. 11:2133-2148(1991).
CC -1- FUNCTION: INVOLVED IN THE DEPHOSPHORYLATION OF THE LARGE SUBUNIT
CC OF RNA POLYMERASE II. IS REQUIRED IN LATE G1 FOR NORMAL G1 CYCLIN
CC EXPRESSION, BUD INITIATION AND EXPRESSION OF CERTAIN GENES THAT
CC ARE PERIODICALLY EXPRESSED DURING LATE G1. ASSOCIATES WITH THE
CC SAP PROTEINS IN A CELL CYCLE-DEPENDENT MANNER.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DEVELOPMENTAL STAGE: FUNCTIONS IN THE LATE CELL CYCLE G1 PHASE FOR
CC PROGRESSION INTO THE S PHASE, POSSIBLY ASSOCIATED IN TWO SEPARATE
CC COMPLEXES WITH THE PHOSPHORYLATED FORMS OF P155 AND P190, TWO HIGH
CC MW PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; M24395; AAA56864.1; -
DR EMBL; Z71781; CAA96442.1; -
DR EMBL; Z74095; CAA98609.1; -
DR PIR; A31874; PABY1.
DR HSSP; P08129; LEJM.
DR SGD; S0002205; SIT4.
DR InterPro; IPR000934; Ser_thr_phosphatase.
DR Pfam; PF00149; STphosphatase; 1.
DR PRINTS; PR00114; STPHPTASE.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolyase; Iron; Manganese; Cell cycle; Mitosis; Multigene family.
FT METAL 53 53 IRON (BY SIMILARITY).
FT METAL 55 55 IRON (BY SIMILARITY).
FT METAL 82 82 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 114 114 MANGANESE (BY SIMILARITY).
FT ACT_SITE 115 115 GENERAL ACID (BY SIMILARITY).
FT METAL 164 164 MANGANESE (BY SIMILARITY).
FT METAL 238 238 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 311 AA; 35537 MW; AF52BC65E4E715EC CRC64;

Query Match 0.6%; Score 7; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 TLIMCLK 214
|1111111
Db 95 TLIMCLK 101

RESULT 22
YG54_ARCFU STANDARD; PRT; 329 AA.
ID YG54_ARCFU
AC O28619;

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DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein AF1654.  
GN AF1654.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
OC Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE-98049343; PubMed-9389475;  
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.R., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Goeyne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).  
CC -----  
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CC -----  
CC EMBL; AE000989; AAB89615.1; -.  
DR TIGR; AF1654; -.  
DR Hypothetical protein; Transmembrane; Complete proteome.  
KW TRANSMEM 13 35 POTENTIAL.  
FT TRANSMEM 229 248 POTENTIAL.  
SQ SEQUENCE 329 AA; 37776 MW; E307CA1A61193DE CRC64;  
  
Query Match 0.6%; Score 7; DB 1; Length 329;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 893 ETEFHLF 899  
DB 301 ETEFHLF 307  
  
RESULT 23  
KCCL\_SCHPO  
ID KCCL\_SCHPO STANDARD; PRT; 335 AA.  
AC 09P712; 074235;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)  
DE (CaMK-I).  
GN CMK1 OR SPAC25D11.02C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomyces.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND MUTAGENESIS OF THR-192.  
RX MEDLINE-20085094; PubMed-10617667;  
RA Rasmussen C.D.;  
RT "Cloning of a calmodulin kinase I homologue from Schizosaccharomyces

RT pome.";  
RL J. Biol. Chem. 275:685-690(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-972;  
RA Wood V., Rajandream M.A., Barrell B.G., Rieger M.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: IMPORTANT IN CELL CYCLE REGULATION.  
CC -1- CATALYTIC ACTIVITY: ATP + protein -> ADP + O-phosphoprotein.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CAMK SUBFAMILY.  
CC -----  
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CC -----  
CC EMBL; AF073893; AAC26005.1; -.  
DR EMBL; AL157993; CAB76233.1; -.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Serine/threonine-protein kinase; Transferase;  
KW Calmodulin-binding; Phosphorylation.  
FT DOMAIN 31 291 PROTEIN KINASE.  
FT NP\_BIND 37 45 ATP (BY SIMILARITY).  
FT DOMAIN 310 334 CALMODULIN-BINDING (POTENTIAL).  
FT ACT\_SITE 154 154 BY SIMILARITY.  
FT MOD\_RES 192 192 PHOSPHORYLATION (AUTO-).  
FT MUTAGEN T->D: 15-FOLD INCREASE IN ACTIVITY.  
FT CONFLICT 115 115 E -> A (IN REF. 1).  
FT CONFLICT 294 295 KR -> NG (IN REF. 1).  
SQ SEQUENCE 335 AA; 38163 MW; 8761B9CF6882B02 CRC64;  
  
Query Match 0.6%; Score 7; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 504 FLISGYT 510  
DB 225 FLISGYT 231  
  
RESULT 24  
LEU3\_MYCBO  
ID LEU3\_MYCBO STANDARD; PRT; 336 AA.  
AC P94929;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 3-Isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)  
DE (IMDH) (3-IPM-DH).  
GN LEUB.  
OS Mycobacterium bovis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BG;  
RX MEDLINE-97266124; PubMed-9111927;  
RA Han M.Y., Son M.Y., Lee S.H., Kim J.K., Huh J.S., Kim J.H., Choe I.S.,  
RA Chung T.W., Choe Y.K.;  
RT "Molecular cloning of the leuB genes from Mycobacterium bovis BCG and

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RT  Mycobacterium tuberculosis";
RL  Biochem. Mol. Biol. Int. 41:657-663(1997).
CC  -1- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
CC  NAD(+) -> 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
CC  DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
CC  -1- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC  DEHYDROGENASES FAMILY.
CC  -----
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CC  -----
CC  EMBL; U78886; AAC45173.1; -.
CC  DR  HSSP; P00351; 1XAA.
CC  DR  InterPro; IPR001804; Isodh.
CC  DR  Pfam; PF00180; Isodh; 1.
CC  DR  PROSITE; PS00470; IDH_IMDH; 1.
CC  KM  Oxidoreductase; Leucine biosynthesis; NAD.
CC  SQ  SEQUENCE 336 AA; 35272 MW; 03C95850A6CA51E2 CRC64;

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Query Match      0.6%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  529 VLPDSVV 535
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DB  48 VLPDSVV 54

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RESULT 25
LEU3_MYCTU
ID  LEU3_MYCTU STANDARD; PRT; 336 AA.
AC  P95313;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
DE  (IMDH) (3-IPM-DH).
GN  LEUB OR RV2995C OR MT3073 OR MTV012.09.
OS  Mycobacterium tuberculosis.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX  NCBI_TaxID-1773;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE-97266124; PubMed-9111927;
RA  Han M.Y., Son M.Y., Lee S.H., Kim J.K., Huh J.S., Kim J.H., Choe I.S.,
RA  Chung T.W., Choe Y.K.;
RT  "Molecular cloning of the leuB genes from Mycobacterium bovis BCG and
RT  Mycobacterium tuberculosis."
RL  Biochem. Mol. Biol. Int. 41:657-663(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-H37RV;
RX  MEDLINE-98295987; PubMed-9634230;
RA  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA  Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA  Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA  Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA  Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA  Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA  Rutter S., Seeger K., Skelton S., Squares S., Rogers R.,
RA  Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT  "Deciphering the biology of Mycobacterium tuberculosis from the
RT  complete genome sequence."

```

```

RL  Nature 393:537-544(1998).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CDC 1551 / Oshkosh;
RA  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA  Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA  Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA  Bishai W.;
RT  "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT  laboratory strains."
RL  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC  -1- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
CC  NAD(+) -> 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
CC  DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
CC  -1- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC  DEHYDROGENASES FAMILY.
CC  -----
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CC  -----
CC  EMBL; U78887; AAC45174.1; -.
CC  DR  EMBL; AL021287; CAAL6080.1; -.
CC  DR  EMBL; AE007127; AAK47402.1; -.
CC  DR  HSSP; P00351; 1XAA.
CC  DR  TIGR; MT3073; -.
CC  DR  Tuberculist; RV2995c; -.
CC  DR  InterPro; IPR001804; Isodh.
CC  DR  Pfam; PF00180; Isodh; 1.
CC  DR  PROSITE; PS00470; IDH_IMDH; 1.
CC  KM  Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
CC  SQ  SEQUENCE 336 AA; 35306 MW; E78718100CCA5B42 CRC64;

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Query Match      0.6%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  529 VLPDSVV 535
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DB  48 VLPDSVV 54

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RESULT 26
GGH_SOYBN
ID  GGH_SOYBN STANDARD; PRT; 342 AA.
AC  P93164;
DT  15-JUL-1999 (Rel. 38, Created)
DT  15-JUL-1999 (Rel. 38, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-GLU-X
DE  carboxypeptidase) (Conjugase) (GH).
OS  Glycine max (Soybean).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX  NCBI_TaxID-3847;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. WILLIAMS 82;
RX  MEDLINE-97069645; PubMed-8912628;
RA  Huangpu J., Pak J.H., Burkhardt W., Graham M.C., Rickle S.A.,
RA  Graham J.S.;
RT  "Purification and molecular analysis of an extracellular gamma-
RT  glutamyl hydrolase present in young tissues of the soybean plant."

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RL Biochem. Biophys. Res. Commun. 228:1-6(1996).
CC -1- CATALYTIC ACTIVITY: Cleavage of a gamma-glutamyl bond to release
CC an unsubstituted C-terminal amino acid.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR OR CELL-WALL BOUND.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN YOUNG (1-15 DAY OLD) LEAF,
CC STEM AND ROOT TISSUE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C26.
CC -----
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CC -----
DR EMBL; U63726; AAB26960.1; -.
DR Mendel; 12606; GLYma;1806;1.
KW Hydrolyase; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 342 GAMMA-GLUTAMYL HYDROLASE.
FT CARBOHYD 72 72 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 342 AA; 37676 MW; 515CBAD1E5BA258C CRC64;

Query Match
Best Local Similarity 0.6%; Score 7; DB 1; Length 342;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GKTFFVST 114
   |||||
Db 248 GKTFFVST 254

RESULT 27
SOHB_ECOLI STANDARD; PRT; 349 AA.
ID SOHB_ECOLI
AC P24213; P77676;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Possible protease sohb (EC 3.4.21.-).
GN SOHB OR B1272.
OS Escherichia coli.
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358368; PubMed=1885549;
RA Baird L., Lipinska B., Raina S., Georgopoulos C.;
RT Identification of the Escherichia coli sohb gene, a multicopy
RT suppressor of the HtrA (DegP) null phenotype.";
RL J. Bacteriol. 173:5763-5770(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,

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RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -1- FUNCTION: MULTICOPY SUPPRESSOR OF THE HTRA (DEGP) NULL PHENOTYPE.
CC IT IS POSSIBLY A PROTEASE, NOT ESSENTIAL FOR BACTERIAL VIABILITY.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
CC -----
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CC -----
DR EMBL; M73320; AAA24639.1; -.
DR EMBL; AE000225; AAC74354.1; -.
DR EMBL; D90764; BAA14809.1; -.
DR EMBL; D90765; BAA14824.1; -.
DR PIR; A38115; A38115.
DR MEROPS; S49.002; -.
DR EcoGene; EG10956; sohb.
DR InterPro; IPR002142; Peptidase_U7.
DR Pfam; PF01343; Peptidase_U7; 1.
DR ProDom; PD002897; Peptidase_U7; 1.
KW Protease; Hydrolyase; Transmembrane; Complete proteome.
FT TRANSMEM 9 29 POTENTIAL.
FT CONFLICT 85 85 A -> R (IN REF. 1).
FT CONFLICT 90 90 A -> R (IN REF. 1).
FT CONFLICT 296 296 T -> A (IN REF. 1).
SQ SEQUENCE 349 AA; 39366 MW; 3362AE74C33C5F5C CRC64;

Query Match
Best Local Similarity 0.6%; Score 7; DB 1; Length 349;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 ADKIVSA 290
   |||||
Db 187 ADKIVSA 193

RESULT 28
SOHB_HAEIN STANDARD; PRT; 353 AA.
ID SOHB_HAEIN
AC P45315;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Possible protease sohb (EC 3.4.21.-).
GN SOHB OR H11682.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: POSSIBLE PROTEASE (BY SIMILARITY).

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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.  
CC -----  
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CC -----  
DR EMBL; U32841; AAC23328.1; -  
DR MEROPS; S49.002; -  
DR TIGR; H11682; -  
DR InterPro; IPR002142; Peptidase\_U7.  
DR Pfam; PF01343; Peptidase\_U7; 1.  
DR ProDom; PD002897; Peptidase\_U7; 1.  
KW Protease; Hydrolase; Transmembrane; Complete proteome.  
FT TRANSMEM 11 31 POTENTIAL.  
SQ SEQUENCE 353 AA; 39872 MW; 4C2E6D75B0F88070 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 353;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 284 ADRIYSA 290  
Db 190 ADRIYSA 196

RESULT 29  
CHSB\_PHANI STANDARD; PRT; 363 AA.  
ID CHSB\_PHANI  
AC P48396;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Chalcone synthase B (EC 2.3.1.74) (Naringenin-chalcone synthase B)  
DE (CHS-B) (Fragment).  
GN CHSB.  
OS Pharbitis nil (Violet) (Japanese morning glory).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.  
OX NCBI\_TaxID=35883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95241498; PubMed-7724563;  
RA Durbin M.L., Learn G.H., Hutley G.A., Clegg M.T.;  
RT "Evolution of the chalcone synthase gene family in the genus  
RT Ipomoea."  
RL Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).  
CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-  
CC TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)  
CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO  
CC NARINGENIN.  
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA -> 4 CoA +  
CC naringenin-chalcone + 3 CO(2).  
CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF  
CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY  
CC OF WHICH ARE BRIGHTLY COLORED.  
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.  
CC -----  
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CC -----  
DR EMBL; U15944; AAC49029.1; -  
DR InterPro; IPR001099; Chal\_stil\_synt.

DR Pfam; PF00195; Chal\_stil\_synt; 1.  
DR Pfam; PF02797; Chal\_stil\_synt; 1.  
DR PROSITE; PS00441; CHALCONE\_SYNTH; 1;  
KW Flavonoid biosynthesis; Transferase; Acyltransferase;  
KW Multigene family.  
FT ACT\_SITE 170 170 BY SIMILARITY.  
FT NON\_TER 363 363  
SQ SEQUENCE 363 AA; 40483 MW; 9349FABA60C7C3FA CRC64;

Query Match 0.6%; Score 7; DB 1; Length 363;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 545 AEITINI 551  
Db 197 AEITINI 203

RESULT 30  
RCLL\_HUMAN STANDARD; PRT; 373 AA.  
ID RCLL\_HUMAN  
AC Q9Y2P8; Q9NY00; Q9P044; Q9H9D0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE RNA 3'-terminal phosphate cyclase-like protein (HSPC338).  
DE RNA 3' OR RPC2 OR RTC2 OR RCL1.  
GN RNAC OR RPC2 OR RTC2 OR RCL1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20253086; PubMed-10790377;  
RA Billy E., Wegierski T., Nasr F., Filipowicz W.;  
RT "Rclp, the yeast protein similar to the RNA 3'-phosphate cyclase,"  
RT associates with U3 snRNP and is required for 18S rRNA biogenesis.";  
RL EMBO J. 19:2115-2126(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retinoblastoma;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuko Y., Oshima A.;  
RT "NEO human cDNA sequencing project."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 8-373 FROM N.A.  
RA Kan L., Zhang Q.H., Fu G., Zhou J., Ye M., Shen Y., Wu J., He K.,  
RA Chen S.J., Mao M., Chen Z.;  
RT "Human hematopoietic cell derived RNA cyclase (HPRC) homolog.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 46-373 FROM N.A.  
RC TISSUE=Blood;  
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,  
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;  
RT "Human partial CDS from cd34+ stem cells."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: DOES NOT HAVE CYCLASE ACTIVITY. PLAYS A ROLE IN 40S-  
CC RIBOSOMAL-SUBUNIT BIOGENESIS IN THE EARLY PRE-RNA PROCESSING  
CC STEPS AT SITES A0, A1 AND A2 THAT ARE REQUIRED FOR PROPER  
CC MATURATION OF THE 18S RNA (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.  
CC SUBFAMILY 2.

CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS  
 CC IN POSITIONS 13 AND 58.  
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 CC -----  
 DR EMBL; AJ276894; CAB89811.1; -  
 DR EMBL; BC001025; AAH01025.1; -  
 DR EMBL; AK022904; BAB14300.1; -  
 DR EMBL; AF067172; AAD32456.1; ALT\_FRAME.  
 DR EMBL; AF161456; AAF29016.1; -  
 DR InterPro: IPR000228; RTC.  
 DR Pfam; PF01137; RTC; 1.  
 DR PROSITE; PS01287; RTC; 1.  
 KW Nuclear protein.  
 FT CONFLICT 6 6 H -> Y (IN REF. 3).  
 FT CONFLICT 46 46 D -> S (IN REF. 5).  
 FT CONFLICT 49 49 A -> S (IN REF. 5).  
 FT CONFLICT 153 153 K -> N (IN REF. 3).  
 FT CONFLICT 310 310 R -> Q (IN REF. 2 AND 3).  
 SQ SEQUENCE 373 AA; 40870 MW; 51EFAC56F0AF93C8 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 1; Length 373;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 79 FSNLSKT 85  
 Db 365 FSNLSKT 371  
 RESULT 31  
 RCL\_MOUSE  
 ID RCL\_MOUSE STANDARD; PRT; 373 AA.  
 AC Q9JUT0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE RNA 3'-terminal phosphate cyclase-like protein.  
 GN RNAC OR RCL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20253086; PubMed=10790377;  
 RA Billy E., Weglarski T., Nasr F., Filipowicz W.;  
 RT "Rclp, the yeast protein similar to the RNA 3'-phosphate cyclase,"  
 RL EMBO J. 19:2115-2126(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Mikado I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection,";  
 RL Nature 409:685-690(2001).  
 CC -1- FUNCTION: DOES NOT HAVE CYCLASE ACTIVITY. PLAYS A ROLE IN 40S-  
 CC RIBOSOMAL-SUBUNIT BIOGENESIS IN THE EARLY PRE-RNA PROCESSING  
 CC STEPS AT SITES A0, A1 AND A2 THAT ARE REQUIRED FOR PROPER  
 CC MATURATION OF THE 18S RNA (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.  
 CC SUBFAMILY 2.  
 CC -----  
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 CC -----  
 DR EMBL; AJ276895; CAB89817.1; -  
 DR EMBL; AK009709; BAB26454.1; -  
 DR MGD; MGI:1913275; Rnac.  
 DR InterPro: IPR000228; RTC.  
 DR Pfam; PF01137; RTC; 1.  
 DR PROSITE; PS01287; RTC; 1.  
 KW Nuclear protein.  
 SQ SEQUENCE 373 AA; 40840 MW; 3BE97CA47A8CEFA1 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 1; Length 373;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 79 FSNLSKT 85  
 Db 365 FSNLSKT 371  
 RESULT 32  
 Y801\_METJA  
 ID Y801\_METJA STANDARD; PRT; 379 AA.  
 AC Q58211;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical ATP-binding protein M0801.  
 GN M0801.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
 OC Methanococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 RL jannaschii.";  
 RN Science 273:1058-1073(1996).  
 RN [2]  
 RP SIMILARITY.

RX MEDLINE-97197912; PubMed-9045616;  
RA Koonin E.V.;  
RT "Evidence for a family of archaeal ATPases.";  
RL Science 275:1489-1490(1997).  
CC -1- SIMILARITY: BELONGS TO THE ARCHAEOAL ATPASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; U67524; AAB98799.1; -.  
DR TIGR; MJ0801; -.  
DR InterPro: IPR002576; Archaeal\_ATPase.  
DR Pfam: PF01637; Archaeal\_ATPase; 1.  
DR ProDom: PD003808; Archaeal\_ATPase; 1.  
KW Hypothetical protein; ATP-binding; Complete proteome.  
FT NP\_BIND 29 36 ATP (POTENTIAL).  
SQ SEQUENCE 379 AA; 44716 MW; 1BAF2567E0C5D0B4 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 379;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1124 VENNINL 1130  
Db 243 VENNINL 249

RESULT 33  
ID PURT\_BACSU STANDARD; PRT; 384 AA.  
AC P39771; O31450;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-) (GART 2)  
DE (GAR transformylase 2) (5'-phosphoribosylglycinamide transformylase  
DE 2) (Formate-dependent GAR transformylase).  
GN PURT.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-168;  
RX MEDLINE-96118702; PubMed-7496533;  
RA Saxild H.H., Jacobsen J.H., Nygaard P.;  
RT "Functional analysis of the Bacillus subtilis purt gene encoding  
RT formate-dependent glycinamide ribonucleotide transformylase.";  
RL Microbiology 141:2211-2218(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-168;  
RA Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;  
RT "Sequence analysis of the 70kb region between 17 and 23 degree of the  
RT Bacillus subtilis chromosome.";  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CATALYZES TWO REACTIONS:THE FIRST ONE IS THE PRODUCTION  
CC OF BETA-FORMYL GLYCINAMIDE RIBONUCLEOTIDE (GAR) FROM FORMATE, ATP  
CC AND BETA GAR; THE SECOND, A SIDE REACTION, IS THE PRODUCTION OF  
CC ACETYL PHOSPHATE AND ADP FROM ACETATE AND ATP.  
CC -1- CATALYTIC ACTIVITY: FORMATE + ATP + 5'-PHOSPHO-RIBOSYLGICINAMIDE  
CC = 5'-PHOSPHORIBOSYL-N-FORMYLGICINAMIDE + ADP + PYROPHOSPHATE.  
CC -1- COFACTOR: MAGNESIUM (BY SIMILARITY).  
CC -1- PATHWAY: THIRD STEP (FIRST OF TWO TRANSFORMYLATION REACTIONS)  
CC IN DE NOVO PURINE BIOSYNTHESIS. THIS IS AN ALTERNATIVE ENZYME TO  
CC THE PURN GAR TRANSFORMYLASE.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE PURK / PURT FAMILY.  
CC -----  
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CC -----  
DR EMBL; X78962; CA55557.1; -.  
DR EMBL; AB006424; BAA33120.1; -.  
DR EMBL; Z99105; CAB12017.1; -.  
DR PIR; S47267; S47267.  
DR Subtilist; BG10924; PURT.  
DR InterPro: IPR003135; ATP-grasp.  
DR Pfam; PF02222; ATP-grasp; 1.  
KW purine biosynthesis; Transferase; Magnesium; Complete proteome.  
FT CONFLICT 240 241 KH -> ND (IN REF. 1).  
SQ SEQUENCE 384 AA; 42093 MW; 5E3642CD6CA9F9F7.CRC64;

Query Match 0.6%; Score 7; DB 1; Length 384;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1058 DELIKLE 1064  
Db 81 DELIKLE 87

RESULT 34  
ID RPA2\_METVA STANDARD; PRT; 386 AA.  
AC P14247;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE DNA-directed RNA polymerase subunit A\* (EC 2.7.7.6).  
GN RPOA2.  
OS Methanococcus vannielii.  
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
OC Methanococcus.  
OX NCBI\_TaxID=2187;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 1224;  
RA Palm P., Arnold-Ammer I., Lechner K.A., Zillig W.;  
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 171-386 FROM N.A.  
RC STRAIN-DSM 1224;  
RX MEDLINE-89362493; PubMed-2475640;  
RA Lechner K., Heller G., Boeck A.;  
RT "Organization and nucleotide sequence of a transcriptional unit of  
RT Methanococcus vannielii comprising genes for protein synthesis  
RT elongation factors and ribosomal proteins.";  
RL J. Mol. Evol. 29:20-27(1989).  
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
CC SUBSTRATES.  
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +  
CC (RNA)(N).  
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
CC -----  
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CC -----  
 DR EMBL: X73293; CAA51729.1; -  
 DR EMBL: X15970; CAA34086.1; -  
 DR PIR: S06620; S06620.  
 DR InterPro: IPR002879; RNA\_pol\_A2.  
 DR Pfam: PF01854; RNA\_pol\_A2; 1.  
 KW Transferase; Transcription; DNA-directed RNA polymerase; Zinc.  
 SQ SEQUENCE 386 AA; 42982 MW; 0D26292FB45BA6A7 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 919 SEDISVD 925  
 Db 143 SEDISVD 149

RESULT 35  
 CHSB\_IPOPU STANDARD; PRT; 396 AA.  
 ID CHSB\_IPOPU STANDARD; PRT; 396 AA.  
 AC P48398;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Chalcone synthase B (EC 2.3.1.74) (Naringenin-chalcone synthase B)  
 DE (CHS-B).  
 GN CHSB.  
 OS Ipomoea purpurea (Common morning glory).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.  
 OX NCBI\_TaxID=4121;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95241498; Pubmed-7724563;  
 RA Durbin M.L., Learn G.H., Huttley G.A., Clegg M.T.;  
 RT "Evolution of the chalcone synthase gene family in the genus  
 Ipomoea."  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).  
 CC -1- FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4',2',4',6'-  
 TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)  
 CC WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO  
 CC NARINGENIN.  
 CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumaroyl-CoA -> 4 CoA +  
 CC naringenin-chalcone + 3 CO(2).  
 CC -1- PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF  
 CC FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY  
 CC OF WHICH ARE BRIGHTLY COLORED.  
 CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U15947; AAC49030.1; -  
 DR InterPro: IPR001099; Chal\_stil\_synt.  
 DR Pfam: PF00195; Chal\_stil\_synt; 1.  
 DR Pfam: PF02797; Chal\_stil\_syntc; 1.  
 DR PROSITE: PS00441; CHALCONE\_SYNTH; 1.  
 KW Flavonoid biosynthesis; Transferase; Acyltransferase;  
 KW Multigene family.  
 FT ACT\_SITE 170 170 BY SIMILARITY.  
 SQ SEQUENCE 396 AA; 43926 MW; 352C478C1AF892B6 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 68;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 545 AEITINI 551  
 Db 197 AEITINI 203

RESULT 36  
 YMS7\_YEAST  
 ID YMS7\_YEAST STANDARD; PRT; 420 AA.  
 AC Q03694;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 47.3 kDa protein in TOM40-PFK2 intergenic region.  
 GN YMR204C OR YMR8325.05C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RA Odell C., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -----

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 CC -----

DR EMBL: Z48755; CAA88645.1; -  
 DR SGD: S0004817; YMR204C.  
 KW Hypothetical protein.  
 SQ SEQUENCE 420 AA; 47314 MW; A11EF51211DEF675 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1131 GTSSKKT 1137  
 Db 63 GTSSKKT 69

RESULT 37  
 EXLP\_TOBAC  
 ID EXLP\_TOBAC STANDARD; PRT; 426 AA.  
 AC Q03211;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Pistil-specific extensin-like protein precursor (PELP).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. PETITE HAVANA; TISSUE=Pistil;  
 RX MEDLINE-93005740; Pubmed-1392607;  
 RA Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;  
 RT "Developmental expression of tobacco pistil-specific genes encoding  
 RT novel extensin-like proteins."  
 RL Plant Cell 4:1041-1051(1992).  
 CC -1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER  
 CC PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING



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CC FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE
CC AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
CC POLLINATION.
CC -----
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CC -----
DR EMBL; Z14019; CAA78397.1; -
DR PIR; JQ1696; JQ1696.
DR InterPro; IPR000419; Pollen_Ole_e_1.
DR Pfam; PF01190; Pollen_Ole_e_1; 1.
KW Structural protein; Signal; Repeat; Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 426 PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.
FT DOMAIN 69 182 4 X 5 AA REPEATS OF S-P(4).
FT REPEAT 69 73 1.
FT REPEAT 76 80 2.
FT REPEAT 83 87 3.
FT REPEAT 178 182 4.
FT CARBOHYD 310 310 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 426 AA; 44278 MW; 51A495CC94017812 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 534 VVKPLPP 540
Db 278 VVKPLPP 284

RESULT 38
TBB2_PHYPO
ID TBB2_PHYPO STANDARD; PRT; 454 AA.
AC P12458;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin beta-2 chain (Tubulin beta-major chain).
GN BETA.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88216603; PubMed=2835667;
RA Burland T.G., Paul E.C.A., Oetliker M., Dove W.F.;
RT "A gene encoding the major beta tubulin of the mitotic spindle in
RT Physarum polycephalum plasmodia.";
RL Mol. Cell. Biol. 8:1275-1281(1988).
CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -!- FUNCTION: THIS IS THE MAJOR BETA TUBULIN OF MITOTIC SPINDLE.
CC -!- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -!- SUBCELLULAR LOCATION: MITOSIS IN THE SLIME MOLD PLASMODIUM DIFFERS
CC FROM THE PROCESS IN MANY EUKARYOTES. THE TUBULIN CHAINS MUST BE
CC TRANSPORTED TO THE NUCLEI FOR INTRANUCLEAR ASSEMBLY OF THE
CC SPINDLE.
CC -!- DEVELOPMENTAL STAGE: PREFERENTIALLY EXPRESSED IN PLASMODIUM.
CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
CC -----
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CC -----
DR EMBL; M20191; AAA29977.1; -
DR PIR; A33655; A33655.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; tubulin; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
KW Microtubules; GTP-binding; Multigene family; Nuclear protein.
FT NP_BIND 140 146 GTP (POTENTIAL).
SQ SEQUENCE 454 AA; 50364 MW; A913D46AF63F1AD4 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 454;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 857 LGTLIS 863
Db 147 LGTLIS 153

RESULT 39
TBB_DICDI
ID TBB_DICDI STANDARD; PRT; 455 AA.
AC P32256;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tubulin beta chain.
GN TUBB.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94043557; PubMed=8227212;
RA Trivinos-Lagos L., Ohmachi T., Albrigtonson C., Burns R.G.,
RA Ennis H.L., Chisholm R.L.;
RT "The highly divergent alpha- and beta-tubulins from Dictyostelium
RT discoideum are encoded by single genes.";
RL J. Cell Sci. 105:903-911(1993).
CC -!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.
CC -!- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
CC -!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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CC -----
DR EMBL; L14000; AAC37344.1; -
DR Dictydb; DD01044; tubB.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR000217; Tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; tubulin; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
KW Microtubules; GTP-binding.
FT NP_BIND 145 151 GTP (POTENTIAL).
```

SO SEQUENCE 455 AA; 51279 MW; EE214EE050285EEC CRC64;

Query Match 0.6%; Score 7; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 857 LGTLLIS 863

DB 152 LGTLLIS 158

RESULT 40  
ZNT1\_MOUSE STANDARD; PRT; 503 AA.

ID ZNT1\_MOUSE  
AC Q60738;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zinc transporter 1 (Znt-1).  
GN SLC30A1 OR ZNT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Brain;  
RX MEDLINE=9518868; PubMed=7882967;  
RA Palmer R.D., Findley S.D.;  
RT "Cloning and functional characterization of a mammalian zinc transporter that confers resistance to zinc.";  
RL EMBO J. 14:639-649(1995).  
CC -1- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.  
CC LETHALITY OF KNOCKOUT EARLY IN GESTATION SUGGESTS A ROLE OF THE PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.  
CC -1- SUBUNIT: MULTIMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE).  
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.  
CC -1- SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.  
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CC -----  
DR EMBL; U17132; AAA79233.1; -.  
DR MGD; MGI:1345281; SLC30a1.  
DR InterPro; IPR002524; Cation\_efflux.  
DR Pfam; PF01545; Cation\_efflux; 1.  
KW Zinc; Transport; Transmembrane; Multigene family; Repeat.  
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 11 31 POTENTIAL.  
FT DOMAIN 32 35 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 36 56 POTENTIAL.  
FT DOMAIN 57 78 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 79 99 POTENTIAL.  
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 114 134 POTENTIAL.  
FT DOMAIN 135 243 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 244 264 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 265 303 POTENTIAL.  
FT TRANSMEM 304 324 POTENTIAL.  
FT DOMAIN 325 503 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 145 156 6 X 2 AA APPROXIMATE REPEATS OF H-G.  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 503 AA; 54716 MW; 7C4FF93FC13CDA22 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 84;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 NTSNSNG 62

DB 190 NTSNSNG 196

RESULT 41

G6PD\_CHLMU STANDARD; PRT; 507 AA.

ID G6PD\_CHLMU  
AC Q9PKR8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).  
GN ZWF OR TC0457.  
OS Chlamydia muridarum.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Mopn / Nigg;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-1,5-lactone 6-phosphate + NADPH.  
CC -1- PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.  
CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; AE002314; AAF73556.1; -.  
DR TIGR; TC0457; -.  
DR InterPro; IPR001282; G6PD.  
DR Pfam; PF00479; G6PD; 1.  
DR PRINTS; PR0079; G6PDHCRGNASE.  
DR ProDom; PD001129; G6PD; 1.  
DR PROSITE; PS00069; G6P\_DEHYDROGENASE; 1.  
KW Oxidoreductase; NADP; Glucose metabolism; Complete proteome.  
FT ACT\_SITE 202 202 BY SIMILARITY.  
SQ SEQUENCE 507 AA; 58547 MW; C66F3FE1562391A6 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 507;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 963 NFSEAE 969

DB 100 NFSEAE 106

RESULT 42

ZNT1\_RAT STANDARD; PRT; 507 AA.

AC Q62720;

DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Zinc transporter 1 (Znt-1).  
 GN SLC30A1 OR ZNT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95188868; PubMed=7882967;  
 RA Palmer R.D., Findley S.D.;  
 RT "Cloning and functional characterization of a mammalian zinc  
 transporter that confers resistance to zinc.";  
 RL EMBO J. 14:639-649(1995).  
 RN [2]  
 RP INDUCTION BY ZINC.  
 RC TISSUE=Intestine;  
 RX MEDLINE=98226729; PubMed=9560190;  
 RA McMahon R.J., Cousins R.J.;  
 RT "Regulation of the zinc transporter ZNT-1 by dietary zinc.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:4841-4846(1998).  
 CC -1- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.  
 CC -1- SUBUNIT: MULTIMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE  
 CC BASOLATERAL SURFACE OF THE ENTEROCYTES.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN IS DETECTED IN  
 CC DUODENUM AND JEJUNUM BUT NOT IN ILEUM AND COLON.  
 CC -1- INDUCTION: SLIGHTLY BY ZINC IN THE INTESTINE, BUT NOT THE LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.  
 CC -----  
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 CC -----  
 DR EMBL: U17133; AAA79234.1; -  
 DR InterPro: IPR002524; Cation\_efflux.  
 DR Pfam: PF01545; Cation\_efflux; 1.  
 KW Zinc; Transport; Transmembrane; Multigene family; Repeat.  
 RN DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT DOMAIN 32 35 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 36 56 POTENTIAL.  
 FT DOMAIN 57 78 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 79 99 POTENTIAL.  
 FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 114 134 POTENTIAL.  
 FT DOMAIN 135 247 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 248 268 POTENTIAL.  
 FT DOMAIN 269 307 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 308 328 POTENTIAL.  
 FT DOMAIN 329 507 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 145 156 6 X 2 AA APPROXIMATE REPEATS OF H-G.  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 507 AA; 55142 MW; 9F9770017C2455FC CRC64;

Query Match 0.6%; Score 7; DB 1; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 56 NTSNSNG 62  
 |||||  
 Db 194 NTSNSNG 200

RESULT 43  
 SPA2\_STAUV  
 ID SPA2\_STAUV STANDARD; PRT; 508 AA.  
 AC P38507;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Immunoglobulin G binding protein A precursor (IGG binding protein A).  
 GN SPA.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COWAN 1 / NCTC 8530;  
 RX MEDLINE=88112878; PubMed=2828190;  
 RA Shuttleworth H.L., Duggleby C.J., Jones S.A., Atkinson T.,  
 RA Minton N.P.;  
 RT "Nucleotide sequence analysis of the gene for protein A from  
 RT staphylococcus aureus Cowan 1 (NCTC8530) and its enhanced expression  
 RT in Escherichia coli.";  
 RL Gene 58:283-295(1987).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC STRAIN-COWAN 1 / NCTC 8530;  
 RX MEDLINE=78023926; PubMed=913410;  
 RA Sjoedahl J.;  
 RT "Structural studies on the four repetitive Fc-binding regions in  
 RT protein A from Staphylococcus aureus.";  
 RL Eur. J. Biochem. 78:471-490(1977).  
 RN [3]  
 RP STRUCTURE BY NMR OF 211-270.  
 RX MEDLINE=93003122; PubMed=1390743;  
 RA Gouda H., Torigoe H., Saito A., Sato M., Arata Y., Shimada I.;  
 RT "Three-dimensional solution structure of the B domain of  
 RT staphylococcal protein A: comparisons of the solution and crystal  
 RT structures.";  
 RL Biochemistry 31:9665-9672(1992).  
 RN [4]  
 RP STRUCTURE BY NMR OF 37-92.  
 RX MEDLINE=97110349; PubMed=8952510;  
 RA Starovasnik M.A., Skelton N.J., O'Connell M.P., Kelley R.F.,  
 RA Reilly D., Fairbrother W.J.;  
 RT "Solution structure of the E-domain of staphylococcal protein A.";  
 RL Biochemistry 35:15558-15569(1996).  
 RN [5]  
 RP STRUCTURE BY NMR OF 212-269.  
 RX MEDLINE=97467196; PubMed=9325113;  
 RA Tashiro M., Tejero R., Zimmerman D.E., Celda B., Nilsson B.,  
 RA Montellone G.T.;  
 RT "High-resolution solution NMR structure of the Z domain of  
 RT staphylococcal protein A.";  
 RL J. Mol. Biol. 272:573-590(1997).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.  
 CC -1- DOMAIN: THE C-TERMINAL HALF CONTAINS THE IG-BINDING REGION.  
 CC WHILST THE N-TERMINAL HALF IS THE CELL-WALL-BINDING DOMAIN.  
 CC -1- MISCELLANEOUS: IMPORTANT IMMUNODIAGNOSTIC REAGENT BECAUSE OF ITS  
 CC ABILITY TO BIND THE FC FRAGMENT OF A WIDE RANGE OF MAMMALIAN  
 CC IMMUNOGLOBULINS.  
 CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS  
 CC IN THE REGION OF THE MEMBRANE ANCHOR.  
 CC -----  
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 CC -----  
 DR EMBL: M18264; AAA26677.1; -  
 DR PIR: A29605; A29605.

DR PDB; 1BDC; 11-JAN-97.  
 DR PDB; 1BDD; 11-JAN-97.  
 DR PDB; 1EDI; 01-APR-97.  
 DR PDB; 1EDJ; 01-APR-97.  
 DR PDB; 1EDK; 01-APR-97.  
 DR PDB; 1EDL; 01-APR-97.  
 DR PDB; 2SPZ; 21-APR-00.  
 DR InterPro; IPR003132; B\_domain.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR InterPro; IPR002482; LysM.  
 DR Pfam; PF02216; B; 5.  
 DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
 DR Pfam; PF01476; LysM; 1.  
 DR SMART; SM00257; LysM; 1.  
 DR PROSITE; PS00343; GRAM\_POS\_ANCHORING; 1.  
 KW Igg-binding protein; Repeat; Transmembrane; Cell wall; Signal;  
 3D-structure.  
 FT SIGNAL 1 36  
 FT CHAIN 37 508  
 FT DOMAIN 37 482  
 FT TRANSMEM 483 503  
 FT DOMAIN 504 508  
 FT DOMAIN 37 332  
 FT REPEAT 37 100  
 FT REPEAT 101 158  
 FT REPEAT 159 216  
 FT REPEAT 217 274  
 FT REPEAT 275 332  
 FT DOMAIN 333 408  
 FT REPEAT 333 340  
 FT REPEAT 341 348  
 FT REPEAT 349 356  
 FT REPEAT 357 364  
 FT REPEAT 365 372  
 FT REPEAT 373 380  
 FT REPEAT 381 388  
 FT REPEAT 389 396  
 FT REPEAT 397 405  
 FT REPEAT 406 413  
 FT REPEAT 414 421  
 FT REPEAT 422 429  
 FT DOMAIN 474 479  
 FT CONFLICT 273 273  
 SQ SEQUENCE 508 AA; 55439 MW; E78C538D4B5E88F5 CRC64;  
 K -> D (IN REF. 2).  
 PROTEINS.  
 CONSERVED IN GRAM-POSITIVE COCCI SURFACE

Query Match 0.6%; Score 7; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 857 LGTLLIS 863  
 |||||  
 DB 21 LGTLLIS 27

RESULT 44  
 SPAL\_STAAU STANDARD; PRT; 524 AA.  
 AC P02976;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Immunoglobulin G binding protein A precursor (IGG binding protein A).  
 GN SPA.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NCTC 8325-4;  
 RX MEDLINE=84111639; PubMed=6319407;

RA Uhlen M., Guss B., Nilsson B., Gatenbeck S., Philipson L.,  
 RA Lindberg M.;  
 RT "Complete sequence of the staphylococcal gene encoding protein A. A  
 RT gene evolved through multiple duplications."  
 RL J. Biol. Chem. 259:1695-1702(1984).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=8325-4;  
 RA Uhlen M., Guss B., Nilsson B., Gatenbeck S., Philipson L.,  
 RA Lindberg M.;  
 RL J. Biol. Chem. 259:13628-13628(1984).  
 RN [3]  
 RP SEQUENCE OF 1-186 FROM N.A.  
 RC STRAIN=8325-4;  
 RX MEDLINE=83143997; PubMed=6338496;  
 RA Loeferdahl S., Guss B., Uhlen M., Philipson L., Lindberg M.;  
 RT "Gene for staphylococcal protein A."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:697-701(1983).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.  
 CC -1- DOMAIN: THE N-TERMINAL HALF CONTAINS THE IGG-BINDING REGION  
 CC -1- MISCELLANEOUS: IMPORTANT IMMUNODIAGNOSTIC REAGENT BECAUSE OF ITS  
 CC ABILITY TO BIND THE FC FRAGMENT OF A WIDE RANGE OF MAMMALIAN  
 CC IMMUNOGLOBULINS.  
 CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS  
 CC IN THE REGION OF THE MEMBRANE ANCHOR.  
 CC -----  
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 CC -----  
 DR EMBL; V01287; CAA24596.1; -.  
 DR EMBL; J01786; AAA26676.1; -.  
 DR PIR; A03500; QVSAA.  
 DR PIR; A19498; A19498.  
 DR HSSP; P38507; 1BDD.  
 DR InterPro; IPR003132; B\_domain.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR InterPro; IPR002482; LysM.  
 DR Pfam; PF02216; B; 5.  
 DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
 DR Pfam; PF01476; LysM; 1.  
 DR SMART; SM00257; LysM; 1.  
 DR PROSITE; PS00343; GRAM\_POS\_ANCHORING; 1.  
 DR Igg-binding protein; Repeat; Transmembrane; Cell wall; Signal.  
 KW Igg-binding protein; Repeat; Transmembrane; Cell wall; Signal;  
 3D-structure.  
 FT SIGNAL 1 36  
 FT CHAIN 37 524  
 FT DOMAIN 37 498  
 FT TRANSMEM 499 519  
 FT DOMAIN 520 524  
 FT DOMAIN 37 332  
 FT REPEAT 37 100  
 FT REPEAT 101 158  
 FT REPEAT 159 216  
 FT REPEAT 217 274  
 FT REPEAT 275 332  
 FT DOMAIN 333 408  
 FT REPEAT 333 340  
 FT REPEAT 341 348  
 FT REPEAT 349 356  
 FT REPEAT 357 364  
 FT REPEAT 365 372  
 FT REPEAT 373 380  
 FT REPEAT 381 388  
 FT REPEAT 389 396  
 FT REPEAT 397 404  
 FT REPEAT 406 412  
 FT REPEAT 413 420  
 FT REPEAT 421 428

FT DOMAIN 490 495 CONSERVED IN GRAM-POSITIVE COCCI SURFACE  
FT FT PROTEINS.  
FT CONFLICT 101 101 N-> D (IN REF. 3).  
SQ SEQUENCE 524 AA; 57320 MW; 0A615C73C61316EF CRC64;  
Query Match 0.6%; Score 7; DB 1; Length 524;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 857 LGTLIS 863  
Db 21 LGTLIS 27  
RESULT 45  
IL2B\_MOUSE  
ID IL2B\_MOUSE STANDARD; PRT; 539 AA.  
AC P16297;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)  
DE (High affinity IL-2 receptor beta subunit) (CD122).  
GN IL2RB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90175385; PubMed=2155425;  
RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,  
RA Miyasaka M., Miyata T., Taniguchi T.;  
RT "Murine interleukin 2 receptor beta chain: dysregulated gene,  
expression in lymphoma line EL-4 caused by a promoter insertion.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).  
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS  
INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE  
MITOGENIC SIGNALS OF IL-2.  
CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R  
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE  
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA  
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE  
WITH A GAMMA CHAIN.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
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CC -----  
DR EMBL; M28052; AAA39283.1; -.  
DR PIR; A35052; A35052.  
DR HSSP; P14784; 1ILN.  
DR MGD; MGI:96550; 1L2PB.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_ILI.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_FL.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_FL; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 539 INTERLEUKIN-2 RECEPTOR BETA CHAIN.  
FT DOMAIN 27 240 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 241 268 POTENTIAL.  
FT DOMAIN 269 539 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 74 86 BY SIMILARITY.  
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 539 AA; 60538 MW; 365C9D206B6FE14 CRC64;  
Query Match 0.6%; Score 7; DB 1; Length 539;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 303 SYEQVR 309  
Db 204 SYEQVR 210  
RESULT 46  
C166\_CARAU  
ID C166\_CARAU STANDARD; PRT; 555 AA.  
AC Q90304;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE CD166 antigen homolog precursor (Neurolin) (DM-GRASP homolog).  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Carassius.  
OX NCBI\_Taxid=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Retina;  
RA Laessing U.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 30-552 FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE-Retina;  
RX MEDLINE=94299040; PubMed=8026643;  
RA Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.;  
RT "Molecular characterization of fish neurolin: a growth-associated  
RT cell surface protein and member of the immunoglobulin superfamily in  
RT the fish retinotectal system with similarities to chick protein  
RT DM-GRASP/SC-1/BEN.";  
RL Differentiation 56:21-29(1994).  
CC -1- FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION BY  
CC NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GANGLION CELLS (RGCs)  
CC AND THEIR AXONS (IN EMBRYO). ABSENT FROM MATURE AXONS ALONG MOST  
CC OF THEIR LENGTH, BUT IS PRESENT ON NEW AND GROWING AXONS DERIVED  
CC FROM THE RGCs AT THE RETINAL MARGIN. REMAINS ON ADULT RGCs ONLY AT  
CC CELL-CELL CONTACT SITES AND IS CONTINUOUSLY FOUND IN THE RETINAL  
CC AXON TERMINAL ARBOR LAYERS OF THE ADULT TECTUM.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.  
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CC -----  
DR EMBL; L25056; AAC38015.2; -.  
DR HSSP; Q13740; 1KJC.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003600; IG\_Like.  
DR InterPro; IPR003596; IG\_V.



DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_Like; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Signal; Developmental protein; Cell adhesion; Immunoglobulin domain;  
 KW Repeat; Glycoprotein; Transmembrane.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 555 CD166 ANTIGEN HOMOLOG.  
 FT DOMAIN 23 499 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 500 520 POTENTIAL.  
 FT DOMAIN 521 555 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 31 117 IG-LIKE V-TYPE DOMAIN 1.  
 FT DOMAIN 147 224 IG-LIKE V-TYPE DOMAIN 2.  
 FT DOMAIN 256 313 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 340 392 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 419 477 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DISULFID 38 110 POTENTIAL.  
 FT DISULFID 154 217 POTENTIAL.  
 FT DISULFID 263 306 POTENTIAL.  
 FT DISULFID 426 470 POTENTIAL.  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 555 AA; 60371 MW; 5A4AB014F00BFF68 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 838 SDAGLYV 844  
 Db 378 SDAGLYV 384

RESULT 47  
 C166\_BRARE STANDARD; PRT; 564 AA.  
 ID C166\_BRARE 090460; 090480;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE CD166 antigen homolog precursor (Neurolin) (DM-GRASP homolog).  
 GN CD166.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94376084; PubMed-8089660;  
 RA Kanki J.P., Chang S., Kuwada J.Y.;  
 RT "The molecular cloning and characterization of potential chick  
 RT DM-GRASP homologs in zebrafish and mouse."  
 RL J. Neurobiol. 25:831-845(1994).  
 RN [2]  
 RP SEQUENCE OF 398-561 FROM N.A.  
 RX MEDLINE-94299040; PubMed-8026643;  
 RA Laessle U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.;  
 RT "Molecular characterization of fish neurolin: a growth-associated  
 RT cell surface protein and member of the immunoglobulin superfamily in  
 RT the fish retinotectal system with similarities to chick protein  
 RT DM-GRASP/SC-1/BEN."  
 RL Differentiation 56:21-29(1994).  
 RN [1]  
 RP FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION BY  
 CC NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.  
 CC SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

CC EMBL; L25273; AAA50024.1; -  
 CC EMBL; L25057; AAA50048.1; -  
 CC HSSP; Q13740; IKUC.  
 CC ZFIN; ZDB-GENE-990415-30; cd166.  
 CC InterPro; IPR003006; Ig\_MHC.  
 CC InterPro; IPR003600; Ig\_Like.  
 CC InterPro; IPR003596; Ig\_V.  
 CC Pfam; PF00047; Ig; 5.  
 DR SMART; SM00410; Ig\_Like; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;  
 KW Repeat; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 564 CD166 ANTIGEN HOMOLOG.  
 FT DOMAIN 25 507 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 508 528 POTENTIAL.  
 FT DOMAIN 529 564 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 31 117 IG-LIKE V-TYPE DOMAIN 1.  
 FT DOMAIN 147 222 IG-LIKE V-TYPE DOMAIN 2.  
 FT DOMAIN 256 314 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 340 389 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 419 477 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DISULFID 38 110 POTENTIAL.  
 FT DISULFID 154 217 POTENTIAL.  
 FT DISULFID 263 306 POTENTIAL.  
 FT DISULFID 426 470 POTENTIAL.  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 488 497 LFEEDKPKPG -> R (IN REF. 2).  
 SQ SEQUENCE 564 AA; 61273 MW; ADA7C293A607929 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 838 SDAGLYV 844  
 Db 378 SDAGLYV 384

RESULT 48  
 IL1R\_HUMAN STANDARD; PRT; 569 AA.  
 ID IL1R\_HUMAN  
 AC P14778;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-1 receptor, type I precursor (IL-1R-1) (IL-1R-alpha)  
 DE (P80) (Antigen CD121a).  
 GN IL1R OR IL1RA OR IL1R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Liver;  
 RX MEDLINE-90098789; PubMed-2532321;  
 RA Chua A.O., Gubler U.;  
 RT "Sequence of the cDNA for the human fibroblast type interleukin-1

RT receptor.";  
 RL Nucleic Acids Res. 17:10114-10114(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-cell;  
 RX MEDLINE=90046906; Pubmed=2530587;  
 RA Sims J.E., Acres R.B., Grubin C.E., McMahon C.J., Wignall J.M.,  
 RA March C.J., Dower S.K.;  
 RT "Cloning the interleukin 1 receptor from human T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8946-8950(1989).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 18-332 IN COMPLEX WITH IL1B.  
 RX MEDLINE=97215903; Pubmed=9062193;  
 RA Vigers G.P., Anderson L.J., Cafes P., Brandhuber B.J.;  
 RT "Crystal structure of the type-I interleukin-1 receptor complexed  
 RT with interleukin-1beta.";  
 RL Nature 386:190-194(1997).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 21-331 IN COMPLEX WITH IL1RA.  
 RX MEDLINE=97215904; Pubmed=9062194;  
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,  
 RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;  
 RT "A new cytokine-receptor binding mode revealed by the crystal  
 RT structure of the IL-1 receptor with an antagonist.";  
 RL Nature 386:194-200(1997).  
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),  
 CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BINDING TO  
 CC THE AGONIST LEADS TO THE ACTIVATION OF NF-KAPPA B.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.  
 CC -1- DATABASE: NAME-PRO; NOTE-CD guide CD121a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd121a.htm".  
 CC -----  
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 CC -----  
 DR EMBL; X16896; CA34773.1; -;  
 DR EMBL; M27492; AAS59137.1; -;  
 DR PIR; S06928; S06928.  
 DR PIR; A36187; A36187.  
 DR PDB; 1ITB; 04-FEB-98.  
 DR PDB; 1IRA; 17-JUN-98.  
 DR MIM; 147810; -;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR004076; Intlik1\_receptor1\_pre.  
 DR InterPro; IPR004075; Intlik1\_receptor1.  
 DR InterPro; IPR004074; Intlik1\_receptor1\_II.  
 DR InterPro; IPR000157; TIR.  
 DR Pfam; PF00047; Ig; 2.  
 DR Pfam; PF01582; TIR; 1.  
 DR PRINTS; PRO1538; INTERLEUKIN1R1.  
 DR PRINTS; PRO1536; INTERLEUKIN1R12F.  
 DR PRINTS; PRO1537; INTERLEUKIN1R1F.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR SMART; SM00255; TIR; 1.  
 DR PROSITE; PS50104; TIR; 1.  
 KW Immunoglobulin domain; Transmembrane; Glycoprotein; Receptor; Signal;  
 KW Repeat; 3D-structure.  
 FT SIGNAL 1 17  
 FT CHAIN 18 569 INTERLEUKIN-1 RECEPTOR, TYPE I.  
 FT DOMAIN 18 336 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 337 356 POTENTIAL.  
 FT DOMAIN 357 569 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 37 103 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 135 203 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 241 319 IG-LIKE C2-TYPE DOMAIN 3.

FT DOMAIN 383 541 TIR.  
 FT DISULFID 23 104  
 FT DISULFID 44 96  
 FT DISULFID 121 164  
 FT DISULFID 142 196  
 FT DISULFID 248 312  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 569 AA; 65402 MW; 5BAA83F8F0225C25 CRC64;  
 Query Match 0.6%; Score 7; DB 1; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 164 VLPEVLE 170  
 Db 410 VLPEVLE 416  
 RESULT 49  
 ERGL\_HUMAN  
 ID ERGL\_HUMAN STANDARD; PRT; 574 AA.  
 AC Q14534; Q9UEK6;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Squalene monooxygenase (EC 1.14.99.7) (Squalene epoxidase) (SE).  
 GN SQUAL OR ERGL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97432831; Pubmed=9286711;  
 RA Nagai M., Sakakibara J., Wakui K., Fukushima Y., Igarashi S.,  
 RA Tsuji S., Arakawa M., Ono T.;  
 RT "Localization of the squalene epoxidase gene (SQLE) to human  
 RT chromosome region 8q24.1";  
 RL Genomics 44:141-143(1997).  
 RN [2]  
 RP SEQUENCE OF 187-535 FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE=96215195; Pubmed=8626488;  
 RA Nakamura Y., Sakakibara J., Izumi T., Shibata A., Ono T.;  
 RT "Transcriptional regulation of squalene epoxidase by sterols and  
 RT inhibitors in Hela cells.";  
 RL J. Biol. Chem. 271:8053-8056(1996).  
 CC -1- FUNCTION: CATALYZES THE FIRST OXYGENATION STEP IN STEROL  
 CC BIOSYNTHESIS AND IS SUGGESTED TO BE ONE OF THE RATE-LIMITING  
 CC ENZYMES IN THIS PATHWAY.  
 CC -1- CATALYTIC ACTIVITY: Squalene + AH(2) + O(2) -> (S)-squalene-2,3-  
 CC epoxide + A + H(2)O.  
 CC -1- COFACTOR: FAD.  
 CC -1- SUBUNIT: MAY FORM A COMPLEX WITH SQUALENE SYNTHASE.  
 CC -1- SUBCELLULAR LOCATION: Microsomal.  
 CC -1- SIMILARITY: BELONGS TO THE SQUALENE MONOOXYGENASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; D78130; BAA22372.1; -;  
 DR EMBL; D78129; BAA11209.1; -;

DR MIM; 602019; -  
DR InterPro; IPR000205; NAD\_binding.  
DR InterPro; IPR003042; Rng\_monooxygenase.  
DR InterPro; IPR000733; Flavo\_monooxygenase.  
DR Pfam; PF01360; Monooxygenase; 1.  
DR PRINTS; PR00420; RINGMONOXGNASE.  
KW Oxidoreductase; Flavoprotein; FAD; Transmembrane.  
FT TRANSMEM 20 40 POTENTIAL.  
FT TRANSMEM 61 81 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
FT TRANSMEM 546 566 POTENTIAL.  
FT NP\_BIND 126 153 FAD (ADP PART) (POTENTIAL).  
FT CONFLICT 247 247 E -> G (IN REF. 2).  
FT CONFLICT 336 336 R -> Q (IN REF. 2).  
FT CONFLICT 389 389 L -> P (IN REF. 2).  
FT CONFLICT 451 451 N -> K (IN REF. 2).  
FT CONFLICT 518 518 A -> V (IN REF. 2).  
SQ SEQUENCE 574 AA; 63329 MW; DD4F95308864FD09 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 574;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 LPSSSVK 544  
|||||||  
DB 393 LPSSSVK 399

RESULT 50

GTBL\_MOUSE  
ID GTBL\_MOUSE STANDARD; PRT; 583 AA.

AC 008582;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE GTP-binding protein 1 (G-protein 1) (GP-1).

GN GTPBP1 OR GTPBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97223458; PubMed=9070279;

RA Senju S., Nishimura Y.;

RT "Identification of human and mouse GP-1, a putative member of a novel

G-protein family.";

RL Biochem. Biophys. Res. Commun. 231:360-364(1997).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, THYMUS, LUNG, AND KIDNEY.

CC -1- SIMILARITY: BELONGS TO THE AGPI/GTPBP1 FAMILY OF GTP-BINDING

PROTEINS.

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CC -----

DR EMBL; U87965; AAB51274.1; -

DR MGD; MGI:109443; Gtpbp1.

DR InterPro; IPR000795; GTP\_EFTU.

DR InterPro; IPR004161; GTP\_EFTU\_D2.

DR InterPro; IPR004160; GTP\_EFTU\_D3.

DR Pfam; PF00009; GTP\_EFTU; 1.

DR Pfam; PF03144; GTP\_EFTU\_D2; 1.

DR Pfam; PF03143; GTP\_EFTU\_D3; 1.

KW GTP-binding.

FT NP\_BIND 82 89 GTP (POTENTIAL).

FT NP\_BIND 167 171 GTP (POTENTIAL).

FT NP\_BIND 223 226 GTP (POTENTIAL).

SQ SEQUENCE 583 AA; 63329 MW; A17F297D214247F9 CRC64;

Query Match 0.6%; Score 7; DB 1; Length 583;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 KLNDTLL 210  
|||||||  
DB 337 KLNDTLL 343

Search completed: May 18, 2002, 07:08:25  
Job time: 248 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:04:02 ; Search time 37.5 Seconds  
(without alignments)  
5374.376 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 1165

Sequence: 1 MICQKPCVLLHMEFIVIT.....QTCSTQTHKIMENKCDLTV 1165

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1165	100.0	1165	4 Q92921	Q92921 homo sapien
2	891	76.5	896	4 Q92919	Q92919 homo sapien
3	891	76.5	958	4 Q92920	Q92920 homo sapien
4	681	58.5	896	4 Q13594	Q13594 homo sapien
5	681	58.5	906	4 Q13593	Q13593 homo sapien
6	681	58.5	958	4 Q13592	Q13592 homo sapien
7	84	7.2	894	6 Q9MYL1	Q9MYL1 macaca mula
8	84	7.2	925	6 Q9MYK9	Q9MYK9 macaca mula
9	84	7.2	1163	6 Q9MYL2	Q9MYL2 macaca mula
10	84	7.2	1194	6 Q9MYL0	Q9MYL0 macaca mula
11	53	4.5	848	6 Q9MZS2	Q9MZS2 sus scrofa
12	53	4.5	1165	6 Q02671	Q02671 sus scrofa
13	43	3.7	57	6 Q97778	Q97778 elephas max
14	43	3.7	57	6 Q97779	Q97779 loxodonta a
15	42	3.6	1162	11 Q9QWG3	Q9QWG3 mus musculu
16	41	3.5	895	11 Q62960	Q62960 rattus norv

17	26	2.2	203	6 Q28604	Q28604 ovis aries
18	20	1.7	152	6 P79115	P79115 bos taurus
19	18	1.5	74	11 Q9ERI4	Q9ERI4 rattus norv
20	18	1.5	173	6 Q9XSN9	Q9XSN9 sus scrofa
21	18	1.5	246	11 Q35773	Q35773 rattus norv
22	17	1.5	102	6 Q9XSH3	Q9XSH3 equus caball
23	17	1.5	145	13 Q9IA32	Q9IA32 gallus gall
24	17	1.5	1146	13 Q9IBV6	Q9IBV6 gallus gall
25	17	1.5	1147	13 Q9DDK1	Q9DDK1 meleagris g
26	17	1.5	1148	13 Q9IBAT	Q9IBAT gallus gall
27	13	1.1	123	6 Q9NIF9	Q9NIF9 sus scrofa
28	13	1.1	161	6 Q28606	Q28606 ovis aries
29	13	1.1	273	11 Q9QWV5	Q9QWV5 mus musculu
30	10	0.9	147	6 Q95257	Q95257 sus scrofa
31	9	0.8	26	11 Q9WV88	Q9WV88 mus musculu
32	9	0.8	121	6 Q18980	Q18980 bos taurus
33	9	0.8	901	4 Q9HCE2	Q9HCE2 homo sapien
34	9	0.8	919	4 Q9BUMB	Q9BUMB homo sapien
35	9	0.8	919	4 Q96HY7	Q96HY7 homo sapien
36	8	0.7	30	11 Q9JHF4	Q9JHF4 rattus norv
37	8	0.7	103	12 Q9ID21	Q9ID21 respiratory
38	8	0.7	104	12 Q9ID20	Q9ID20 respiratory
39	8	0.7	104	12 Q9IDU1	Q9IDU1 respiratory
40	8	0.7	107	12 Q9IDU0	Q9IDU0 respiratory
41	8	0.7	124	3 Q13894	Q13894 schizosacch
42	8	0.7	184	5 Q9BHJ6	Q9BHJ6 trypanosoma
43	8	0.7	217	13 P70016	P70016 xenopus lae
44	8	0.7	222	16 Q97185	Q97185 clostridium
45	8	0.7	236	17 P95945	P95945 sulfolobus
46	8	0.7	322	13 Q9IBG4	Q9IBG4 xenopus lae
47	8	0.7	325	13 Q9IBG2	Q9IBG2 xenopus lae
48	8	0.7	326	13 Q9IBB2	Q9IBB2 xenopus lae
49	8	0.7	326	13 Q9IBG3	Q9IBG3 xenopus lae
50	8	0.7	335	12 Q9DH41	Q9DH41 meleagrid h
51	8	0.7	383	8 Q9B205	Q9B205 calman croc
52	8	0.7	425	16 Q9K9C3	Q9K9C3 bacillus ha
53	8	0.7	459	16 Q9I6E9	Q9I6E9 pseudomonas
54	8	0.7	498	12 Q88525	Q88525 turkey herp
55	8	0.7	850	16 Q9CKA8	Q9CKA8 pasteurella
56	8	0.7	864	10 Q9L219	Q9L219 arabidopsis
57	8	0.7	937	16 Q9A3P1	Q9A3P1 caulobacter
58	8	0.7	952	1 Q9P915	Q9P915 haloarcula
59	8	0.7	1270	5 Q19736	Q19736 caenorhabdi
60	8	0.7	1291	5 Q19734	Q19734 caenorhabdi
61	8	0.7	1318	5 Q19733	Q19733 caenorhabdi
62	8	0.7	1327	5 Q19735	Q19735 caenorhabdi
63	7	0.6	47	11 Q63139	Q63139 rattus norv
64	7	0.6	64	16 Q9PH48	Q9PH48 xylella fas
65	7	0.6	78	5 Q9NIE5	Q9NIE5 leishmania
66	7	0.6	94	2 Q9AGE7	Q9AGE7 listeria mo
67	7	0.6	94	16 Q929U9	Q929U9 listeria in
68	7	0.6	101	3 Q07236	Q07236 saccharomyc
69	7	0.6	104	16 Q92DX8	Q92DX8 listeria in
70	7	0.6	111	4 Q9H4W3	Q9H4W3 homo sapien
71	7	0.6	120	8 Q9BBT8	Q9BBT8 lotus japon
72	7	0.6	120	13 Q9UAD1	Q9UAD1 eptatretus
73	7	0.6	125	2 Q47664	Q47664 escherichia
74	7	0.6	127	16 Q92FK4	Q92FK4 listeria in
75	7	0.6	128	2 Q53089	Q53089 rhodobacter

#### ALIGNMENTS

RESULT 1  
ID Q92921 PRELIMINARY: PRT; 1165 AA.  
AC Q92921: 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96398968; PubMed=8805376;  
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,  
 RA Matthews W.;  
 RT "A role for leptin and its cognate receptor in hematopoiesis."  
 RL Curr. Biol. 6:1170-1180(1996).  
 DR EMBL; U66497; AAB07497.1; -.  
 DR HSSP; P16471; 1BP3.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
 DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 100.0%; Score 1165; DB 4; Length 1165;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60  
 1 MICQFCVLLHWEFIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60  
 DB 1 MICQFCVLLHWEFIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60  
 QY 61 NGHYETAEPKFNSSGTHFSNLSTKTHCCFRSEODRNCISLADNIEGKTFVSTVNSL 120  
 61 NGHYETAEPKFNSSGTHFSNLSTKTHCCFRSEODRNCISLADNIEGKTFVSTVNSL 120  
 DB 61 NGHYETAEPKFNSSGTHFSNLSTKTHCCFRSEODRNCISLADNIEGKTFVSTVNSL 120  
 QY 121 QOIDANWNIQWLKGLKFLICVYESLEKLNERNYKVKHLLVLEVLLEDSPVLPQKS 180  
 121 QOIDANWNIQWLKGLKFLICVYESLEKLNERNYKVKHLLVLEVLLEDSPVLPQKS 180  
 DB 121 QOIDANWNIQWLKGLKFLICVYESLEKLNERNYKVKHLLVLEVLLEDSPVLPQKS 180  
 QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGSVIFQSPMLSVQPINMKPDP 240  
 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGSVIFQSPMLSVQPINMKPDP 240  
 DB 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGSVIFQSPMLSVQPINMKPDP 240  
 QY 241 LGLHMETDDGNLKLISWSSPPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
 241 LGLHMETDDGNLKLISWSSPPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
 DB 241 LGLHMETDDGNLKLISWSSPPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
 QY 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTQDVIFPPKILTSVGSNVSEHCYKKEKNI 360  
 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTQDVIFPPKILTSVGSNVSEHCYKKEKNI 360  
 DB 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTTQDVIFPPKILTSVGSNVSEHCYKKEKNI 360  
 QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
 DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
 QY 421 RYAEIYVIDVNIINISCEIDGILTKMTCRMSTSTIQSLAESTLQLRHRSLLYCSIDPSIH 480  
 421 RYAEIYVIDVNIINISCEIDGILTKMTCRMSTSTIQSLAESTLQLRHRSLLYCSIDPSIH 480  
 DB 421 RYAEIYVIDVNIINISCEIDGILTKMTCRMSTSTIQSLAESTLQLRHRSLLYCSIDPSIH 480  
 QY 481 PISEPKCYLQSDGFYECIFQPIFLSLGYTMIRINHSLSGLSPPTCVLPDSVVKPLRP 540  
 481 PISEPKCYLQSDGFYECIFQPIFLSLGYTMIRINHSLSGLSPPTCVLPDSVVKPLRP 540  
 DB 481 PISEPKCYLQSDGFYECIFQPIFLSLGYTMIRINHSLSGLSPPTCVLPDSVVKPLRP 540  
 QY 541 SSYKAEITINIGLKLISWEKPVFPENNLQFQIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
 541 SSYKAEITINIGLKLISWEKPVFPENNLQFQIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
 DB 541 SSYKAEITINIGLKLISWEKPVFPENNLQFQIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600  
 QY 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPDEFWRILNGDTMKKEKNV 660  
 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPDEFWRILNGDTMKKEKNV 660  
 DB 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATYVMDIKVPMRGPDEFWRILNGDTMKKEKNV 660  
 QY 661 TLMLKPLMKNDSLCSQRYVINHTSCNGTWSDEVGNHTKFTPLMTEQAHTVTALAINSI 720  
 661 TLMLKPLMKNDSLCSQRYVINHTSCNGTWSDEVGNHTKFTPLMTEQAHTVTALAINSI 720

DB 661 TLMLKPLMKNDSLCSQRYVINHTSCNGTWSDEVGNHTKFTPLMTEQAHTVTALAINSI 720  
 QY 721 GASVANENLTFSPMSKVNIVQSLGAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNED 780  
 721 GASVANENLTFSPMSKVNIVQSLGAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNED 780  
 DB 721 GASVANENLTFSPMSKVNIVQSLGAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNED 780  
 QY 781 GEIKWLRISSSVKYYIHDHFIPLEKYQSLYPIFMEGVGKPKINSFTQDDIEKHQSDA 840  
 781 GEIKWLRISSSVKYYIHDHFIPLEKYQSLYPIFMEGVGKPKINSFTQDDIEKHQSDA 840  
 DB 781 GEIKWLRISSSVKYYIHDHFIPLEKYQSLYPIFMEGVGKPKINSFTQDDIEKHQSDA 840  
 QY 841 GLYVIVPVISSSILLGLTLLISHQNMKLFMEDVNPKNCSNAQGLNFQKPEFELHFI 900  
 841 GLYVIVPVISSSILLGLTLLISHQNMKLFMEDVNPKNCSNAQGLNFQKPEFELHFI 900  
 DB 841 GLYVIVPVISSSILLGLTLLISHQNMKLFMEDVNPKNCSNAQGLNFQKPEFELHFI 900  
 QY 901 KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPPTVSVLSLTDLEKGSVCISDQFN 960  
 901 KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPPTVSVLSLTDLEKGSVCISDQFN 960  
 DB 901 KHTASVTCGPLLLEPETISEDIVDTSWKNKDEMPPTVSVLSLTDLEKGSVCISDQFN 960  
 QY 961 SVNFSEAEGETEYVEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
 961 SVNFSEAEGETEYVEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
 DB 961 SVNFSEAEGETEYVEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTCKFSSKNSPL 1020  
 QY 1021 KDSFNSWMEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
 1021 KDSFNSWMEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
 DB 1021 KDSFNSWMEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
 QY 1081 GVTISIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
 1081 GVTISIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
 DB 1081 GVTISIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
 QY 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165  
 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165  
 DB 1141 YMPQFOTCSTQTHKIMENKMDLTIV 1165  
 RESULT 2  
 Q92919  
 ID Q92919 PRELIMINARY; PRT; 896 AA.  
 AC Q92919;  
 DT 01-FEB-1997 (TREMBLREL. 02, Created)  
 DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)  
 DE LEPTIN RECEPTOR.  
 GN DB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,  
 RA Matthews W.;  
 RT Curr. Biol. 6:0-0(0).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97215244; PubMed=9061609;  
 RA Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,  
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;  
 RT "Cloning and characterization of a human leptin receptor using a  
 RT biologically active leptin immunoadhesin."  
 RL J. Mol. Endocrinol. 18:77-85(1997).  
 DR EMBL; U66495; AAB07495.1; -.  
 DR EMBL; U50748; AAC23650.1; -.  
 DR HSSP; P16471; 1BP3.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
 DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.

SO 'SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3.CRC64;

Query Match 76.5%; Score 891; DB 4; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYE 120
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYE 120
QY 121 QOIDANMNIOQWLKGDCLKFICVESLFFKNLFRNRYNKHLLYLPLEVLEDSPLVPQKGS 180
DB 121 QOIDANMNIOQWLKGDCLKFICVESLFFKNLFRNRYNKHLLYLPLEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVFPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP 240
DB 181 FQWVHCNCSVHECCCECLVFPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFENLNKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFENLNKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
DB 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKSISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKSISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPNATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPNATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHVTVALAINSI 720
DB 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQAHVTVALAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
DB 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKKYYIHDHPIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCSWAQGLNFQK 891
DB 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFMEDVPPNPKNCSWAQGLNFQK 891
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RESULT 3  
ID Q92920 PRELIMINARY; PRT; 958 AA.  
AC Q92920;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)

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DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96398968; Pubmed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Mathews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis.";
RL Curr. Biol. 6:1170-1180(1996).
DR EMBL; U66496; AAB07496.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 958 AA; 109392 MW; 3F65BC5A187E803A.CRC64;
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Query Match 76.5%; Score 891; DB 4; Length 958;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYE 120
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYE 120
QY 121 QOIDANMNIOQWLKGDCLKFICVESLFFKNLFRNRYNKHLLYLPLEVLEDSPLVPQKGS 180
DB 121 QOIDANMNIOQWLKGDCLKFICVESLFFKNLFRNRYNKHLLYLPLEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVFPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP 240
DB 181 FQWVHCNCSVHECCCECLVFPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMKPDP 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVPFPLOYQVKYSENSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFENLNKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFENLNKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
DB 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSLLYCSIDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKSISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKSISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPNATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
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Db 601 PDLCAVYAVQYRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFMRILNGDTMKKEKNV 660  
QY 661 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSEDVGNHTKFTFLMTEQAHTVTVLAINSI 720  
Db 661 TLMKPLMKNDSLCSVQRYVINHTSCNGTWSEDVGNHTKFTFLMTEQAHTVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQK 891  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQK 891

RESULT 4  
Q13594 PRELIMINARY; PRT; 896 AA.  
ID Q13594  
AC Q13594;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; Pubmed=8616721;  
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RA Platika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
RT hemotopolesis and reproduction.";  
RL Nat. Med. 2:585-589(1996).  
DR EMBL; U52914; AAC50511.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.  
SQ SEQUENCE 896 AA; 102516 MW; 73C431F8C578CD07 CRC64;

Query Match 58.5%; Score 681; DB 4; Length 896;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVEQQIDANMNIOQWLKGLKFLICYVESLFXNLFNRYNYKVHLLVLPVYL 169  
Db 110 TFEVSTVNSLVEQQIDANMNIOQWLKGLKFLICYVESLFXNLFNRYNYKVHLLVLPVYL 169  
QY 170 EDSPLVPQKGSFQVHNCNSVHECECLVPVPTAKLNDTLMLCKITSGVIFOSPLMSV 229  
Db 170 EDSPLVPQKGSFQVHNCNSVHECECLVPVPTAKLNDTLMLCKITSGVIFOSPLMSV 229  
QY 230 QPINMYKDDPPLGLHMEITDDGNLKSWSPPPLVPLQYQVKYSENSTVIREADKIYS 289  
Db 230 QPINMYKDDPPLGLHMEITDDGNLKSWSPPPLVPLQYQVKYSENSTVIREADKIYS 289

QY 290 ATSLVDSILPGSSYEVOVRGKRLDGPGLSDMSTPRVFTTQDVITYFPKILTSVGSNV 349  
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QY 350 FHCIIYKKENKIVPSKEIWMNMNLAEKIPQSOYDVSDHVSXVTFNENETKPRGKFTYDA 409  
Db 350 FHCIIYKKENKIVPSKEIWMNMNLAEKIPQSOYDVSDHVSXVTFNENETKPRGKFTYDA 409  
QY 410 VYCCNEHECHHRYAELVIDVININISCEFDGYLTMTCTCRWSTSTIOSLAESTLQRLYHRS 469  
Db 410 VYCCNEHECHHRYAELVIDVININISCEFDGYLTMTCTCRWSTSTIOSLAESTLQRLYHRS 469  
QY 470 SLVCS DIPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINSLGLSDSPPTCV 529  
Db 470 SLVCS DIPSIHPISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINSLGLSDSPPTCV 529  
QY 530 LPDSVVKPLPSSSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589  
Db 530 LPDSVVKPLPSSSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589  
QY 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIT 649  
Db 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIT 649  
QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSEDVGNHTKFTFLMTEQA 709  
Db 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSEDVGNHTKFTFLMTEQA 709  
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMY 769  
Db 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMY 769  
QY 770 FIEMKNLNEDEIKWLRISSSVKYYIHDHFPIEKYQPSLYPIFMEGVGKPKIINSFT 829  
Db 770 FIEMKNLNEDEIKWLRISSSVKYYIHDHFPIEKYQPSLYPIFMEGVGKPKIINSFT 829  
QY 830 QDDIEKHQSDAGLYIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNF 889  
Db 830 QDDIEKHQSDAGLYIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNF 889  
QY 890 QK 891  
Db 890 QK 891

RESULT 5  
Q13593 PRELIMINARY; PRT; 906 AA.  
ID Q13593  
AC Q13593;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; Pubmed=8616721;  
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RA Platika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
RT hemotopolesis and reproduction.";  
RL Nat. Med. 2:585-589(1996).  
DR EMBL; U52913; AAC50510.1; -.  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.

DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.  
SQ SEQUENCE 906 AA; 103487 MW; 6D51126F33076626 CRC64;

Query Match 58.5%; Score 681; DB 4; Length 906;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFVSTVNSLVFQOIIDANWNIOQWLKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVL 169  
DB 110 TFVSTVNSLVFQOIIDANWNIOQWLKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVL 169  
QY 170 EDSPLVPQKGSFQMVHNCVSHECCCLVPVPTAKLNDTLMLCKITSGGVIFRSPIMSV 229  
DB 170 EDSPLVPQKGSFQMVHNCVSHECCCLVPVPTAKLNDTLMLCKITSGGVIFRSPIMSV 229  
QY 230 QPINWKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVS 289  
DB 230 QPINWKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVS 289  
QY 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDWSTPRVFTTQDVITYFPKILTSVGSNVS 349  
DB 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDWSTPRVFTTQDVITYFPKILTSVGSNVS 349  
QY 350 FHCITYKKENKIIVPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDA 409  
DB 350 FHCITYKKENKIIVPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDA 409  
QY 410 VYCCNEHECHHRYAELVIVDYNINISCEITDGYLTMTCRMSTSTIOSLAESTIQLRYHRS 469  
DB 410 VYCCNEHECHHRYAELVIVDYNINISCEITDGYLTMTCRMSTSTIOSLAESTIQLRYHRS 469  
QY 470 SLVCSIDIPSIHIPISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCV 529  
DB 470 SLVCSIDIPSIHIPISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCV 529  
QY 530 LPDSVVKPLPPSSVKAETITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYEV 589  
DB 530 LPDSVVKPLPPSSVKAETITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYEV 589  
QY 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIT 649  
DB 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIT 649  
QY 650 NGDTMKKEKNVTLLMKPLKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTPLWTEQA 709  
DB 650 NGDTMKKEKNVTLLMKPLKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTPLWTEQA 709  
QY 710 HTVTVLAINSIGASVANRNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKIMY 769  
DB 710 HTVTVLAINSIGASVANRNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKIMY 769  
QY 770 FLEEMKNLNEDEGIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSEFT 829  
DB 770 FLEEMKNLNEDEGIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSEFT 829  
QY 830 QDDIEKHOSDAGLYVIVPVISSSILLGLTLLISHQRMKLFWEDEVNPNKNCSWAOGILNF 889  
DB 830 QDDIEKHOSDAGLYVIVPVISSSILLGLTLLISHQRMKLFWEDEVNPNKNCSWAOGILNF 889  
QY 890 OK 891  
DB 890 OK 891

RESULT 6  
Q13592  
ID Q13592 PRELIMINARY; PRT; 958 AA.

AC Q13592;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=96206286; PubMed=8616721;  
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
RA Platika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
hematopoiesis and reproduction.";  
RL Nat. Med. 2:585-589(1996).  
DR EMBL; U52912; AAC50509.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; FN3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Signal; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.  
SQ SEQUENCE 958 AA; 109419 MW; C7E0E8D18428677B CRC64;

Query Match 58.5%; Score 681; DB 4; Length 958;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFVSTVNSLVFQOIIDANWNIOQWLKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVL 169  
DB 110 TFVSTVNSLVFQOIIDANWNIOQWLKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVL 169  
QY 170 EDSPLVPQKGSFQMVHNCVSHECCCLVPVPTAKLNDTLMLCKITSGGVIFRSPIMSV 229  
DB 170 EDSPLVPQKGSFQMVHNCVSHECCCLVPVPTAKLNDTLMLCKITSGGVIFRSPIMSV 229  
QY 230 QPINWKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVS 289  
DB 230 QPINWKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVS 289  
QY 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDWSTPRVFTTQDVITYFPKILTSVGSNVS 349  
DB 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDWSTPRVFTTQDVITYFPKILTSVGSNVS 349  
QY 350 FHCITYKKENKIIVPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDA 409  
DB 350 FHCITYKKENKIIVPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDA 409  
QY 410 VYCCNEHECHHRYAELVIVDYNINISCEITDGYLTMTCRMSTSTIOSLAESTIQLRYHRS 469  
DB 410 VYCCNEHECHHRYAELVIVDYNINISCEITDGYLTMTCRMSTSTIOSLAESTIQLRYHRS 469  
QY 470 SLVCSIDIPSIHIPISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCV 529  
DB 470 SLVCSIDIPSIHIPISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCV 529  
QY 530 LPDSVVKPLPPSSVKAETITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYEV 589  
DB 530 LPDSVVKPLPPSSVKAETITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYEV 589  
QY 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIT 649  
DB 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIT 649



QY	650	NGDTMKKEKNTVTLWMKPLMKNDLSQVORYVINHHTSCNGTWSQVGNHHTKFTLWTEQA	709
Db	650	NGDTMKKEKNTVTLWMKPLMKNDLSQVORYVINHHTSCNGTWSQVGNHHTKFTLWTEQA	709
QY	710	HFTVTLAINSIGASVANENLTFWPMKSVNIQVLSAYPLNSSCVIVSWILSPDYKLMY	769
Db	710	HFTVTLAINSIGASVANENLTFWPMKSVNIQVLSAYPLNSSCVIVSWILSPDYKLMY	769
QY	770	FILEMKNLNEDEGEIKWLRISSSVKKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKLINSFT	829
Db	770	FILEMKNLNEDEGEIKWLRISSSVKKYYIHDHFPIEIKYQFSLYPIFMEGVGKPKLINSFT	829
QY	830	QDDIEKHQSDAGLYVIVPIISSSILLGTLILSHQRMKLFWEDEVNPNKNCSSAOGLENF	889
Db	830	QDDIEKHQSDAGLYVIVPIISSSILLGTLILSHQRMKLFWEDEVNPNKNCSSAOGLENF	889
QY	890	QK 891	
Db	890	QK 891	

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RESULT      7
O9MYL1
ID O9MYL1 PRELIMINARY; PRT; 894 AA.
AC O9MYL1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RX Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF225873; AAF35387.1; .
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAFF032238BAFB9 CRC64;

Query Match          7.2%; Score 84; DB 6; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 672 SLCSVQRYYVINHTSCNGTWSDEVGNHKTFTFLWTEQAHTVTVLAINSIGASVANFNLTTF 731
   |||||||
Db , 670 SLCSVQRYYVINHTSCNGTWSDEVGNHKTFTFLWTEQAHTVTVLAINSIGASVANFNLTTF 729
-QY 732 SMPMSKVNIVQSLSAYPLNSSCVI 755
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Db      730 SWPMASKVNIVQSLSAFPLNSSCVI 753

RESULT      8
Q9MYK9
ID      Q9MYK9      PRELIMINARY;      PRT;      925 AA.
AC      Q9MYK9;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS      Macaca mulatta (Rhesus macaque);
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98408931; PubMed=9738551;

SEQUENCE FROM N.A.
TISSE-ADIPOSE TISSE;
MEDLINE=98408931; PubMed=9738551;
Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RA      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AF225875; AAF35389.1;
DR      HSSP: P16471; 1BP3.
DR      InterPro: IPR002996; CRIA.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003529; Hematopo_receptor_L_F2.
DR      InterPro: IPR003531; Hematopo_receptor_S_F1.
DR      Pfam: PF00041; fn3; 2.
DR      SMART: SM00060; FN3; 1.
DR      PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR      PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW      Receptor.
SQ      SEQUENCE      925 AA;      105721 MW;      EC09GC27EC29C5F3A CRC64;

Query Match      7.2%; Score 84; DB 6; Length 925;
Best Local Similarity      100.0%; Pred. No. 3e-80;
Matches      84; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      672 SLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLT 731
Db      670 SLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLT 729
QY      732 SWPMASKVNIVQSLSAFPLNSSCVI 755
Db      730 SWPMASKVNIVQSLSAFPLNSSCVI 753

RESULT      9
Q9MYL2
ID      Q9MYL2      PRELIMINARY;      PRT;      1163 AA.
AC      Q9MYL2;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      LEPTIN RECEPTOR LONG FORM.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98408931; PubMed=9738551;

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RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA  
RT expression in the adipose tissue of normal, hyperinsulinemic, and type  
RT 2 diabetic rhesus monkeys."  
RL Obes. Res. 6:353-360(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF222960; AAF34683.1; -  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam: PF00041; fn3; 2.  
DR SMART: SM00060; FN3; 1.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;

Query Match 7.2%; Score 84; DB 6; Length 1163;  
Best Local Similarity 100.0%; Pred. No. 3.6e-80;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 672 SLCSVQRVYVNHHTSCNGTWSGDNHTKFTFLWTEQAHVTVLAINSIGASVANFNLT 731  
Db 670 SLCSVQRVYVNHHTSCNGTWSGDNHTKFTFLWTEQAHVTVLAINSIGASVANFNLT 729  
OY 732 SWPMKVNIVQSLAYPLNSSCVI 755  
Db 730 SWPMKVNIVQSLAYPLNSSCVI 753

RESULT 10  
O9MYL0 PRELIMINARY; PRT; 1194 AA.  
AC O9MYL0;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR LONG INSERT ISOFORM.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADIPOSE TISSUE;  
RX MEDLINE=98408931; PubMed=9738551;  
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA  
RT expression in the adipose tissue of normal, hyperinsulinemic, and type  
RT 2 diabetic rhesus monkeys."  
RL Obes. Res. 6:353-360(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADIPOSE TISSUE;  
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF225874; AAF35388.1; -  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam: PF00041; fn3; 2.  
DR SMART: SM00060; FN3; 1.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.

KW Receptor.  
SQ SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;  
Query Match 7.2%; Score 84; DB 6; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 3.7e-80;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 672 SLCSVQRVYVNHHTSCNGTWSGDNHTKFTFLWTEQAHVTVLAINSIGASVANFNLT 731  
Db 670 SLCSVQRVYVNHHTSCNGTWSGDNHTKFTFLWTEQAHVTVLAINSIGASVANFNLT 729  
OY 732 SWPMKVNIVQSLAYPLNSSCVI 755  
Db 730 SWPMKVNIVQSLAYPLNSSCVI 753

RESULT 11  
O9MZS2 PRELIMINARY; PRT; 848 AA.  
AC O9MZS2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).  
GN OBR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Hu X., Dai R., Li N., Wu C.;  
RT "Expression, Detection, and Partial Cloning of Porcine Leptin Receptor  
RT (OBR) Gene."  
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF167719; AAF89633.1; -  
DR HSSP: P16471; 1BP3.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro: IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam: PF00041; fn3; 1.  
DR SMART: SM00060; FN3; 2.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE: PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 848 848  
SQ SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;

Query Match 4.5%; Score 53; DB 6; Length 848;  
Best Local Similarity 100.0%; Pred. No. 3.9e-47;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 399 TKPRGFTYDAVYCCNEHCHRYAEIVYDVNINISCEETDGYLTKTCRWST 451  
Db 393 TKPRGFTYDAVYCCNEHCHRYAEIVYDVNINISCEETDGYLTKTCRWST 445

RESULT 12  
O02671 PRELIMINARY; PRT; 1165 AA.  
AC O02671;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE TRANSMEMBRANE LEPTIN RECEPTOR.  
GN LEPR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.F.,
RT Murphy B.D.;
RL "Porcine Leptin (Ob) receptor complete coding sequence.";
RN Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 408-470 FROM N.A.
RX MEDLINE=97222487; PubMed=9069130;
RA Ernst C.W., Kapke P.A., Yerie M., Rothschild M.F.;
RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";
RL Mamm. Genome 8:226-226(1997).
DR EMBL; AF092422; AAC61766.1; -.
DR EMBL; U72070; AAC48707.1; -.
DR HSSP; P16471; IBP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F12 CRC64;

Query Match 4.5%; Score 53; DB 6; Length 1165;
Best Local Similarity 100.0%; Pred. No. 5.2e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 399 TKPRGKFTYDAVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 451
DB 399 TKPRGKFTYDAVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 451

RESULT 13
O97778 PRELIMINARY; PRT; 57 AA.
AC O97778;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE LEPTIN RECEPTOR (FRAGMENT).
GN LEPR.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE FROM N.A.
RA Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.;
RT "Identification of Sequence Tagged Sites in the Asian Elephant
(Elephas maximus) and the African Elephant (Loxodonta africana).";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95048; AAD00769.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 6605 MW; 667857030937BA26 CRC64;

Query Match 3.7%; Score 43; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 409 AVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 451
DB 3 AVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 45
```

```
RESULT 14
O97779 PRELIMINARY; PRT; 57 AA.
AC O97779;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE LEPTIN RECEPTOR (FRAGMENT).
GN LEPR.
OS Loxodonta africana (African elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
OX NCBI_TaxID=9785;
RN [1]
RP SEQUENCE FROM N.A.
RA Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.;
RT "Identification of Sequence Tagged Sites in the Asian Elephant
(Elephas maximus) and the African Elephant (Loxodonta africana).";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95049; AAD00770.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 6605 MW; 667857030937BA26 CRC64;

Query Match 3.7%; Score 43; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 409 AVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 451
DB 3 AVYCCNEHECHHRYAELVIDVNINISCETDGYLTMTCRWST 45

RESULT 15
O90WG3 PRELIMINARY; PRT; 1162 AA.
AC O90WG3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEPTIN RECEPTOR B.
GN LEPR OR LEPRB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-KK OBESSE; TISSUE-BRAIN, HYPOTHALAMUS;
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joost H.G.;
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
hyperinsulinemic KK mouse strain.";
RL J. Endocrinol. 21:337-345(1998).
DR EMBL; Y10296; CAA71342.1; -.
DR HSSP; P16471; IBP3.
DR MGD; MGI:104993; Lepr.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
FT VARIANT 600
FT VARIANT 600 N -> D.
SQ SEQUENCE 1162 AA; 130787 MW; 541E77CBA46EC00D CRC64;
```

Query Match 3.6%; Score 42; DB 11; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 3e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 541  
|||||  
DB 498 FQPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 539

## RESULT 16

Q62960 PRELIMINARY; PRT; 895 AA.  
AC Q62960;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE LEPTIN RECEPTOR.  
GN ROB-R.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID-10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RA Wang M.-Y., Unger R.H.;  
RT "Characterization of leptin receptors in normal and Zucker diabetic  
RT fatty rats."  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U53144; AAB03088.1; -  
DR HSSP; P16471; 1BP3.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR InterPro; IPR003531; Hematopo\_receptor\_S\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;

Query Match 3.5%; Score 41; DB 11; Length 895;  
Best Local Similarity 100.0%; Pred. No. 2.8e-34;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 QPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 541  
|||||  
DB 499 QPIFLLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 539

## RESULT 17

Q28604 PRELIMINARY; PRT; 203 AA.  
AC Q28604;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE LEPTIN RECEPTOR LONG FORM (FRAGMENT).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID-9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HYPOTHALAMUS;  
RX MEDLINE-97217693; PubMed-9063654;  
RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;  
RT "Leptin receptor mRNA is expressed in ewe anterior pituitary and  
RT adipose tissues and is differentially expressed in hypothalamic  
RT regions of well-fed and feed-restricted ewes.";

RL Domest. Anim. Endocrinol. 14:119-128(1997).

DR EMBL; U62124; AAC48708.1; -  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 203 203  
SQ SEQUENCE 203 AA; 22398 MW; 94CAC2852950AD03 CRC64;

Query Match 2.2%; Score 26; DB 6; Length 203;  
Best Local Similarity 100.0%; Pred. No. 8.3e-19;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 GPILLEPETISEDISVDTSWKNKDEM 934  
|||||  
DB 18 GPILLEPETISEDISVDTSWKNKDEM 43

## RESULT 18

P79115 PRELIMINARY; PRT; 152 AA.  
AC P79115;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE OBES RECEPTOR (FRAGMENT).  
GN OB-R.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID-9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfister-Genskow M., Eggen A., Hayes H., Bishop M.D.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U62385; AAB40624.1; -  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 152 152  
SQ SEQUENCE 152 AA; 16749 MW; 1B58BFED05EBD8DB CRC64;

Query Match 1.7%; Score 20; DB 6; Length 152;  
Best Local Similarity 100.0%; Pred. No. 1.7e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1053 FSEGLDELKLEGNFPEENN 1072  
|||||  
DB 120 FSEGLDELKLEGNFPEENN 139

## RESULT 19

Q9ER14 PRELIMINARY; PRT; 74 AA.  
AC Q9ER14;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE LEPTIN RECEPTOR OB-RA (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID-10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MUNICH-WISTAR; TISSUE=KIDNEY;  
RA Totsume K., Takahashi K., Mackenzie H.S., Murakami O., Arihara Z.,  
RA Sone M., Satoh F., Mouri T., Brenner B.M., Ito S.;  
RT "Leptin receptor gene expression in rat kidney."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF304191; AAG22823.1; -  
KW Receptor.  
FT NON\_TER 1 1

SO SEQUENCE 74 AA; 8357 MW; E6ABC5C4FA7CE3D6 CRC64;

Query Match  
Best Local Similarity 1.5%; Score 18; DB 11; Length 74;  
Matches 18; Conservative 100.0%; Pred. No. 1.2e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 855 LLGLTLLSHQRMKLLFW 872  
|||||  
Db 33 LLGLTLLSHQRMKLLFW 50

RESULT 20

O9XSN9

PRELIMINARY; PRT; 173 AA.

ID O9XSN9;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE LEPTIN RECEPTOR (FRAGMENT).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-HYPOTHALAMUS;

RA Materl R.L.;

RT "Partial CDNA sequence of the porcine leptin receptor."

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF036908; AAB88825.1; -.

KW Receptor.

FT NON\_TER 1 1

SO SEQUENCE 173 AA; 19539 MW; 678897C04BFDD842 CRC64;

Query Match  
Best Local Similarity 1.5%; Score 18; DB 6; Length 173;  
Matches 18; Conservative 100.0%; Pred. No. 2.6e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 917 TISEDIVDTSWKNKDEM 934  
|||||

Db 1 TISEDIVDTSWKNKDEM 18

RESULT 21

O35773

PRELIMINARY; PRT; 246 AA.

ID O35773;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LEPTIN RECEPTOR OB-RE (FRAGMENT).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA Chien E.K.; Hara M.; Rouard M.; Yano H.; Phillippe M.; Polonsky K.S.;

RA Bell G.I.;

RT "Rat leptin splice variant Ob-Re.";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF007819; AAB63202.1; -.

DR HSSP; P40189; 1BQU.

DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.

DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.

KW Receptor.

FT NON\_TER 1 1

SO SEQUENCE 246 AA; 28085 MW; 4A469748F2B6ED8E CRC64;

Query Match  
Best Local Similarity 1.5%; Score 18; DB 11; Length 246;  
Matches 18; Conservative 100.0%; Pred. No. 3.5e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 EKPVPENNLOFQIRYGL 576  
|||||  
Db 1 EKPVPENNLOFQIRYGL 18

RESULT 22

O9XSH3

PRELIMINARY; PRT; 102 AA.

ID O9XSH3;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE LEPTIN RECEPTOR (FRAGMENT).

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Dodds A.C.; Whitley N.C.; Keisler D.H.;

RT "Equine leptin receptor."

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF139663; AAD31284.1; -.

KW Receptor.

FT NON\_TER 1 1

FT NON\_TER 102 102

SO SEQUENCE 102 AA; 11025 MW; 6AB008D11B6CE783 CRC64;

Query Match  
Best Local Similarity 1.5%; Score 17; DB 6; Length 102;  
Matches 17; Conservative 100.0%; Pred. No. 1.9e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1034 QAFITLSDQHPNIIISP 1050  
|||||

Db 86 QAFITLSDQHPNIIISP 102

RESULT 23

O9IA32

PRELIMINARY; PRT; 145 AA.

ID O9IA32;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LEPTIN RECEPTOR (FRAGMENT).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20539125; PubMed=11086550;

RA Dunn I.C.; Boswell T.; Friedman-Einat M.; Eshdat Y.; Burt D.W.;

RA Paton I.R.;

RT "Mapping of the leptin receptor gene (LEPR) to chicken chromosome 8.";

RL Anim. Genet. 31:290-290(2000).

DR EMBL; AF222783; AAF63467.1; -.

KW Receptor.

FT NON\_TER 1 1

FT NON\_TER 145 145

SO SEQUENCE 145 AA; 16684 MW; 71CFA3A2AE942DAD CRC64;

Query Match  
Best Local Similarity 1.5%; Score 17; DB 13; Length 145;  
Matches 17; Conservative 100.0%; Pred. No. 2.6e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 339 KILTSVGSNVSFHCITYK 355  
 |||||||  
 Db 55 KILTSVGSNVSFHCITYK 71

## RESULT 24

Q918V6

ID Q918V6 PRELIMINARY; PRT; 1146 AA.

AC Q918V6;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LEPTIN RECEPTOR.

GN LEPR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEGHORN;

RX MEDLINE-20314392; Pubmed-10854702;

RA Horev G., Einat P., Aharoni T., Eshdat Y., Friedman-Einat M.;

RT "Molecular cloning and properties of the chicken leptin-receptor (CLEPR) gene."

RL Mol. Cell. Endocrinol. 162:95-106(2000).

DR EMBL; AF169827; AAF31355.1; -.

DR HSSP; P40189; 1BQU.

DR InterPro; IPR002996; CRIA.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.

DR Receptor.

KW RECEPTOR.

SQ SEQUENCE 1146 AA; 129036 MW; 403161267D437BE4 CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1146;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355

|||||

Db 329 KILTSVGSNVSFHCITYK 345

## RESULT 25

Q9DDK1

ID Q9DDK1 PRELIMINARY; PRT; 1147 AA.

AC Q9DDK1;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LEPTIN RECEPTOR.

GN OB-R.

OS Meleagris gallopavo (Common turkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.

OX NCBI\_TaxID=9103;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Richards M.P., Poch S.M., Ashwell C.M.;

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF321982; AAG40323.1; -.

DR HSSP; P40189; 1BQU.

DR InterPro; IPR002996; CRIA.

DR InterPro; IPR003961; FN\_III.

DR Pfam; PF00041; fn3; 2.

DR SMART; SM00060; FN3; 4.

DR Receptor.

FT VARIANT 1133 1133 Q -> R  
 SQ SEQUENCE 1147 AA; 129131 MW; 34197B7908F734F4 CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1147;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355

|||||

Db 330 KILTSVGSNVSFHCITYK 346

## RESULT 26

Q91BA7

ID Q91BA7 PRELIMINARY; PRT; 1148 AA.

AC Q91BA7;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LEPTIN RECEPTOR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20225474; Pubmed-10760595;

RA Ohkubo T., Tanaka M., Nakashima K.;

RT "Structure and tissue distribution of chicken leptin receptor (cob-R) mRNA."

RL Biochim. Biophys. Acta 1491:303-308(2000).

DR EMBL; AB033383; BAA94292.1; -.

DR HSSP; P40189; 1BQU.

DR InterPro; IPR002996; CRIA.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 2.

DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.

DR Receptor.

KW RECEPTOR.

SQ SEQUENCE 1148 AA; 129195 MW; 06Q13EF295D7CEDB CRC64;

Query Match 1.5%; Score 17; DB 13; Length 1148;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 KILTSVGSNVSFHCITYK 355

|||||

Db 330 KILTSVGSNVSFHCITYK 346

## RESULT 27

Q9N1F9

ID Q9N1F9 PRELIMINARY; PRT; 123 AA.

AC Q9N1F9;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 15, Last annotation update)

DE LEPTIN RECEPTOR (FRAGMENT).

GN LEPR.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRED YORKSHIRE/MEISHAN;

RA Lacroix D.A., Gevery N.Y., Ruiz-Cortes Z.T., Murphy B.D.;

RT "Porcine leptin receptor intron 3, partial."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF184173; AAF66822.1; -  
DR EMBL; AF184172; AAF66822.1; JOINED.  
KW Receptor.  
SQ SEQUENCE 123 AA; 13696 MW; 91C8ED51BCCA7B5B CRC64;

Query Match  
Best Local Similarity 100.0%; Score 13; DB 6; Length 123;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LLHMEFYVITAF 22  
|||||  
DB 10 LLHMEFYVITAF 22

## RESULT 28

ID Q28606 PRELIMINARY; PRT; 161 AA.  
AC Q28606;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR (FRAGMENT).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HYPOTHALAMUS;  
RA Dyer C.J., Simmons J.M., Matteri R.L., Kelsler D.H.;  
RT "Ovine partial leptin receptor cDNA.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U63719; AAB51695.1; -.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 161 161  
SQ SEQUENCE 161 AA; 18678 MW; 308DFC03621E6A19 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 13; DB 6; Length 161;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FCVVLHMEFYV 18  
|||||  
DB 1 FCVVLHMEFYV 13

## RESULT 29

ID Q9QWV5 PRELIMINARY; PRT; 273 AA.  
AC Q9QWV5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE LEPTIN RECEPTOR LONG ISOFORM RB (FRAGMENT).  
GN LEPR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RA Banks A.S., Myers M.G.Jr.;  
RT "Murine Leptin Receptor Genomic Exon 18b and Surrounding Sequence.";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF098792; AAD13218.1; -.  
DR MGD; MGI:104993; Lepr.  
KW Receptor.

FT NON\_TER 1 1  
SQ SEQUENCE 273 AA; 30335 MW; AB00AE611EBB5F96 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 13; DB 11; Length 273;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1153 HKIMENKMDLTV 1165  
|||||  
DB 261 HKIMENKMDLTV 273

## RESULT 30

ID Q95257 PRELIMINARY; PRT; 147 AA.  
AC Q95257;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE LEPTIN RECEPTOR (FRAGMENT).  
GN LEPR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HYPOTHALAMUS;  
RA Matteri R.L., Carroll J.A.;  
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 97-111 FROM N.A.  
RA Stratil A., Kopecky M., Moser G., Schroff J., Cepica S.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U67739; AAB07892.1; -.  
DR EMBL; AJ223162; CAA11142.1; -.  
DR EMBL; AJ223163; CAA11143.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16811 MW; 96AC8E929D0FED2F CRC64;

Query Match  
Best Local Similarity 100.0%; Score 10; DB 6; Length 147;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 WEFIYVITAF 22  
|||||  
DB 1 WEFIYVITAF 10

## RESULT 31

ID Q9WV88 PRELIMINARY; PRT; 26 AA.  
AC Q9WV88;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE LEPTIN RECEPTOR (FRAGMENT).  
GN LEPR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CD-1;  
RA Brown J.A., Chua S.C., Liu S.M., Andrews M.T., Vandenbergh J.G.;  
RT "A spontaneous mutation in the db gene results in obesity and diabetes in CD-1 outbred mice.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152957; AAD41084.1; -.

KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 26 26  
SQ SEQUENCE 26 AA; 3087 MW; AA471248894FCBB CRC64;

Query Match 0.8%; Score 9; DB 11; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 639 PMRGPFW 647  
Db 1 PMRGPFW 9

RESULT 32

018980 PRELIMINARY; PRT; 121 AA.  
AC 018980;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LEPTIN RECEPTOR (FRAGMENT).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Morrison C., Yan X., Ramsay T.G.;  
RT "Bovine ovarian leptin receptor partial cDNA sequence and mRNA  
expression in response to stimuli."  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U83512; AAB62399.1; -.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 13823 MW; 1C6775E2783FE373 CRC64;

Query Match 0.8%; Score 9; DB 6; Length 121;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 TVNSLVFQQ 122  
Db 84 TVNSLVFQQ 92

RESULT 33

09HCE2 PRELIMINARY; PRT; 901 AA.  
AC 09HCE2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE KIAA1630 PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=20450683; PubMed=10997877;  
RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes.  
XVIII. The complete sequences of 100 new cDNA clones from brain which  
code for large proteins in vitro."  
RL DNA Res. 7:273-281(2000).  
DR EMBL; AB046850; BAB13456.1; -.

DR InterPro; IPR001017; El\_dh.  
DR Pfam; PF00676; El\_dehydrog; 1.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 901 AA; 101085 MW; B32C84628EDCC2F6 CRC64;

Query Match 0.8%; Score 9; DB 4; Length 901;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSSLYCSDI 476  
Db 390 RSSLYCSDI 398

RESULT 34

09BUM8 PRELIMINARY; PRT; 919 AA.  
AC 09BUM8;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 103.0 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY, RENAL CELL ADENOCARCINOMA;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002477; AAH02477.1; -.  
DR InterPro; IPR001017; El\_dh.  
DR InterPro; IPR000360; Transketolase.  
DR Pfam; PF00676; El\_dehydrog; 1.  
DR Pfam; PF02779; transket\_pyr; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 919 AA; 102969 MW; 938716BD65A1D605 CRC64;

Query Match 0.8%; Score 9; DB 4; Length 919;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSSLYCSDI 476  
Db 378 RSSLYCSDI 386

RESULT 35

096HY7 PRELIMINARY; PRT; 919 AA.  
AC 096HY7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 103.0 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS, AND LEIOMYOSARCOMA;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC007955; AAH07955.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 919 AA; 103042 MW; E07A3137BDD2CBD4 CRC64;

Query Match 0.8%; Score 9; DB 4; Length 919;

Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 RSSLYCSDI 476  
DB 378 RSSLYCSDI 386

RESULT 36

O9JHF4 PRELIMINARY; PRT; 30 AA.  
AC Q9JHF4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE LEPTIN RECEPTOR (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY;  
RA Lindell K., Bennett P.A., Itoh Y., Robinson I.C.A.F., Carlsson L.M.S.,  
RA Carlsson B.;  
RT "5' alternate splicing of leptin receptor transcripts."; Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lindell K., Bennett P.A., Itoh Y., Robinson I.C.A.F., Carlsson L.M.S.,  
RA Carlsson B.;  
RT "5' Alternate splicing of leptin receptor transcripts."; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF139208; AAF63410.1; -  
DR EMBL; AF121331; AAF61190.1; -  
DR EMBL; AF121332; AAF61191.1; -  
DR EMBL; AF121333; AAF61192.1; -  
KW Receptor.  
FT NON\_TER 30 30  
SQ SEQUENCE 30 AA; 3562 MW; E99F8168A5A7AB67 CRC64;

Query Match 0.7%; Score 8; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 VVLLHWEF 15  
DB 8 VVLLHWEF 15

RESULT 37

O9IDZ1 PRELIMINARY; PRT; 103 AA.

AC Q9IDZ1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GLYCOPROTEIN (FRAGMENT).  
OS respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=12814;  
[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-A965C;  
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;  
RT "Influenza and RSV."; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A965C;  
RA Stockton J.D.;

RL Thesis (2000), Department of Life Sciences, Open University, London,  
RL United Kingdom.  
DR EMBL; AJ410801; CAC44814.1; -  
FT NON\_TER 1 1  
FT NON\_TER 103 103  
SQ SEQUENCE 103 AA; 11018 MW; 1FD8CAAC99CA92C1 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 103;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86  
DB 43 FSNLSKTT 50

RESULT 38

O9IDZ0 PRELIMINARY; PRT; 104 AA.  
AC Q9IDZ0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GLYCOPROTEIN (FRAGMENT).  
OS respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=12814;  
[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-A966C;  
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;  
RT "Influenza and RSV."; Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A966C;  
RA Stockton J.D.;  
RL Thesis (2000), Department of Life Sciences, Open University, London,  
RL United Kingdom.  
DR EMBL; AJ410802; CAC44815.1; -  
FT NON\_TER 1 1  
FT NON\_TER 104 104  
SQ SEQUENCE 104 AA; 11036 MW; 6AC87C999F92FF34 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 104;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 FSNLSKTT 86  
DB 45 FSNLSKTT 52

RESULT 39

O9IDU1 PRELIMINARY; PRT; 104 AA.

AC Q9IDU1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GLYCOPROTEIN (FRAGMENT).  
OS respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=12814;  
[1]

RP SEQUENCE FROM N.A.  
RC STRAIN-BIRM/12291/96;  
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;  
RT "Influenza and RSV.";

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

RL (2)  
RN SEQUENCE FROM N.A.  
RC STRAIN-BIRM/12291/96;  
RA Stockton J.D.;  
RL Thesis (2000), Department of Life Sciences, Open University, London,  
United Kingdom.  
DR EMBL; AJ410851; CAC44864.1; -  
FT NON\_TER 1 1  
FT NON\_TER 104 104  
SQ SEQUENCE 104 AA; 11046 MW; 74DA86F1FB54D4AB CRC64;

Query Match 0.7%; Score 8; DB 12; Length 104;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 FSNLSKTT 86  
|||||  
Db 48 FSNLSKTT 55

RESULT 40

ID Q91DU0 PRELIMINARY; PRT; 107 AA.

AC Q91DU0;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE GLYCOPROTEIN (FRAGMENT).  
OS respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=12814;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BIRM/12344/96;  
RA Zambon M.C., Stockton J.D., Clewley J.P., Fleming D.M.;  
RT "Influenza and RSV."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BIRM/12344/96;  
RA Stockton J.D.;  
RL Thesis (2000), Department of Life Sciences, Open University, London,  
United Kingdom.  
DR EMBL; AJ410852; CAC44865.1; -  
FT NON\_TER 1 1  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11537 MW; 252B57C6CCAB5382 CRC64;

Query Match 0.7%; Score 8; DB 12; Length 107;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 FSNLSKTT 86  
|||||  
Db 42 FSNLSKTT 49

RESULT 41

ID Q13894 PRELIMINARY; PRT; 124 AA.

AC Q13894;  
DT 01-JAN-1999 (TREMBlrel. 09, Created)  
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)  
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)  
DE HYPOTHETICAL 14.7 KDA PROTEIN C22A12.02C IN CHROMOSOME I.  
GN SPAC22A12.02C.  
OS Schizosaccharomyces pombe (fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-972;  
RA Pearson D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z99295; CAB16572.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 124 AA; 14736 MW; C93DDEAB43D03544A CRC64;

Query Match 0.7%; Score 8; DB 3; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGLSKNTS 58  
|||||  
Db 45 AGLSKNTS 52

RESULT 42

ID Q9BHJ6 PRELIMINARY; PRT; 184 AA.

AC Q9BHJ6;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE 14-3-3-LIKE PROTEIN (FRAGMENT).  
GN TBS1.  
OS Trypanosoma brucei brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-427;  
RA Hara T., Fukuma T.;  
RT "Trypanosoma brucei 14-3-3 protein homologue."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ306572; CAC35518.1; -  
DR HSSP; P29312; 1A4O.  
DR InterPro; IPR000308; 14-3-3.  
DR pfam; PF00244; 14-3-3; 1.  
DR PRINTS; PR00305; 1433ZETA.  
DR ProDom; PD000600; 14-3-3; 1.  
DR SMART; SM00101; 14-3-3; 1.  
DR PROSITE; PS00796; 1433\_1; 1.  
FT NON\_TER 1 1  
FT NON\_TER 184 184  
SQ SEQUENCE 184 AA; 21422 MW; 6FC796E64689E07A CRC64;

Query Match 0.7%; Score 8; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 655 KKEKNVTL 662  
|||||  
Db 34 KKEKNVTL 41

RESULT 43

ID P70016 PRELIMINARY; PRT; 217 AA.

AC P70016;  
DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE OLFACTORY RECEPTOR (FRAGMENT).  
GN Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.



OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Freitag J.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96112032; PubMed=8845161;  
RA Freitag J., Krieger J., Strotman J., Breer H.;  
RT "Two classes of olfactory receptors in *Xenopus laevis*.";  
RL Neuron 15:1383-1392(1995).  
DR EMBL; Y08347; CAA69633.1; -;  
DR InterPro; IPR00276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KM Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 217 217  
SQ SEQUENCE 217 AA; 24498 MW; 633D47D9F2E30D35 CRC64;

Query Match 0.7%; Score 8; DB 13; Length 217;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524  
Db 35 HSLGSLDS 42

RESULT 44  
O97185 PRELIMINARY; PRT; 222 AA.  
AC O97185;  
DT 01-OCT-2001 (TREMBLrel. 18, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE HYPOTHETICAL PROTEIN CAC1767.  
GN CAC1767.  
OS Clostridium acetobutylicum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
RX MEDLINE=21359325; PubMed=11466286;  
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I., Daly M.J.,  
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
RA Bennett G.N., Koonin E.V., Smith D.R.;  
RT "Genome sequence and comparative analysis of the solvent-producing  
bacterium *Clostridium acetobutylicum*.";  
RL J. Bacteriol. 183:4823-4838(2001).  
DR EMBL; AE007685; AAK79733.1; -;  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 222 AA; 26089 MW; 15DA54912724B246 CRC64;

Query Match 0.7%; Score 8; DB 16; Length 222;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 KNLFRRYN 156  
Db 4 KNLFRRYN 11

RESULT 45  
ID P95945 PRELIMINARY; PRT; 236 AA.  
AC P95945;

DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE ENDONUCLEASE III (DNA ENDONUCLEASE III, PROBABLE) (NTH-1)  
DE (EC 4.2.99.18).  
GN NTH-1.  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Awayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,  
RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
DR EMBL; Y08257; CAA69576.1; -;  
DR EMBL; AE006650; AAK40470.1; -;  
DR HSP; P20625; 2ABK.  
DR InterPro; IPR004035; Endonuclease\_III\_FCL.  
DR InterPro; IPR003265; Endo\_3c.  
DR InterPro; IPR003651; Fes\_bind.  
DR InterPro; IPR003583; HHH\_1.  
DR Pfam; PF00730; HNH-GPD; 1.  
DR SMART; SM00478; ENDO3c; 1.  
DR SMART; SM00525; FES; 1.  
DR SMART; SM00278; Hnh1; 1.  
DR PROSITE; PS00764; ENDONUCLEASE\_III\_1; 1.  
KM Endonuclease; Lyase; Complete proteome.  
SQ SEQUENCE 236 AA; 26843 MW; 6FF5CADB280ECCD2 CRC64;

Query Match 0.7%; Score 8; DB 17; Length 236;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1058 DELKLEG 1065  
Db 122 DELKLEG 129

RESULT 46  
O918C4 PRELIMINARY; PRT; 322 AA.  
ID O918C4;  
AC O918C4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE OLFACTORY RECEPTOR CLASS I.  
GN XB238.  
OS *Xenopus laevis* (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; *Xenopus*.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OLFACTORY EPITHELIUM;  
RA Mezler M., Breer H.;  
RT "Two classes of olfactory receptors: molecular and functional  
studies.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ250750; CAC00721.1; -;  
DR InterPro; IPR00276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.

DR PROSITE: PS50262; G\_PROTEIN\_RECCEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 322 AA; 36469 MW; F42E6A910188F3A3 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 8; DB 13; Length 322;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524  
Db 108 HSLGSLDS 115

RESULT 47

OY18C2 PRELIMINARY; PRT; 325 AA.  
AC OY18C2;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE OLFACTORY RECEPTOR CLASS I.  
GN XB242.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-OLFACTORY EPITHELIUM;  
RA Mezier M., Breer H.;  
RT "Two classes of olfactory receptors: molecular and functional studies.";  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AJ250752; CAC00723.1;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR PROSITE: PS00237; G\_PROTEIN\_RECCEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECCEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 8; DB 13; Length 325;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524  
Db 108 HSLGSLDS 115

RESULT 48

OY19B2 PRELIMINARY; PRT; 326 AA.  
AC OY19B2;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE OLFACTORY RECEPTOR CLASS I.  
GN XB107.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-OLFACTORY EPITHELIUM;  
RA Mezier M., Breer H.;  
RT "Two classes of olfactory receptors: molecular and functional

RT analyses.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ249404; CAB86884.1;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR PROSITE: PS00237; G\_PROTEIN\_RECCEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECCEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 326 AA; 36971 MW; 9475EBF6E5EA5C4 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 8; DB 13; Length 326;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524  
Db 108 HSLGSLDS 115

RESULT 49

OY18C3 PRELIMINARY; PRT; 326 AA.  
AC OY18C3;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE OLFACTORY RECEPTOR CLASS I.  
GN XB239.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-OLFACTORY EPITHELIUM;  
RA Mezier M., Breer H.;  
RT "Two classes of olfactory receptors: molecular and functional studies.";  
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AJ250751; CAC00722.1;  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR PROSITE: PS00237; G\_PROTEIN\_RECCEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECCEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 326 AA; 36923 MW; D575EBFD82F71878 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 8; DB 13; Length 326;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 517 HSLGSLDS 524  
Db 108 HSLGSLDS 115

RESULT 50

OY19B2 PRELIMINARY; PRT; 335 AA.  
AC OY19B2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE US8 MEMBRANE GLYCOPROTEIN E (SORE1 C-TERMINUS GE PARTIAL HOMOLOG).  
GN HVT083 OR SORF1.  
OS Meleagrid herpesvirus 1 (herpesvirus of turkeys).  
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae.  
OX NCBI\_TaxID=37108;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FC126;  
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Rock D.L., Kutish G.K.;  
RT "The genome of turkey herpesvirus.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FC126;  
RA Kingham B.J., Zelnik V., Kopacek J., Majerciak V., Ney E., Chen Y.,  
RA Schmidt C.J.;  
RT "Coding potential of herpesvirus of turkey: comparative genetic  
RT analysis of Marek's disease serologically related viruses.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF291866; AAG45808.1; -  
DR EMBL; AF282130; AAG30104.1; -  
DR InterPro; IPR003404; Herpes\_glycopE.  
DR Pfam; PF02480; Herpes\_gE; 1.  
SQ SEQUENCE 335 AA; 36810 MW; 619E53C08A1D42AD CRC64;

Query Match 0.7%; Score 8; DB 12; Length 335;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 839 DAGLYVIV 846  
|||||||  
Db 155 DAGLYVIV 162

Search completed: May 18, 2002, 07:08:02  
Job time: 240 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 06:55:06 ; Search time 39.35 Seconds  
(without alignments)  
3288.462 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVVLHMEFIVIT.....QTCSQTHKIMENKMDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

A\_Geneseq\_032802:\*

1: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
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9: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
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22: /net/abs06/SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1165	100.0	1165	18	AAW24051 Human WSX receptor
2	1165	100.0	1165	22	AAE12609 Human Ob receptor
3	1165	100.0	1220	18	AAW34500 Obesity receptor D
4	1140	97.9	1165	22	AAE12551 Human Ob receptor
5	1064	91.3	1165	20	AAV13474 Peptide Seq ID No:
6	963	82.7	1165	18	AAW19116 Human Ob receptor.
7	891	76.5	896	18	AAW24052 Human WSX receptor
8	891	76.5	923	18	AAW24053 Human WSX receptor
9	891	76.5	970	18	AAW34499 Obesity receptor C
10	891	76.5	972	18	AAW34497 Obesity receptor A
11	891	76.5	999	18	AAW34498 Obesity receptor B

12	839	72.0	839	18	AAW34502	Obesity receptor p
13	815	70.0	815	20	AAV05701	Human OB receptor
14	798	68.5	804	18	AAW34501	Obesity receptor p
15	742	63.7	883	19	AAW62543	Human ob-receptor
16	681	58.5	896	18	AAW50003	Human OB-R variant
17	681	58.5	904	18	AAW50002	Human OB-R variant
18	681	58.5	958	18	AAW38214	Human OB-R variant
19	681	58.5	958	18	AAW19111	Human OB-R Leptin
20	681	58.5	958	18	AAW19535	Human OB-R Leptin
21	681	58.5	958	18	AAW22773	Human haematopoiet
22	580	49.8	908	17	AAW88912	Haematopoietin rec
23	580	49.8	960	17	AAW88910	Haematopoietin rec
24	580	49.8	960	17	AAW88910	Haematopoietin rec
25	568	48.8	1221	19	AAW62544	Human ob-receptor
26	474	40.7	908	18	AAW19536	Variant form of hu
27	388	33.3	896	18	AAW14841	Human haemopoietin
28	388	33.3	896	18	AAW14841	Amino acid sequenc
29	213	18.3	213	22	AAW63999	Soluble leptin bin
30	42	3.6	805	18	AAW22106	Murine leptin rece
31	42	3.6	842	18	AAW22102	Murine leptin rece
32	42	3.6	892	18	AAW34260	Rat ob receptor is
33	42	3.6	894	18	AAW37338	Ob protein recepto
34	42	3.6	894	18	AAW37337	Murine short form
35	42	3.6	894	18	AAW24064	Murine short form
36	42	3.6	894	18	AAW19114	Murine short form
37	42	3.6	894	22	AAE12608	Rat ob receptor is
38	42	3.6	895	18	AAW34258	Murine leptin rece
39	42	3.6	900	18	AAW22105	Rat ob receptor is
40	42	3.6	1015	18	AAW34259	Rat ob receptor is
41	42	3.6	1162	18	AAW34257	Rat ob receptor is
42	42	3.6	1162	18	AAW23399	Rat ob receptor (f
43	42	3.6	1162	18	AAW23398	Rat ob receptor (w
44	42	3.6	1162	18	AAW19115	Murine long form O
45	42	3.6	1162	20	AAV13473	Peptide Seq ID No:
46	42	3.6	1162	22	AAE12615	Murine long form O
47	33	2.8	783	18	AAW24054	Murine long form O
48	25	2.1	25	22	AAW48723	Murine long form O
49	23	2.0	23	18	AAW32073	Human leptin recep
50	23	2.0	23	20	AAW39406	Human leptin recep
51	23	2.0	581	18	AAW22103	Human leptin recep
52	19	1.6	19	22	AAW37114	Murine leptin rece
53	18	1.5	18	21	AAW57839	Lipid accumulation
54	18	1.5	319	18	AAW22104	Human leptin recep
55	17	1.5	17	21	AAW57840	Human leptin recep
56	17	1.5	17	21	AAW57841	Human leptin recep
57	15	1.5	1146	22	AAE00961	Chicken leptin-rec
58	15	1.3	15	21	AAV57842	Human leptin recep
59	15	1.3	15	22	AAE10383	Human leptin recep
60	15	1.3	15	22	AAE10383	Human leptin recep
61	14	1.2	14	22	AAW64509	Gene 25 human secr
62	14	1.2	14	22	AAW48706	Human leptin recep
63	14	1.2	14	22	AAW48707	Human leptin recep
64	10	0.9	19	18	AAW22109	Leptin receptor an
65	10	0.9	276	18	AAW37420	Leptin receptor C-
66	9	0.8	9	18	AAW23358	Ligand-specific sl
67	9	0.8	9	22	AAE12613	Murine Ob receptor
68	8	0.7	8	22	AAE12612	Murine Ob receptor
69	8	0.7	8	22	AAE12614	Murine Ob receptor
70	8	0.7	58	22	AAW99675	Human excretory re
71	8	0.7	58	22	AAW42490	Human kidney relat
72	8	0.7	217	22	AAW73056	Olfactory receptor
73	7	0.6	17	22	AAW39623	Peptide #7129 enco
74	7	0.6	17	22	AAW60329	Human brain expres
75	7	0.6	17	22	AAW72962	Human bone marrow

ALIGNMENTS

RESULT. 1  
ID AAW24051 standard; Protein; 1165 AA.  
xx

AC AAW24051;  
XX 17-MAR-1998 (first entry)  
XX Human WSX receptor variant 13.2.  
DE  
XX  
KW Human; WSX receptor; variant 13.2; identification; purification;  
KW ligand; activator; antibody; agonist; proliferation; obesity;  
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;  
KW Type II diabetes; polycystic ovarian disease;  
KW cardiovascular disease; osteoarthritis; dermatological disorder;  
KW hypertension; insulin resistance; hypercholesterolaemia;  
KW hypertriglyceridaemia; cancer; cholelithiasis.  
XX  
OS Homo sapiens.  
XX  
PN WO9725425-A1.  
XX 17-JUL-1997.  
XX  
PF 07-JAN-1997; 97WO-US00325.  
XX  
XX 20-JUN-1996; 96US-0667197.  
PR 08-JAN-1996; 96US-0585005.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;  
PI Rodrigues ML;  
XX  
XX MPI; 1997-372864/34.  
DR N-PSDB; AAT85575.  
XX  
XX MSX receptor and related antibodies and ligands - used to develop  
PT products for diagnosis and therapy, e.g. for improving  
PT haematopoiesis or for treating tumours  
XX  
PS Claim 2; Pages 81-85; 219pp; English.  
XX  
CC The present sequence is the human WSX receptor variant 13.2,  
CC which can be used to identify and purify ligands and activators.  
CC An anti-WSX receptor antibody can be used as an agonist to activate  
CC the WSX receptor, leading to enhanced proliferation or  
CC differentiation of a cell expressing the WSX receptor. It can also  
CC be used to decrease body weight and/or fat-depot weight and/or food  
CC intake in an obese mammal. WSX receptor ligands can be used to  
CC enhance proliferation or differentiation of lymphoid, myeloid or  
CC erythroid blood cell lineages. This is useful when a mammal,  
CC especially a human, is suffering from decreased blood cell levels,  
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone  
CC marrow transplantation therapy. It can also be used to repopulate  
CC blood cells in a mammal. The products can also be used to treat,  
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,  
CC polycystic ovarian disease, cardiovascular diseases,  
CC osteoarthritis, dermatological disorders, hypertension, insulin  
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer  
CC and cholelithiasis.  
XX  
SQ Sequence 1165 AA;  
  
Query Match 100.0%; Score 1165; DB 18; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 QOIDANMNIOCWLGKDLKLFICVYESLFKNLFRNYKVHLLVYLPEVLEDSPLVPQKS 180  
DB 121 qqidanwniqcwkkgdtklficyveslfknlfrnykvhllylpevledsplvpqks 180  
QY 181 FQMVHNCNVHECCCLVVPPTAKLNDTLMLCKLITSGVIFQSPMLSVQPIINWVKPDP 240  
DB 181 fgmvhncnsvheccclvvpptaklndtlmlcklitsgvi fgsplmsvqpiinwvkpdp 240  
QY 241 LGLHMETDDGNLKTSSWSPPLVPPLOQVKSSENSTTVIREADKIVATSLLVDSILP 300  
DB 241 lglhmetddgnlktsswspplvpplpqvksensttvireadkivatsllvdsilp 300  
QY 301 GSSYEVQVRGKRLDGPISWSDSTPRVFTQDVLYFPFKILTSVGSNVSFHCYKKEKNI 360  
DB 301 gssyevqvrgrldgpgi swdstprvftqdvlyfppk ltsvgsnvsfhciykkenki 360  
QY 361 VPSKEIWMNNLAERIPQSQYDVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 vpskeiwmnnlaekipqsqydvshvskvtfpflnetkprgkftdaycnehech 420  
QY 421 RYAEIYVIDVNIINISGETDGYLTFTKMTCRMSTSTIOSLAESTLQLRHRSLSYCSIDPSIH 480  
DB 421 ryaelividvniinisetdgy ltkmtcrwststioslaestlqlyrhrrslscsidspsih 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
DB 481 pisepkdcylsdfeyecifqipifllsgytmwirinhs lsglsdspptcvlpdsvvpklpp 540  
QY 541 SSVKAEITINIGLKISWEKVPFPENNLOFOIRGLSGKEVQWKMEVYDASKSVSLPV 600  
DB 541 ssvkaeitiniglkiswekvpfpennlofoirglsgkevqwkmyevyda sksvslpv 600  
QY 601 PDLCAVAVQVRCKRLDGLGYWSMNSNPAYTVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 pdlcavavqvrckrldglgywsnwnspaytvymdikvpmrgp efwriingdtmkkenv 660  
QY 661 TLLMKPLMKNDSLCSQVRVYVNHHTSCNGTSEEDVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 tllwplmkndslcsvqrvynhhtscngtseedvgnhckftflwteqah tvtlainssi 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLASAPPLNSGCIIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 gasvanfnltfswpmkvnivqslasayplnscv i vswilspsdylmyfiemknlne 780  
QY 781 GEIKWLRISSSVKYYIHDFPIPIEKYQESLYPIFMEGVGPKIINSFTODDIEKHQSDA 840  
DB 781 geikwlri ssvkyyihdfpi piekyqeslypifmegv gpk i nsftoddiekhgsda 840  
QY 841 GLYIVIVPVISSILLGLTLLISHQRMKLEWEDVPNPKNSWAQGLNFKQPETFEHLFI 900  
DB 841 glyvivpvi ssillgl tllishqrmklewedvpnpknswaqgl nfkqpetfehlf i 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNDEMPTTVVSLSTTDLKGSVCISDOFN 960  
DB 901 khtasvtcgp ll epetisedisvdtswkn dempttvvslstt dlkgsvcisdo fn 960  
QY 961 SVNFSAEGETEYTEDESQROPFVKYATLISNSKPSSETGEOGLINSVYKCFSSKNSPL 1020  
DB 961 svnfsaegeteytedesqropfvkyatl isnskpssetgeoglin svykcfssknspl 1020  
QY 1021 KDSFNSNWETEAQAFILSDQHPNITSPHLTSEGLDELKLEGNFPENNDKKSIIYYL 1080  
DB 1021 kdsfnssnwet eaqafil s dqhpnit sphl tsegl delkl egnfpenndkksiiyyl 1080  
QY 1081 GVTISIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTBAS 1140  
DB 1081 gvtisikkresgvlltdksrvsc pfpapclftdirv lqdscshfvenninlgtsskktbas 1140  
QY 1141 YMPOFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 ympofotcstqthkimenkmdltv 1165





Db 361 vpskelvwmlaeklpqsgydvsvdhvskvtfflnetkprgkftydavygcnehech 420  
QY 421 RYAEIYVIDVININISCEIDGYLTMTCRWSTSTIOSLAESTLQLRHRSYLCCDIPSIH 480  
Db 421 ryaelvidvniiniscetdgylltkmtrwststioslaestlqlyhrrslycsdipsih 480  
QY 481 PISEPKDCYLQSDCFECIFQPIFLSLGYTMIRINHSLSGLSDSPICVLPQSVYKPLP 540  
Db 481 pisepkdcylqsdgfyecifqipflilsgytmirinhslsldspicvlpqsvykpilp 540  
QY 541 SSVKAEITINIGLKISWEKVPFPENNLOFOIRYGLSGKEVQWKMYEYDAKSVSLPV 600  
Db 541 ssvkaeltiniglkswekvpfpennlqfdiryglsgkevqwkmyevdaksvsllpv 600  
QY 601 PDLCAVAVQVRCKRDLGLGYWSNWSNPATYVMDIKVPMRGPEFWHIIINGDMKKEKNV 660  
Db 601 pdlcavavqvrckridglgywsnwnspatvymdikvpmrgpefwiiingdmkkekvn 660  
QY 661 TLLMKPLMKNDSLCSYQRYVINHTSCNGTSEEDVGNHTKFTFLWTEQAHYTVLAINSI 720  
Db 661 tllwplmkndslcsqryvinhtscngtseedvgnhtkftflwteqahvclainsi 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAPLNSCVIWSILSPSDYKIMFYIEWKNLNE 780  
Db 721 gasvanfnltfswpmkvnivqslaysaplnscvswilspdykimyfiiewknlne 780  
QY 781 GEIKWLRISSSVKYYIHDFPIEIKYQFSLYPIFMEGVGPKTIINSFTQDDIEKHQSDA 840  
Db 781 geikwlri:sssvkyyihdfpieikyqfslpyl fmevgv gpk tiinsftqddiekhqsd 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFWEDEVNPNKCSWAQGLNFOKPEFTEHLFI 900  
Db 841 glyivpvii:sssillgl tllishqrmklfwedevnpnkcswaqgl nfo kpe ftehlfi 900  
QY 901 KHTASVTCGPLLEPITISEDISVTSWKNKDEMPPTVSLSTTDLEKGSVCISDOFN 960  
Db 901 khtasvtcgplllepitisedisvtswnkndempptvslsttdlekgsvcisdofn 960  
QY 961 SVNFSEAGTEVTEDESQROPFVKYATLISNSKPSSETGEEOGLINSSVTKGFSSKNSPL 1020  
Db 961 svnfseagtevytedesqrpfvkatlinsnkspssetgeeglinssvtrkcfssknspl 1020  
QY 1021 KDSFNSWEIEAGAFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNDRKSIYYL 1080  
Db 1021 kdsfnssweieagafilsdqhpniiisphltfseglldellklegnpeenndrkksiyyl 1080  
QY 1081 GVTISIKKRESGVLLDLSKRVSCPPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 gvtisikkresgvlltdksrvscppapclftdirvldscshfvennlnlgtsskktffas 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 ympqfqtcsqtghkimenkmdltv 1165  
RESULT 3  
AAW34500  
ID AAW34500 standard; protein: 1220 AA.  
AC AAW34500;  
XX  
DT 18-MAR-1998 (first entry)  
XX  
DE Obesity receptor D protein.  
XX  
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;  
KW high blood lipid level; obesity; diabetes; high cholesterol level;  
KW weight loss; therapy; weight maintenance.  
XX  
OS 'Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..1165

FT /note- "encoded by AAT98531"  
FT Misc-difference 1166  
FT /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 1169  
FT /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 1187  
FT /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 1207  
FT /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 1.1165  
FT /note- "encoded by AAT98531"  
PN W09725424-A1.  
PD 17-JUL-1997.  
XX  
PE 02-JAN-1997; 97WO-US00128.  
PR 31-DEC-1996; 96US-0774414.  
PR 04-JAN-1996; 96US-0582825.  
XX (AMGE-) AMGEN INC.  
XX Chang M, Fletcher FA, Welcher AA;  
PI N-PSDB; AAT98531.  
DR WPI; 1997-384981/35.  
XX  
XX Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood lipid levels  
XX  
PS Claim 31; Page 76; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor D protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The CC proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 1220 AA;  
Query Match 100.0%; Score 1165; DB 18; Length 1220;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHMERIVITAFNLSTPITPMRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 micqkfcvllhmerivita fnlst p i t p m r f k l s c m p n s t y d y f l p a g l s k n t s n s 60  
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 nghyetapepkfnssgthf snl sk t f h c c e f r s e q d r n c s l c a d n i e g k t f v s t v n s l v f 120  
QY 121 QOIDANWNIQCIWKGDCLKFICYVESLFEKMFERNYKVVHLLYVLPEVLEDSPLVPQKS 180  
Db 121 qoidanwniqciwkgdclkficyveslfe kmf ernykvvhll yvlpevle dsplvpqks 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMWKPPDP 240  
Db 181 fqmvhcnscsvheccclvpvptaklndtlmlckitsggvifosplmsvqipnmwkpdpdp 240  
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPIQYQVYKSENSTTVIREADKIVATSLLVDSILP 300  
Db 241 lglhmeitddgnlkswsppplvpfpilqyqvykysensttvireadkivsatsllvdsilp 300



PR 22-JAN-1996; 96US-0599455.  
PR 26-APR-1996; 96US-0638524.  
PR 03-SEP-1996; 96US-0708123.  
PR 28-MAY-1997; 97US-0864564.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
XX  
DR WPI; 2001-624489/72.  
XX  
XX Identifying compounds for treating body weight disorder, e.g. obesity,  
PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob  
PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test  
PT compound -  
XX  
PS Disclosure; Page -; 109pp; English.  
XX  
XX The patent discloses obese receptor (Obr) proteins and nucleic acids  
CC encoding them. Obr protein participates in the regulation of mammalian  
CC body weight. The invention also relates to a method of identifying  
CC therapeutic compounds for the treatment of a body weight disorder.  
CC The method involves contacting a cell that expresses a mammalian Obr  
CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test  
CC compound. The method is useful for identifying compounds which modulate  
CC Obr gene expression and gene product activity, which can be used as  
CC agents to control body weight particularly as therapeutic agents for  
CC treating body weight disorders, including obesity, cachexia and anorexia.  
CC The present sequence is human Obr protein mutant (Y114F).  
CC Note: This sequence is not shown in the specification but is derived  
CC from the wild-type human Obr protein shown in figure 3 of the  
CC specification (AAE12609).  
XX  
SQ Sequence 1165 AA;

Query Match 97.9%; Score 1140; DB 22; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSPYTPFRFKLSCMPNSTDYDFLLPAGLSKNTSNS 60  
DB 1 micqkfcvllhwehlyvitafnlspyltpfrfklscompnstydyfllpagslksntns 60  
QY 61 NGHYETAVERKNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGTFVSTVNSLVF 120  
DB 61 nghyetavetrknsstghfshnlstktfhccfrseqdrcnslcadniegkftvstvnslvf 120  
QY 121 QOIDANNMIQCMKGLDKLFICYVESLEFKLFRNRYNYKVLHLYLEVLDSPLVPQKGS 180  
DB 121 qqidanmngcwlkgdtklficyveslfnlfrnynykvhllylpevljedsplvpqkgs 180  
QY 181 FOMVHCNCSYHECCCLVPVPTAKLNDTLNCLKITSGVIFOSPLMSVOPINWVKPDDP 240  
DB 181 fgmvhcnscsyheccclvpvptaklndtlmclkitsgvifosplmsvopimwvkpddp 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPPIQYQVKSSENSTTVIREADKIVSATSLVDSILP 300  
DB 241 lglhmeitddgnlkiswsspplvpfpilqyqvksensttvireadkivsatsllvdsilp 300  
QY 301 GSSYEYQVRKRLDGPGLMSDSTPRVFTQDVLYFPFKILTSVGSNVSFHCYKKNKI 360  
DB 301 gssyevqvrkrlldgpglmsdstprvftqdvlyfppkiltsvgsnvsfhcykknki 360  
QY 361 VPSKEIVAMNLAEKIPQSQYDVSDHVSVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 vpskeivamnlakipqsqydvsvdhvsvtffnlnetkprgkftydavycnehechh 420  
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKCRNSTSTIOSLAESTLQRLYHRSLSYCS DIPSIH 480  
DB 421 ryaelyvldvniiniscetdgyltmtcrwststioslaestlqrlhrrslsycsdipsih 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPP 540

DB 481 pisepkdcylqsdgfyecifqpfllslsgytmirinhslsglspptcvlpdsvvklpp 540  
QY 541 SSVKAEITINIGLKISWEKVPPEPNLQFQIRYGLSGKEVQWKNEYVDYDAKSKVSLPV 600  
DB 541 ssvkaeitiniglkiswekvpfpennlqfqiiryglsgkevqwkneyvdakskvslpv 600  
QY 601 PDLCAVYAVQVRKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEVWRIINGDTMKREKNV 660  
DB 601 pdlcavayavvrkrlldglgywsnmsnpaytvvmdikvpmrgpevwrilingdtmkreknv 660  
QY 661 TLLMKPLMKNDSLCSQVRVINHHTSCNGTWSGVDGNHTKFTPLNTEQAHVTVLAINSI 720  
DB 661 tllmkplmkndslcsvqrvinhhtscngtwsedvgnhtkftplnteqahvtvlainsl 720  
QY 721 GASVANFNLTFSWPKSVNIVQSLSAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 gasvanfnltfswpksvniqvslsayplnsscvlyswilspdyklymfiemknlne 780  
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIHMEGVGKPKTNSFTODDIEKHQSDA 840  
DB 781 geikwlri:sssvkryihdhfi:piekyqfsl:ypihme:gv:gpkt:nsft:oddie:khq:sd 840  
QY 841 GLYVIVPVISSSILGLTLLISHORMKLLFWEDEVNPNKNCWAQGLNFQKPTFEHLFT 900  
DB 841 glyvivpvi:sssillgl:tl:lishormkllfwe:devn:pnkncwa:qgl:nf:qkpt:feh:lf 900  
QY 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVSLSTOLEKGSVCISDQFN 960  
DB 901 khtasvtcgp:llpept:ised:isvdt:smknkde:mpptv:slstole:kgs:vcis:dqfn 960  
QY 961 SVNFSEAGTEVTEDEDSORQPEVKYATLLISNKPSETGEEQGLNSSVTKCRSSKN SPL 1020  
DB 961 svnfseagtevt:ed:esor:qpevk:ya:tl:lsnkp:se:tg:eeqgl:nssv:tkcr:sskn:sp 1020  
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIISPHLTPSGLDDELKLEGNFPEENNKKSIYYL 1080  
DB 1021 kdsfnsnsweiea:qaf:il:sdq:hpni:isph:lt:psgl:del:kle:gnf:pe:enn:kk:si:yy 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPAPACFLTDIRVLQDSCSHFVNNINILGTSKKTFFAS 1140  
DB 1081 gvt:si:kkres:gv:lltd:ksrv:sc:pa:pa:cl:ft:dir:vl:qd:scsh:f:vn:nnil:g:tsk:kt:ff 1140  
RESULT 5  
AAV13474  
ID AAV13474 standard; Protein; 1165 AA.  
XX  
AC AAV13474;  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE Peptide Seq ID No: 4 of W09923493.  
XX  
KW leptin; phosphorylated leptin receptor; tyrosine phosphatase 1D; PTP-1D;  
KW modulator; drug; weight loss; adiposity; hypertension; heart disease;  
KW type II diabetes; cancer; AIDS; agriculture.  
XX  
OS Homo sapiens.  
XX  
PN W09923493-A1.  
PN  
PD 14-MAY-1999.  
PD  
XX  
PF 27-OCT-1998; 98WO-US22797.  
PF  
XX  
PR 26-OCT-1998; 98US-0178691.  
PR  
PR 31-OCT-1997; 97US-0961809.  
PR  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
PA  
XX  
PI Friedman JM, Li C;  
PI





FT	Peptide	622..626	receptors"
FT	Peptide	622..626	receptors"
FT	Modified-site	/note- "motif conserved in class F cytokine receptors"	
FT	Modified-site	23	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	41	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
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FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	98	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	187	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	206	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
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FT	Modified-site	/note- "potential N-linked glycosylation site"	
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FT	Modified-site	/note- "potential N-linked glycosylation site"	
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FT	Modified-site	/note- "potential N-linked glycosylation site"	
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FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	624	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	658	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	670	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	688	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	697	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	728	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	750	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
FT	Modified-site	/label- Glycosylation	
FT	Modified-site	/note- "potential N-linked glycosylation site"	
PN	WO9719952-A1.		
XX			
PD	05-JUN-1997.		
XX			
PF	27-NOV-1996;	96WO-US19128.	
XX			
PR	03-SEP-1996;	96US-0708123.	
PR	27-NOV-1995;	95US-0562663.	
PR	04-DEC-1995;	95US-0566622.	
PR	08-DEC-1995;	95US-0569485.	
PR	11-DEC-1995;	95US-0570142.	
PR	28-DEC-1995;	95US-0583153.	
PR	22-JAN-1996;	96US-0599455.	
XX	26-APR-1996;	96US-0638524.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			

[illegible]

Db 661 tllwplmkndslcsvgryinhhtscngtswedvgnhktflwlegahvtvlatnsi 720  
QY 721 GASVANFNLFPSWPMKSVNIQSLAYPLNSSCVIWSIIPSDYKIMYFIIEWKNINED 780  
Db 721 gasvanfnlftswpmkskvniqslaysplnsscviwsiipspdylmyfiiewklned 780  
QY 781 GEIKWLRISSSVKKYVIHDFPIEKYOFSLYPIFMGVGKPKIINSFTQDDIEKHSDA 840  
Db 781 geikwlri:sssvkkyvihdfpiekyqfslpylfmvggkpkinsftqddiekhsda 840  
QY 841 GLYIVPVYIISILLGLTLLISHORMKLFMEDVPNPKNSWAQGLNFQKPEFEEHLEI 900  
Db 841 glyivpvli:ssillgltlilshqrmkklfmedvpnpknswaqglnfqkpetfehlf 900  
QY 901 KHTASVTCGPILLEPETISEDIVDTSWKNKDEMPITYVSLSTTDLEKGSVCISDPN 960  
Db 901 khtasvtcgp1llepetisedivdtswnkndemplyvslsttdlekgsvcisdqfn 960  
QY 961 SVNFSEAEGETEYTEDESQRPVFKYATLISNSKPSSETGEEQGLINSSVTKCFSSKN SPL 1020  
Db 961 svnfseaegetevtyedesqrpvfkyaatlisnkspssetgeegglinsvtkcfsskn spl 1020  
QY 1021 KDSFNSSSWEIEAOAFITLSQHPNITSPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
Db 1021 kdsfnssweieaafitlsqhpnlisphltfseglde1lklegnfppeenndkksityl 1080  
QY 1081 GVTSIKKRESGLVLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
Db 1081 gvtsikkr:esgvlvltDKSRVSCppapclftdirvLQDSCSHFVENNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 ymqfqtctstqthkimenkmdltv 1165  
RESULT 7  
AAW24052  
ID AAW24052 standard; Protein; 896 AA.  
XX  
AC AAW24052;  
XX  
DT 17-MAR-1998 (first entry)  
XX  
DE Human WSX receptor variant 6.4.  
XX  
KW Human; WSX receptor; variant 6.4; identification; purification;  
KW ligand; activator; antibody; agonist; proliferation; obesity;  
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;  
KW Type II diabetes; polycystic ovarian disease;  
KW cardiovascular disease; osteoarthritis; dermatological disorder;  
KW hypertension; insulin resistance; hypercholesterolaemia;  
KW hypertriglyceridaemia; cancer; cholelithiasis.  
XX  
OS Homo sapiens.  
XX  
PN WO9725425-A1.  
XX  
PD 17-JUL-1997.  
XX  
PF 07-JAN-1997; 97WO-US00325.  
XX  
PR 20-JUN-1996; 96US-0667197.  
PR 08-JAN-1996; 96US-0585005.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W,  
PI Rodrigues ML;  
XX  
DR WPI; 1997-372864/34.  
DR N-PSDB; AAT85576.  
XX

PT WSX receptor and related antibodies and ligands - used to develop  
PT products for diagnosis and therapy, e.g. for improving  
PT haematopoiesis or for treating tumours  
XX  
PS Claim 2; Pages 86-89; 219pp; English.  
XX  
CC The present sequence is the human WSX receptor variant 6.4,  
CC which can be used to identify and purify ligands and activators.  
CC An anti-WSX receptor antibody can be used as an agonist to activate  
CC the WSX receptor, leading to enhanced proliferation or  
CC differentiation of a cell expressing the WSX receptor. It can also  
CC be used to decrease body weight and/or fat-depot weight and/or food  
CC intake in an obese mammal. WSX receptor ligands can be used to  
CC enhance proliferation or differentiation of lymphoid, myeloid or  
CC erythroid blood cell lineages. This is useful when a mammal,  
CC especially a human, is suffering from decreased blood cell levels,  
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone  
CC marrow transplantation therapy. It can also be used to repopulate  
CC blood cells in a mammal. The products can also be used to treat,  
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,  
CC polycystic ovarian disease, cardiovascular diseases,  
CC osteoarthritis, dermatological disorders, hypertension, insulin  
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer  
CC and cholelithiasis.  
XX  
SQ Sequence 896 AA;  
Query Match 76.5%; Score 891; DB 18; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHWEFIYVITAFNISTYPTPWRFKLSQMPNPNSTYDYELLPAGLSKNTS 60  
Db 1 micqkfcvllhwefiyvitafnisltpwrfklsqmpnplydyellpaglskntns 60  
QY 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCISCADNIEGKTFVSTVNSLVF 120  
Db 61 nghyetapepkfnssgthf:snlskttfhccfrseqdrnciscadniegktfvstvnslvf 120  
QY 121 QOIDANWNIQWLKGDCLKFICVYESLEKNIERNYNYKVHLLVYLPVLEDSPLVPQKS 180  
Db 121 qoidanwniqwlgdclkficyveslfknlfrnynykvhllvylpveledsplvpqks 180  
QY 181 FQWVHCNCSVHECCGLVVPVPTAKLNDTLMLCKITSGGVTFQSPILNSVQPINMVKPDP 240  
Db 181 fqwvhcnscsvheccclvvpvtaklndtlmlckitsggvtfqspilmsvqpinmvkpdpp 240  
QY 241 IGLHMETDDGNLKISWSSPPLVPPLOQYVKYSENSTVIREADKIVSATSLVDSILP 300  
Db 241 iglhmetddgnlkiswsspplvpploqyvkysenstvir:eadkivsat:slvdsilp 300  
QY 241 Iglhmeitddgnlkiswsspplvfp1qyvkysenstvir:eadkivsat:slvdsilp 300  
QY 301 GSSYEVOVRGKRLDGPGLSDWSTPRVFTQDIVYFPFKILTSVGSNVSEHCYKKEENKI 360  
Db 301 gssyevovrgkrl:dgpglswdstprvftqdivyfpfkiltsvgsnvsehc:ykkeenki 360  
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSQVTEFNLNETKPRGKFTYDAVYCCNEHECH 420  
Db 361 vpskelvwmnlaekipsgydvvdshvskvtffnlnetkprgkft:yavycnehech 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRMSTSTIQSLAESTIQLKVRKSLYCS DIPSIH 480  
Db 421 ryaelyv:ivdininiscetdgy:ltkmtrcmststiqslaest:qlkvrkslycsdipsih 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGLSPPTCVLPDSVVKPLPP 540  
Db 481 pisepkdcylsdfeyecifqpfifilsgytmirinhslsglspp:tcvlpdsvkvkplpp 540  
QY 541 SSVKAEITINIGLKLISWEKVPVPENNLOQIRYGLSGKEVQKMYEYDAKSKSVSLPV 600  
Db 541 ssvkaeitinigllk:iswekvpvpennloqirylsgskevqkmyeydaksksvslpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSMNSNPAYTVVMDIKVPMRGPDEFWRIINGDTMKKEKNV 660

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|||||
Db 601 pdlcavayavqrckridglgyswnsnpaytlvmdikvpmrgpewrlngdtmkkeknv 660
OY 661 TLLMKPLMKNDSLCSQVRVYNHHTSCNGTSEDEGNHTKFTPLWTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDSLCSQVRVYNHHTSCNGTSEDEGNHTKFTPLWTEQAHVTVLAINSI 720
OY 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 gasvanfnltfswpmksvniqslasayplnsscviwswilspdyklyfiemknlne 780
OY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 geikwlriSSsvkkyYhdhfiPiekyfslpifmegvgkpkilnsftqddiekhsda 840
OY 841 GLYVIVPVIISSSILLGTLTLLISHQRMKLFMEDVNPKNCSWAQGLNFOK 891
Db 841 glyvivpviisssillgtlillshqrmklfmedvnpknscswaglnfok 891

```

## RESULT 8

AAW24053

ID AAW24053 standard; Protein; 923 AA.

XX

AC AAW24053;

XX

DT 17-MAR-1998 (first entry)

XX

DE Human WSX receptor variant 12.1.

XX

KW Human; WSX receptor; variant 12.1; identification; purification;

KW ligand; activator; antibody; agonist; proliferation; obesity;

KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;

KW Type II diabetes; polycystic ovarian disease;

KW cardiovascular disease; osteoarthritis; dermatological disorder;

KW hypertension; insulin resistance; hypercholesterolaemia;

KW hypertriglyceridaemia; cancer; cholelithiasis.

KM

XX Homo sapiens.

OS

PN WO9725425-A1.

XX

PD 17-JUL-1997.

XX

PF 07-JAN-1997; 97WO-US00325.

XX

PR 20-JUN-1996; 96US-0667197.

XX

PR 08-JAN-1996; 96US-0585005.

XX

PA (GETH ) GENENTECH INC.

XX

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI

PI Rodrigues ML;

XX

DR WPI: 1997-372864/34.

XX

DR N-PSDB; AAT85577.

XX

XX Claim 2; Pages 89-93; 219pp; English.

XX

XX The present sequence is the human WSX receptor variant 12.1,

CC

CC which can be used to identify and purify ligands and activators.

CC

CC An anti-WSX receptor antibody can be used as an agonist to activate

CC

CC the WSX receptor, leading to enhanced proliferation or

CC

CC differentiation of a cell expressing the WSX receptor. It can also

CC

CC be used to decrease body weight and/or fat-depot weight and/or food

CC

CC enhance proliferation or differentiation of lymphoid, myeloid or

CC

CC erythroid blood cell lineages. This is useful when a mammal,

CC

i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and cholelithiasis.

XX Sequence 923 AA;

Query Match 76.5%; Score 891; DB 18; Length 923;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MICOKFCVLLHMEFIVITAENLSYPTTPWREKISCMPPNSIYDYELLPAQISKNTSNS 60
Db 1 micokfcvllhweflyvitaenlsypttpwrfkiscmpnstlydyellpaqiskntns 60
OY 61 NGHETAVEPKENSSGTHFSNLSTTFHCCFRSEQDRNCSLCADNTEGKTPVSTVNSLVF 120
Db 61 nghetavepkfnssgthfnslnsttfhccfrseqdncslcadnlegkftvstvnslvf 120
OY 121 QOIDAMNIIQCWLTGDIKLFICYVESLFKNLFRNRYKVHLLVYLPVLEDSPLVPQKGS 180
Db 121 qoidanwniqcwlkgdlkfcyveslfknlfrnykvhllyvpvleedsplvpqkgs 180
OY 181 FOMVHCNCSVHECECTVPPPTAKLNDTLMLCKITSGGVIFQSPINSVOPINWVKPDP 240
Db 181 fgmvhcnscvhecectlvppptaklndtlmlckltsggvifqspimsvqplnmvdkpdp 240
OY 241 LGLHMEITDDGNLKISWSSPPLVPFPLQYQVYSENSTTVIREADKIVSATSLVDSILP 300
Db 241 lglhmeitddgnlkiswsspplvplqyqvyseunsttvireadkivsatsllvdsilp 300
OY 301 GSSYEVOVRGKRLDGPQISWSDSTPRVFTTQDVITFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 gssyevqvrqkrlidgpgiwsdstprvfttqdvlyfpklltsvgsnvsfhcilykknki 360
OY 361 VPSKEIWMNMNLAEKIPQSOQYDVVSDHVSQVTFEFLNETKPRGKIYDAVVCNEHECHH 420
Db 361 vpskeiwmnmnlaekipqsgydvvsdhvskvtfeflnetkprgkilydavycnehechh 420
OY 421 RYAEIYVIDVININISCTEDGYLTMTCRMWSTSTIOSLAESTLQLRHSSSLXCSIDIPSIH 480
Db 421 ryaelyvldvnniscetdgyltmtcrwststioslaestlqlrhrssslxcsidipsih 480
OY 481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMWIRINHSLSGLCSPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylsdfeyecifqpfllsgytmwirinhsisglslsptcvlpdsvvpkplpp 540
OY 541 SSVKAEITINIGLKISWEKVPPEPENNLOFQIRYGLSGKEVQKNEYVDASKSVSLPV 600
Db 541 ssvkaeitiniglkiswekvppeennlofqirylsgkevqwkneyvdasksvslpv 600
OY 601 PDLCAVAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavayavqrckridglgyswnsnpaytlvmdikvpmrgpewrlngdtmkkeknv 660
OY 661 TLLMKPLMKNDSLCSQVRVYNHHTSCNGTSEDEGNHTKFTPLWTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDSLCSQVRVYNHHTSCNGTSEDEGNHTKFTPLWTEQAHVTVLAINSI 720
OY 721 GASVANFNLTFSWPMKSVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 gasvanfnltfswpmksvniqslasayplnsscviwswilspdyklyfiemknlne 780
OY 781 GEIKWLRISSSVKKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 geikwlriSSsvkkyYhdhfiPiekyfslpifmegvgkpkilnsftqddiekhsda 840
OY 841 GLYVIVPVIISSSILLGTLTLLISHQRMKLFMEDVNPKNCSWAQGLNFOK 891

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Db      841 glyvivpviissilllgtllishqrmkklfwevdpnpkncswagjlnfqk 891
RESULT  9
AAW34499
ID      AAW34499 standard; protein; 970 AA.
XX
AC      AAW34499;
XX
DT      18-MAR-1998 (first entry)
XX
DE      Obesity receptor C protein.
XX
KW      Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW      high blood lipid level; obesity; diabetes; high cholesterol level;
KW      weight loss; therapy; weight maintenance.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Misc-difference 959
FT      /label= unknown
FT      /note= "encoded by stop codon"
XX
PN      WO9725424-A1.
XX
PD      17-JUL-1997.
XX
PF      02-JAN-1997; 97WO-US00128.
XX
PR      31-DEC-1996; 96US-0774414.
PR      04-JAN-1996; 96US-0582825.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Chang M, Fletcher FA, Welcher AA;
XX
DR      MPI: 1997-384981/35.
DR      N-PSDB; AAT98530.
XX
PT      Obesity protein receptor(s) and related DNA - used to treat weight
PT      disorders, e.g. obesity, diabetes and high cholesterol or blood
PT      lipid levels
XX
PS      Claim 2; Page 72; 151pp; English.
XX
CC      This sequence represents the obesity (OB) receptor C protein. This
CC      sequence has one or more of the biological properties of naturally
CC      occurring OB receptor protein. The OB receptor proteins and OB
CC      receptor/OB protein complexes are used for the treatment of obesity,
CC      diabetes, high blood lipid levels and high cholesterol levels. The
CC      proteins may also be used to treat an individual for weight loss or
CC      weight maintenance required for purely cosmetic purposes.
XX
SQ      Sequence 970 AA;

Query Match      76.5%; Score 891; DB 18; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Endels 0; Gaps 0;
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QY      181 FQMVHCNCSVHECCCLVVPVPAKLNDFLLMCLKITSGGVIFCSPLMSVQPINMKPDP 240
Db      181 fgmvhcnscsvhecceclvpvptaklndflmlclkitsggvifcsplmsvqpinmvpdp 240
QY      241 LGTHMETDDGNLKISWSSPPLVPEPLOYOVKYSSENSTTVIREADKIVSATSLVDSILP 300
Db      241 lglthmetddgnlkiswsspplvpfplogvkvysensttvireadkivsatsllvdsilp 300
QY      301 GSSYEVOVRGRLLDGPGLMSDWSRPVFTTODVIFYFPKILFEVGSNVSFHCYKKENKI 360
Db      301 gssyevovrgkrlldgpplmsdwsrprvfttoddvifyfpkillevgnsvshciykkenk1 360
QY      361 VPSKEIYVWNNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRCKFTYDAVYCCNEHECHN 420
Db      361 vpskeiyvwmnlaekipqsgydvvsdhvskvtfflnetkprgkftydavycnehechn 420
QY      421 RYAEIYVIDVININISCEFDGYLTMTCRWSTSTIQSLAESTLCLRHKSSLYCSDIPSIH 480
Db      421 ryaelyvldvininiscefdgyltkmtcrwststiqslaestlclrhksslycsdipsih 480
QY      481 PISEPKCYLQSDGFYECIFQPIFILSGYTMIRINHSLSGLSPPTCVLPDSVVKPLPP 540
Db      481 pisepkcyiqsdgfyecifqipifilsgytmirinhslsglsppctcvlpdsavvkplpp 540
QY      541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWKNVEYDAKSKSVSLPV 600
Db      541 ssvkaeitinigllkiswekvpfpennloqirylsgskewqwnyevydaksksvslpv 600
QY      601 PDLCAVAVQVRCRRLDGLGYSWNSNDAYTVMDIKVPMRCPFEFWRILINGDTMKKEKNV 660
Db      601 pdlcavayavrcrkrlldglgyswnsndaytlvmdikvpmrgpfeffwrlingdtmkkeknv 660
QY      661 TLLWKPFLMKNDSLCSQVRYVINHHTSCNGTWSERVEDVGNHTKFTFLMTQAHVTVLAINSI 720
Db      661 tllwkpflmkndslcsvqryvinhhtscngtwservedvgnhtkftflwteqahvtvlainsi 720
QY      721 GASVANENLTFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPEDYKLMYFIEMKNLNE 780
Db      721 gasvanenlftspmskvnivqslsavplnsscvivswilspedyklymfiemknlne 780
QY      781 GEIKWLRISSSVKKYIYIHDFIPRIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db      781 geikwlrisssvkkyyihdfipriekyqfslypifmegvgkpkilnsftqddiekhsda 840
QY      841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSKACGLNFOK 891
Db      841 glyvivpviissilllgtllishqrmkklfwevdpnpkncswagjlnfqk 891

RESULT  10
AAW34497
ID      AAW34497 standard; protein; 972 AA.
XX
AC      AAW34497;
XX
DT      18-MAR-1998 (first entry)
XX
DE      Obesity receptor A protein.
XX
KW      Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW      high blood lipid level; obesity; diabetes; high cholesterol level;
KW      weight loss; therapy; weight maintenance.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Misc-difference 897
FT      /label= unknown
FT      /note= "encoded by stop codon"
FT      Misc-difference 919
FT      /label= unknown
FT      /note= "encoded by stop codon"
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FT Misc-difference 948 /label- unknown  
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FT /note- "encoded by stop codon"  
FT Misc-difference 971 /label- unknown  
FT /note- "encoded by stop codon"  
PN WO9725424-A1.  
PD 17-JUL-1997.  
PF 02-JAN-1997; 97WO-US00128.  
PR 31-DEC-1996; 96US-0774414.  
PR 04-JAN-1996; 96US-0582825.  
XX (AMGE-) AMGEN INC.  
XX Chang M, Fletcher FA, Welcher AA;  
XX WPI; 1997-384981/35.  
DR N-PSDB; AAT98528.  
XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight  
PT disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels  
XX  
PS Claim 1; Page 64; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor A protein. This  
CC sequence has one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 972 AA;  
  
Query Match 76.5%; Score 891; DB 18; Length 972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MICQKFCVLLHMEFIYVITAENLSYPTPWRFRKLSGMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 micqkfcvllhweiflyitainlsyptpwrfrklscompnstydyflpagslksntns 60  
  
QY 61 NGHYETAVEPKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
Db 61 nghyetavepkfnsgthfnskskttfhccfrseqdfrncslcadniegkltfvstvnslvf 120  
  
QY 121 QQIDANWNTQGWLGKDLFCYVESLFRNRYNYKVHLLVLPVLELDSPLVPQGS 180  
Db 121 qqidanwniqgwlgkdlfcyveslfrnrynykvhllylpevledsplvpqgs 180  
  
QY 181 FQMVHNCNVHECCFVLPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINWKPDP 240  
Db 181 fqmvhncnsvheccfvlvpvtaklndtlmlckitsgvifqspplmsvqpinwkpdp 240  
  
QY 241 IGLHMEITDDGNLKSMSPPPLVPFPLQYQVKSSENSTVIREADKIVSATSLLVDSILP 300  
Db 241 iglhmeitddgnlksmsppplvpfpplqyqvksenstlvireadkivsatsllvdsilp 300

QY 301 GSSYEYQVRGKRLDGPGLNSDMSTPRVFTTQDVITYFPFKILTSVGSNVSEFCIYKKEKI 360  
Db 301 gssyevqvrgrldgpglndstprvfttqdvityfpfkiltsvgsnvsfchlykkenki 360  
  
QY 361 VPSKEIWMNLAEKIPQSDYVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNHECHH 420  
Db 361 vpskeiwmnlaekipqsdvsvdhvskvtfeflnetkprgkftydavyccnhechh 420  
  
QY 421 RYAEIVIDVNNINISCEFDGVLTKMTCRWSTSTIQSLAESTLQLRYHRSLSYCDIPSIH 480  
Db 421 ryaelvidvnniniscefdgvltkmtcrwststiqslaestlqlryhrslycdipsih 480  
  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLCSPTCVLPDSVVKPLPP 540  
Db 481 pisepkdcylqsdgfyecifqpifllsgytmirinhslsglsdpsptcvlpdsvvkplpp 540  
  
QY 541 SSVKAEITINIGLKSISWEKRVFPENNLOFQIRYGLSGKEVQWKMFEVYDAKSVSLPV 600  
Db 541 ssvkaeitiniglkiswekrfvpennlofqiroyglsgkevqwkmyevydaaksvglpv 600  
  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPETWRIINGDTMKKEKNV 660  
Db 601 pdlcavyavvrckrldglgywsnmsnpaytyvmdikvpmrgpetwriingdtmkkeknv 660  
  
QY 661 TLLMKPLMKNDLSCVQGRVINHHTSCNGTSEDEYGNHTKFTPLITEQAHVYVLAINSI 720  
Db 661 tllmkplmkndlscvqgrvinhhtscngtsedevgnhtkftpliteqahvylvlainsi 720  
  
QY 721 GASVANFNLTFSWPMKYNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 gasvanfnltfswpmkynivqslayplnsscvivswilspdyklymyfiemknlne 780  
  
QY 781 GEIKWLRISSSVKKYVYIHDHFIPIEKYQFSLYPIFMEGVGKPKI::NSFTQDDIEKHQSDA 840  
Db 781 geikwlri:sssvkkyvindhfi:piekyqfsl:ypifmegvgkpk:instqdd:iekhsda 840  
  
QY 841 GLYVIVPVISSSILLGTLISHORMKKLFWEDEVNPKNCSWAQGLNPOK 891  
Db 841 glyvivpvi:sssillgtllshor:mkklfwedev:npkncswaqln:po 891  
  
RESULT 11  
AAW34498  
ID AAW34498 standard; protein; 999 AA.  
XX AC AAW34498;  
XX  
DT 18-MAR-1998 (first entry)  
XX  
DE Obesity receptor B protein.  
XX  
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;  
KW high blood lipid level; obesity; diabetes; high cholesterol level;  
KW weight loss; therapy; weight maintenance.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 905  
FT /label- unknown  
FT /note- "encoded by stop codon"  
FT Misc-difference 933  
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FT /label- unknown  
FT /note- "encoded by stop codon"  
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FT /label- unknown  
FT /note- "encoded by stop codon"  
PN WO9725424-A1.  
XX



PD 17-JUL-1997.  
XX 02-JAN-1997; 97WO-US00128.  
XX 31-DEC-1996; 96US-0774414.  
PR 04-JAN-1996; 96US-0582825.  
XX (AMGE-) AMGEN INC.  
XX Chang M, Fletcher FA, Welcher AA;  
XX WPI: 1997-384981/35.  
DR N-PSDB; AAT98529.  
XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight  
PT disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels  
XX  
PS Claim 2; Page 68; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor B protein. This  
CC sequence has one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 999 AA;

Query Match 76.5%; Score 891; DB 18; Length 999;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICOKFCVLLHMEFIVITAFNLSTPTTPWRFKLSMPNSTYDIFLLPAGLSKNTSNS 60  
DB 1 micqkfcvllhweilvitafnlstpttpwrfklsmpnstydyfllpaglskntns 60  
QY 61 NGHETAVEPKENSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 nghetavepkfnsstgthfslsktffhccfrseodrnscicadniegkftfstvnslvf 120  
QY 121 QOIDANMNIOCWKLKDLKLFICVESLEKFLFRNYNYKVLHLYLPEVLEDSPLVPQKS 180  
DB 121 qqidanwniqcwlkgdtklficyveslfnlfrnynykvhlylpevledsplvpqks 180  
QY 181 FQVHGNCSVHECCCLVPPFARLNDTLMLCLKITSGGVTFQSPFLMSVQPINMVKPPDP 240  
DB 181 fgmvhcnscvheccclvppfarklndtlmlclkitsggvtfqspflmsvqpinmvpkppdp 240  
QY 241 LGLHMEITDDGNLKSWSPPVFPLOQOVKYSNSTVIREADKIVSATSLVDSILP 300  
DB 241 lglhmeitddgnlkiswsspplvfploqovkysenstvirreadkivatsllvdsilp 300  
QY 301 GSSIEVOYRGRRLDGPIMSDMSTPRVFTTODVIYFPPKILTSVGSNVSPHCITYKKENKI 360  
DB 301 gssyevqyrgkrlldgpimsdmstprvfttqdvlyfppkiltsvgsnvshciyksenki 360  
QY 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGFTYDAVYCCNEHECHH 420  
DB 361 vpskeiyvmmnlakqipsoqydvvsdhvskvtfpflnetkprgkfttydavycnehechh 420  
QY 421 RYAEIYVIDVININISCTDGYLTKMTCRMSTSTIOSLAESTIOLRYHRSLSYCSIDIPSIH 480  
DB 421 ryaelyvidvininiscetdgyltkmtcrwststioslaestiolryhrrslycsdipsih 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
DB 481 pisepkdcylqsdgfyecifqpfiflisgytmwirinhsisglspptcylpdsvvpkplpp 540  
QY 541 SSVKAEITINIGLLKISWEKVPPEENNLOFOIRYGLSGKEVQWKEVYDAKSKSVSLPV 600  
DB 541 ssvkaeltiniglkliswekvpfpennlqfdiryglsgkevqwkmyevydaaksksvslpv 600

DB 541 ssvkaeltiniglkliswekvpfpennlqfdiryglsgkevqwkmyevydaaksksvslpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSMSMNSNPATVVMMDIKVPMRGPEFWRIINGDTMKREKNV 660  
DB 601 pdlcavyavqvrckrldglgysmnsnpaytvmmdikvpmrgpefwrilingdtmkreknv 660  
QY 661 TLMLKPLMKNDLSCSVQRYVINHHTSCNGTWSMEDVGNHTRFTFLTEQAHVTYLAANSI 720  
DB 661 tlmlkplmkndslscsvqryvinhhtscngtwsmedvgnhtrftflteqahvtvlaansi 720  
QY 721 GASVANFNLFSPWPMKVNIVOSLSAYPLNSSCVIWSIWSIPSDYKLMYFIIEWKNLNE 780  
DB 721 gasvanfnlftswpmkvnivqslsayplnsscvlswslspsdyklymfiiwknlned 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 gelkwlrissvkkyyihdhfipiekyslypifmegvgkpkinsftoddiekhsda 840  
QY 841 GLYIVPVITISSIILLGTLLISHQRMKKLFWEDVPNPKNCWAGGLNFQK 891  
DB 841 glyivpvitissillgtllishqrmkklfwedvpnpknswagglnfqk 891

RESULT 12

AAW34502  
ID AAW34502 standard; protein: 839 AA.  
XX  
AC AAW34502;  
XX  
DT 18-MAR-1998 (first entry)  
XX  
DE Obesity receptor protein.  
XX  
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;  
KW high blood lipid level; obesity; diabetes; high cholesterol level;  
KW weight loss; therapy; weight maintenance.  
XX  
OS Homo sapiens.  
XX  
PN W09725424-A1.  
XX  
PD 17-JUL-1997.  
XX  
PF 02-JAN-1997; 97WO-US00128.  
XX  
PR 31-DEC-1996; 96US-0774414.  
PR 04-JAN-1996; 96US-0582825.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Chang M, Fletcher FA, Welcher AA;  
XX  
DR WPI: 1997-384981/35.  
DR N-PSDB; AAT98532.  
XX  
PT Obesity protein receptor(s) and related DNA - used to treat weight  
PT disorders, e.g. obesity, diabetes and high cholesterol or blood  
PT lipid levels  
XX  
PS Disclosure; Page 82; 151pp; English.  
XX  
CC This sequence represents the obesity (OB) receptor protein. This  
CC sequence was used to identify the variants shown in AAW34497-W34501. The  
CC variants have one or more of the biological properties of naturally  
CC occurring OB receptor protein. The OB receptor proteins and OB  
CC receptor/OB protein complexes are used for the treatment of obesity,  
CC diabetes, high blood lipid levels and high cholesterol levels. The  
CC proteins may also be used to treat an individual for weight loss or  
CC weight maintenance required for purely cosmetic purposes.  
XX  
SQ Sequence 839 AA;

Query Match 72.0%; Score 839; DB 18; Length 839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 micqkfcvllhwefiyvitafnlspitpwrfklscompnstydyfllpaglskntsns 60  
QY 61 NGHETAVEPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSIVF 120  
Db 61 nghetavepkfnssgthfnslnskttfhccfrseqdrcnscadniegkctfvstvnslvf 120  
QY 121 QOIDANWNIQCMWLGDKLFLCYVESLEFKNLFRNRYNRYKHLVLPVLEDSPLVPQGS 180  
Db 121 qqidanwniqcmwlgdklflcyveslfnlfrnyrykhlvlpvledsplvpqgs 180  
QY 181 FQWVHCNCSVHECCCLVPVPAKLNDTLLMCLKITSGCVTFQSPPLMSVQPINMVKPDP 240  
Db 181 fqwvhcnscvheccclvpvpaklndtllmclkitsgcvtfqspplmsvqpinmvpkdp 240  
QY 241 LGLHMEITDDGNLKLISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLSLVDSILP 300  
Db 241 lglhmeitddgnlkliswssplvpflpqyqvkysenstcvireadkivsatsllvdsilp 300  
QY 301 GSSYEVQVRGKRLDGPFGIMSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCITYKKEKI 360  
Db 301 gssyevqvrgrldgpgfswdstprvftqdvlyfppkiltsvgsnvsfhciykkenki 360  
QY 361 VPSKEIVWMNLAEKIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHCCH 420  
Db 361 vpskeivwmnlaekipqsgdyvsvdhvskvtfenlnektprgkftydavycnechh 420  
QY 421 RYAEIYVIDVININISCEFDGILTMTCRMSTSTIQSLAESTLQRLRYHRSSLYCSIDPSIH 480  
Db 421 ryaelyvldvininscetdgyiltmcrwststiqslaestlqrlryhrsslycsidpsih 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSLSDPTCVLPDSVYKPLPP 540  
Db 481 pisepkdcylqsdgyefecifqpfllsgytmwirinhslsldptcvlpdsvykplpp 540  
QY 541 SSVKAEITINIGLKLISWEKPYEPENNLOFOIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600  
Db 541 ssvkaeitinigllkliswekpyepennlofoirylsglsgkevqwkmyevydaaksksvslpv 600  
QY 601 PDLCAVYAVQVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRTINGDTMKKEKNV 660  
Db 601 pdlcavayavvrckrldglgyswnsnpatyvmmdikvpmrgpewrtindtmkkeknv 660  
QY 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTSESDVGNHTKFTFLMTEQAHTVYLAINSI 720  
Db 661 tllmkplmkndslcsvqryvinhtscngtsestdvgnhtkftflwteqahyvylainsi 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSWILSPSDYKLMYFIIEKNLNEED 780  
Db 721 gasvanenlftspmskvnivqslayplnsscvlswilspsdylmlyfiieknlned 780  
QY 781 GEIKWLRISSSVKKYVTHDHFPIPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHQSD 839  
Db 781 geikwlri:ssvkkylthdhfipiekyqslypifmegvgkpkiiinsftqddiekhqsd 839

RESULT 13  
ID AAY05701 standard; Protein: 815 AA.  
XX AAY05701;  
XX 19-JUL-1999 (first entry)  
DE Human OB receptor extracellular domain.  
XX TRL: TNF receptor-like; tumour necrosis factor receptor; human;  
KW signal transduction; cell differentiation; prostate cancer;

KW inflammation; arthritis; diabetes; insulin resistance; diagnosis;  
KW therapy; OB receptor; leptin receptor.

OS Homo sapiens.  
XX WO915663-A1.  
XX 01-APR-1999.  
XX 25-SEP-1998; 98WO-US20219.  
XX 17-MAR-1998; 98US-0042785.  
XX 26-SEP-1997; 97US-0938896.  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
XX Busfield SJ;  
XX WPI; 1999-254712/21.  
XX Nucleic acid encoding tumor necrosis factor receptor-like protein  
XX Example 8; Page 82-83; 170pp; English.

CC The present sequence represents the extracellular domain of the  
CC human OB receptor (leptin receptor). A fusion protein comprising  
CC the mouse OB receptor signal sequence, the human OB receptor  
CC extracellular domain and the human IgG Fc domain has been  
CC constructed. The ability of the OB receptor signal peptide to  
CC direct secretion of the fusion protein in transfected HEK 293 cells  
CC was compared to the ability of the human TRL signal peptide (see  
CC AAY05696) to direct secretion of a similar construct. The results  
CC showed that the heterologous TRL signal elevated the amount of  
CC transfected cells approximately 10-fold. TRL is a novel member of  
CC the tumour necrosis factor receptor superfamily. The invention  
CC provides full-length human and murine TRL proteins (see AAY05695-97),  
CC TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as  
CC well as TRL nucleic acids (see AAX25320-22), recombinant expression  
CC vectors, host cells and non-human transgenic animals. TRLs are  
CC regulators or modulators of cellular signal transduction, cellular  
CC proliferation or differentiation, cell survival and apoptosis,  
CC immune system cells, and cells involved in insulin resistance or  
CC the diabetic response.

SO Sequence 815 AA;  
Query Match 70.0%; Score 815; DB 20; Length 815;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 NLSYPTPWRFKLSGMPNSTYDYFLPAGLSKNTSNGHYETAVEPKFNSSGTHFSNL 82  
Db 1 nlsyptpwrfklscompnstydyfllpaglskntsnghyetavepkfnsgthfsl 60  
QY 83 SKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVFOQIDANWNIQCMWLGDKLFLIC 142  
Db 61 sktfhccfrseqdrcnscadniegkctfvstvnslvfqidanwniqcmwlgdklflfc 120  
QY 143 YVESLFKNLFRNRYNRYKHLVLPVLEDSPLVPQKGSFQWVHCNCSVHECCCLVPVPT 202  
Db 121 yveslfknlfrynrykhlvlpvledsplvpqkgsfqwvhcnscvheccclvpvpt 180  
QY 203 AKLNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDPPLGLHMEITDDGNLKSWSPP 262  
Db 181 akldntllmclkitsgvifqspplmsvqpinmvpkdpplglhmeitddgnlkswspp 240  
QY 263 VPFLQYQVKSSENSTVIREADKIVSATSLSLVDSILPGSSYEVQVRGKRLDGPFIWSDW 322  
Db 241 vpflpqyqvkysenstcvireadkivsatsllvdsilpgssyevqvrgrldgpgfswd 300  
QY 323 STPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKEKNIVPSKEIVWMNLAEKIPQSOYD 382

Db 301 stprvfttqdvlyfppkiltsvgsnvsfhciykkenklypskeiwwmmlaekipsgyd 360  
QY 383 VVSDHVSQVTFNFNLNETKPRGKFTYDAVCCNEHECHHRYAELVIDVININISCETDYL 442  
Db 361 vvsdhvskvtffnlnetkprgkftydavccnehechhryaelvidvininiscetdyl 420  
QY 443 TKMTCRWSTSTIOSLAESTIQURHRSLSLYCSDIPSIHPRISEPKDCYLQSDGFYECTQP 502  
Db 421 tkmtcrwststiqslaestlqlrhrsslycsdipshpripsepckdcylqsdgfyecitqp 480  
QY 503 IFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPY 562  
Db 481 ifllsgytmwirinhslsgsdspptcvlpdsvvkplppssvkaeitiniglkiswekpy 540  
QY 563 FPENNLOFOIRYGLSGKEVQMKMEYVDAAKSKSVSLPVPDLCAVAVAVQVRCRDLGLGYW 622  
Db 541 fpennlqfdiryglsgkevqmkmyevydaksksvslpvpdlcavayavqvrckrldglgyw 600  
QY 623 SNMSPATYTVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVIN 682  
Db 601 snmnpaytlvmdikvpmrgpewrlingdtmkkekntllmkplmkndslcsvqryvin 660  
QY 683 HHTSCNGTWESEVGNHTKFTFLWTEQAHVTYVLAINSIGASVANFNLTFSWPMKVNIVQ 742  
Db 661 hhtscngtwsedvgnhtkftflwteqahvtvlnslgsvanfnltfswpmkvnivq 720  
QY 743 SLTAYPLNSSCVIVSWILSPSDYKIMYFIEMKLNLEDGFIKWLRISSSVKKYYIHDFI 802  
Db 721 sltayplnsscvivswilspdyklimyfiemklnledgfkwlrlissvkkyyihdfi 780  
QY 803 PIEKQFSLYPIFMEGVGKPKIINSFTQDDIEKHQ 837  
Db 781 piekqfslypifmegvgkpklnstftqddiekhq 815

RESULT 14

AAW34501  
ID AAW34501 standard; protein; 804 AA.

XX AC AAW34501;

XX DT 18-MAR-1998 (first entry)

XX DE Obesity receptor protein splice variant.

XX KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

KW high blood lipid level; obesity; diabetes; high cholesterol level;

KW weight loss; therapy; weight maintenance; splice variant.

XX OS Homo sapiens.

XX PN W09725424-A1.

XX PD 17-JUL-1997.

XX PF 02-JAN-1997; 97WO-US00128.

XX PR 31-DEC-1996; 96US-0774414.

XX PR 04-JAN-1996; 96US-0582825.

XX PA (AMGE-) AMGEN INC.

XX PI Chang M, Fletcher FA, Welcher AA;

XX DR WPI; 1997-384981/35.

XX DR N-PSDB; AAT98534.

XX PT Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol of blood lipid levels

XX PS Claim 4; Page 89; 151pp; English.

XX CC This sequence represents a natural splice variant of the obesity (OB) receptor protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

XX SQ Sequence 804 AA;

Query Match 68.5%; Score 798; DB 18; Length 804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOQFCVLLHMEFIYVITAFNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 micqfcvllhweifyvitafnlsypitpwrfklscompnstydyfllpaglskntsns 60

QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGTFVSTVNSLYF 120  
Db 61 nghyetavepkfnssgthfnslnsktfhccfrsedrncslcadniegktfstvstnslyf 120

QY 121 QQIDANWNIQCWLKGLDLKFLICYESLFLKLFNRYNKVHLVYLPEVLEDSPLVPQKS 180  
Db 121 qqidanwniqcwlkglkflfcyesslflklnfrnykvhllylpevledsplvpqkgs 180

QY 181 FQWVHCNCSVHECCCLVPPVPAKNDTFLMLCKITSGGVIFCSPLMSVQPINMKPDP 240  
Db 181 fqwvhcnscsvheccclvpvptakndtflmlckitsggvifcspmlsvqipnmkpdpp 240

QY 241 LGTHMETDDGNLKLISWSSPPLVPPLOQYQVKSSENSTVTRBAUKTVSATSLVDSILP 300  
Db 241 lgthmetddgnlkliswsspplvpploqyqvksenstvtreadkivsatsllvdsilp 300

QY 301 GSSYEYQVRGKRLDGPGIWSOWSTPRVFTTODVYIFPPKILTSVGSNVSFHCYKKEKNT 360  
Db 301 gssyeqvrgkrlpgpwwsdwstprvfttqdvlyfppkiltsvgsnvsfhciykkenk 360

QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSQVTFNFNLNETKPRGKFTYDAVCCNEHECHH 420  
Db 361 vpskeiwwmmlaekipsgydavsdhvsqvtffnlnetkprgkftydavccnehechh 420

QY 421 RYAEIYVIDVININISCETDGYLTKMTCRWSTSTIOSLAESTIQURHRSLSLYCSDIPSIH 480  
Db 421 ryaelvidvininiscetdgyltkmtcrwststiqslaestlqlrhrsslycsdipsh 480

QY 481 PISEPKDCYLQSDGFYECTIQURHRSLSLYCSDIPSIH 540  
Db 481 pisepkdcylqsdgfyecitqpirlrhrsslycsdipsh 540

QY 541 SSVKAEITINIGLKISWEKPYFPENNLOFOIRYGLSGKEVQMKMEYVDAAKSKSVSLPV 600  
Db 541 ssvkaeitiniglkiswekpyfpennlqfdiryglsgkevqmkmyevydaksksvslpv 600

QY 601 PDLCAVAVQVRCRDLGLGYWSNMSNPATYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 pdlcavayavrcrldglgywsnmsnpaytlvmdikvpmrgpewrlingdtmkkekvn 660

QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWESEVGNHTKFTFLWTEQAHVTYVLAINSI 720  
Db 661 tllmkplmkndslcsvqryvinhhtscngtwsedvgnhtkftflwteqahvtvlnslsi 720

QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKIMYFIEMKLNLED 780  
Db 721 gasvanfnltfswpmkvnivqslayplnsscvivswilspdyklimyfiemklnled 780

QY 781 GEIKWLRISSSVKKYYIH 798  
Db 781 geikwlrlissvkkyyih 798

RESULT 15  
AAW62543  
ID AAW62543 standard; protein; 883 AA.  
XX  
AC AAW62543;  
XX  
DT 12-OCT-1998 (first entry)  
XX  
DE Human ob-receptor deletion mutant D(41-322).  
XX  
KW ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;  
anorexia; cachexia.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 41..42  
FT /note= "Deletion of 281 amino acids"  
XX  
PN WO9824881-A1.  
XX  
PD 11-JUN-1998.  
XX  
XX 26-NOV-1997; 97WO-US22165.  
XX  
XX 02-DEC-1996; 96US-0032367.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Huang RC, Van Der Ploeg L;  
XX  
DR WPI: 1998-333304/29.  
XX  
XX New mutant ob receptor(s) - used to develop products for drug  
PT screening and for gene therapy for weight control, e.g. obesity or  
PT anorexia  
XX  
PS Claim 4; Fig 1; 27pp; English.  
XX  
XX The ob-receptor (OB-R), a member of the cytokine receptor family is  
CC transcribed in the hypothalamus and is involved in obesity. The  
CC deletion mutant D(41-322) has had the first CK-F3 module, present  
CC in the OB-R, removed. The D(41-322) mutant together with mutants lacking  
CC a functional second CK-F3 module or a functional intracellular domain can  
CC be used in assays for the detection of ligands, agonists, antagonists and  
CC ligand mimetics. The leptin agonists identified can be used in  
CC situations where leptin insufficiency causes obesity, diabetes or  
CC infertility. The leptin antagonists identified can be used in the  
CC treatment of anorexia and cachexia. The mutant receptor nucleic acids  
CC can also be used in gene therapy for weight control, e.g. for treating  
CC obesity or anorexia.  
XX  
SQ Sequence 883 AA;  
  
Query Match 63.7%; Score 742; DB 19; Length 883;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 842; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 323 STPRVFTQDVYIFPPKILTSVGSNVSFHCILYKKNKIVPSKEIWMWMMNLAEKIPQSOYD 382  
DB 41 stprvftqdvlyfppkiltsvgsnvshcllykknkiyvspkeiwmwmlaekipqsgyd 100  
QY 383 VSDHVSQVTFENLNETKPRGFTTYDAVYCCNEHECHHRYAELVYIDVNNINISCEFTDGYL 442  
DB 101 vvdhvsqvtffnlnekprgkfttydavycenechhryaelvyidvnniniscetdyl 160  
QY 443 TKMTCRMSTSTIQSLAESTLQLRHRSLSYCDPSIHPISEPKDCYLGSDGYECIFOP 502  
DB 161 tkmtcrwststiqslaestlqlrhrsslycsdpsihpisepkdcylgsdgfyecifop 220  
QY 503 IFLSGYTMWIRINSLGSLDSPPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPV 562  
-|||||

DB 221 ifllsgytmwirinshlsldspptcvlpdsvvkprlppssvkaejcinigllkiswekpv 280  
QY 563 FPENNIQQIRYGLSGKEVQWKMEVYDAKSKSVSLFVPDLCAVAVQVRCRRLDGLGYW 622  
DB 281 fpeennlqqirylsgkevqwkmyevydaksksvslfvpdlcavavqvrckrldglgyw 340  
QY 623 SNWSNPAYTVVMDIKVPMRGPFEFRIINGDTMKKEKNVTLMLKPLMKNDLSLCSVQRYVIN 682  
DB 341 snwnspaytvvmdikvpmrgpfefwringdtmkkekntvllmkplmkndslcsvqrvyin 400  
QY 683 HHTSCNGTSEDVGNHFFTEFLWTEQAHFVVLAINSIGASVANFNLTFSWMSKVNIVQ 742  
DB 401 hhtscngtwsedvgnhffteflwteqahftvvlainsigasvanfnltfswmskvnivq 460  
QY 743 SUSAYPLNSSCVIVSNILSPSDYKLMYFIIEWKNLNDEGEIKWLRISSSVKRYIHDHFI 802  
DB 461 sisayplnsscvtivswilspdyklimyfiilewknlnedgelkwlri:sssvkryihdhfi 520  
QY 803 PIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDAGLYVIVPVISSSILLGLTLII 862  
DB 521 piekyqfslypifmegvgkpkilnsftqddiekhsdaglyvivpvi:sssillgltili 580  
QY 863 SHQRMKKLFWEDEVPMKNCGWAQGLNFOKPEFTEHLFIKHTASVTCGPLLEPETISED 922  
DB 581 shqrmkklfwedevpmkncswagglnfqkpetfehlfikhtasvtcgplllepetisedi 640  
QY 923 SVDTSWKNKDEMPPTVYSLSTDLKSGVCSIDQFNSVNFSEAEGETEYVEDESQROP 982  
DB 641 svdtswknkdemptvyslstdlekgsvcsidqfnsvnfseaegetevyeaesqrqp 700  
QY 983 FVKYATLISNSKPSSETGEQGLINSSVTCKFSSKNSPLKDSFNSSWEIEAQAFILSDQ 1042  
DB 701 fvkylatlisnkspssetgeegglinssvtckfssknsplkdsfnsweieaqaffilisdq 760  
QY 1043 HPNIISPHLTFSEGLDELKLEGNFPEENNKKSTYVLGVTSIKKRESGVLLTDKSRVSC 1102  
DB 761 hpniisphltfseglidelklegnfpeennkkslylgvtsikkresgvlltdksrvsc 820  
QY 1103 PFPAPCLFTDIRVLODSCSHFVENNINLGTSSKKTFFASYMPQFOTCSTQTHKIMENKMD 1162  
DB 821 pfpapclftdirvldscshfvenninlgtsskktffasympqfotcstqthkimenkmd 880  
QY 1163 LTV 1165  
DB 881 ltv 883  
  
RESULT 16  
AAW50003  
ID AAW50003 standard; protein; 896 AA.  
XX  
AC AAW50003;  
XX  
DT 11-JUN-1998 (first entry)  
XX  
DE Human OB-R variant Form 3.  
XX  
KW Detection; defective obese protein receptor; defective OB-R; human;  
defective leptin receptor; variant Form 3; infertility.  
XX  
OS Homo sapiens.  
XX  
PN WO9741263-A1.  
XX  
PD 06-NOV-1997.  
XX  
PF 28-APR-1997; 97WO-US07676.  
XX  
XX 29-APR-1996; 96US-0640389.  
XX  
XX (PROG-) PROGENITOR INC.  
XX  
PI Cioffi J, Shafer AW, Snodgrass RH, Zupancic JU;

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XX      WPI; 1997-549757/50.
DR      N-PSDB; AAT95781.
XX      Detecting defective obese protein or leptin receptor in reproductive
PT      cells - using variant receptor gene specific probes
XX      Disclosure; Fig 3; 40pp; English.
PS      The present sequence was used in the development of a novel method
XX      for detecting a defective obese protein or leptin receptor (OB-R)
CC      in cells. Them method comprises contacting RNA extracted from a
CC      cell population (preferably an ovary, prostate, testis, sperm, ova,
CC      ovarian follicular or blood cell population) with an
CC      oligonucleotide derived from a portion of the human OB-R variant
CC      Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC      associated with infertility, as they are unable to correctly
CC      transduce signals from leptin binding. The detection method can be
CC      used to diagnose infertility, or predisposition to infertility,
CC      while treatments that inhibit or down regulate the variants, gene
CC      therapy to replace them in homozygotes or direct activation of
CC      downstream signal transduction can be used to improve fertility.
CC      Also described is the use of labelled DNA probes based on the OB-R
CC      sequence to screen for other variants.
XX      Sequence      896 AA;
SQ
Query Match      58.5%; Score 681; DB 18; Length 896;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      110 TFEVTVNSLVFOQIDANWNIOCMKGDKLFIQYVESLFLKMLFRNRYNYKVHLLYLPEVL 169
Db      110 tfevtnsvlfgqidanwnioqmkgdklfiqyveslflkmlfrnrynykvhllylpevl 169
QY      170 EDSPLVPQKGSFQMVHNCNSVHECECLVPVPTAKLNDTLLMCLKITSQGVIFOSPLMSV 229
Db      170 edsplvpqkgsfvmvhncnsvhcececlvpvtaklndtllmclkitsqgvifrsplmsv 229
QY      230 QPINVKKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLOYQVYKSENSTTVIREADKIYS 289
Db      230 qpimvkkpdpplglhmeitddgnlkiswsspplpfploqvkyssentstvireadkiys 289
QY      290 ATSLVDSILPGSSYEVQVRGKRLDGPICWSDMSTPRVFTQDVLYFPPKILTSVGSNVS 349
Db      290 atslvdsilpgssyevqvrgrkldgpgiwsdstprvftqdvlyfppkiltsvgsnvs 349
QY      350 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSOYDVNSDHVSKVTFENLNETKPRGKFTYDA 409
Db      350 fhciyykknkivpskeiyvmmnlakipqsodyvnsdhvskvtfenlnetkprgkftyda 409
QY      410 VYCCNEHCCHRYAELVYIDVNNINISCECTDGYLTMTCRWSTSTIOSLAESTLQRLYHRS 469
Db      410 vycnehechryaelvyidvnniniscetdgyltmtcrwststioslaestlqlryhrs 469
QY      470 SLVCSDFIPSIHPISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRIRNHSLSGLSDSPPTCV 529
Db      470 slvcsdfipsihpisepkdcylqsdgeyecifqipifllsgytmwirirnhslsgldspptcv 529
QY      530 LPDSVVKPLPPSSVKAETITINIGLKISWEKVPFENNLOFQIRIGLSGKEVQWKMEYEV 589
Db      530 lpdsvvkplppssvkaetitiniglkiswekvpfennlofqiriglsgekvqwkmyevy 589
QY      590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSMNSNPAYTVVMDIKVPMRGPETWRII 649
Db      590 daksksvslpvpdlcavyavqvrckrlvglgywsnmnsnpaytvvmdikvpmrgpetwrii 649
QY      650 NGDTMRKKEKNVTLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSSEVYGNHTKFTFLWTEQA 709
Db      650 ngdtmrkkeknvtllmkplmkndslcsvqryvinhhtscngtwsedvgnhtkftflwteqa 709
QY      710 HTVTVALAINSIGASVANFNLTFSWPMKVNIVQSLSAVPLNNSCVIVSWILSPSDYKLMY 769

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Db      710 htvvtvalainsigasvanfnltfswpmkvnivqslsavplnnsctvswilspdyklmY 769
QY      770 FLEWKNLNEDGEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSEF 829
Db      770 flewknlnedgeikwlrisssvkrviihdhfi piekyqfslypifmegvgkpkilnsft 829
QY      830 QDDIEKHQSDAGLYVIVPVISSSILLGLTLLISHQRMKLEWENVPNPKNSWAGGLNF 889
Db      830 qddiekhsdaglyvivpvissislllgtllishqrmklfwdvnpnkncswagglnf 889
QY      890 QK 891
Db      890 qk 891

RESULT 17
AAW50002
ID      AAW50002 standard; Protein; 904 AA.
XX      AAW50002;
AC      11-JUN-1998 (first entry)
DT      Human OB-R variant Form 2.
DE      Homo. sapiens.
KW      Defective; defective obese protein receptor; defective OB-R; human;
RW      defective leptin receptor; variant Form 2; infertility.
XX      WO9741263-A1.
PD      06-NOV-1997.
XX      28-APR-1997; 97WO-US07676.
PF      29-APR-1996; 96US-0640389.
PR      (PROG-) PROGENITOR INC.
PA      Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;
XX      WPI; 1997-549757/50.
PI      N-PSDB; AAT95780.
DR      Detecting defective obese protein or leptin receptor in reproductive
XX      cells - using variant receptor gene specific probes
PT      Disclosure; Fig 3; 40pp; English.
PS      The present sequence was used in the development of a novel method
XX      for detecting a defective obese protein or leptin receptor (OB-R)
CC      in cells. Them method comprises contacting RNA extracted from a
CC      cell population (preferably an ovary, prostate, testis, sperm, ova,
CC      ovarian follicular or blood cell population) with an
CC      oligonucleotide derived from a portion of the human OB-R variant
CC      Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC      associated with infertility, as they are unable to correctly
CC      transduce signals from leptin binding. The detection method can be
CC      used to diagnose infertility, or predisposition to infertility,
CC      while treatments that inhibit or down regulate the variants, gene
CC      therapy to replace them in homozygotes or direct activation of
CC      downstream signal transduction can be used to improve fertility.
CC      Also described is the use of labelled DNA probes based on the OB-R
CC      sequence to screen for other variants;
XX      Sequence      904 AA;
SQ
Query Match      58.5%; Score 681; DB 18; Length 904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 110 TFVSTVNSLVFOQIDAMWNIQWLKGDCLKLFICYVESLEFKNLFERNYNYKVHLLVLEPEVL 169
Db 110 tfvstvnslvfqidamwniqcwlkgdclklficyveslfknlfrrnykvhllylpevl 169
OY 170 EDSPLVPKGSFOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPIMSV 229
Db 170 edsplvpqgsfomvhnscsvheccceclvpvptaklndtlmlclkitsgvifrsplmsv 229
OY 230 QPINMVKPDPPLGLHMETDDGNLKLISWSSPPLVPFLQYOVKYSNSTVTIREADKIVS 289
Db 230 qpinmvkppdplglhmetddgnlkliswsspplpvflqyqvkysenstlvireadkivs 289
OY 290 ATSLLDVSLPGSSYEVOYRGKRLDGPGLMSDMSTPRVFTTQDVIFPPKILTSVGSNVS 349
Db 290 atslldvslpgssyevyrgkrlldgpglmsdmsprvfttqdvifppkiltsvgsnvs 349
OY 350 FHCITYKKENKIVPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPNLNETKPRGKFTYDA 409
Db 350 fhciykenkivpskeivwmnlaeqipsgydvvsdhvskvtfpnlnetkprgkftйда 409
OY 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRS 469
Db 410 vycnehechhryaelvidvinniscetdgyltmtcrwststiqslaestlqrllyhrs 469
OY 470 SLVCS DIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCV 529
Db 470 slycsdipshipsepkdcylqsdgyfeci fqpifllsgytmwirinhs lsgldspptcv 529
OY 530 LPDSVVKPLPPSSVKAETINIGLKLISWEKVPFPENNLOQIIRYGLSGKEVQWKMEYV 589
Db 530 lpdsvvkplppssvkaetinigllkliswekvpfpennlqoiryglsgkevqwkmyevy 589
OY 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAVTVMDIKVPMRGPEFRIT 649
Db 590 daksksvslpvpdlcavyavqvrckrlldglgywsnwsnpavtvmidikvpmrgpelfrit 649
OY 650 NGDTMKKEKNVTLLMKNDLSLQVQRYVINHTSCNGTSEDVGNHTKFTFLTEQA 709
Db 650 ngdtmkkekntllwkpmlkndslcsvqryvinhtscngtse dvgnhtkftflwtega 709
OY 710 HTVTYLAINSIGASVANFNLTFSWPMKSVNIQSLATPLNSSCVIVSWILSPSDYKLMY 769
Db 710 htvtyla insigasvanfnltfswpmksvniqslatplnsscvivswilspdyk lmy 769
OY 770 FIEEMKNLNEDEGIKWLRISSSVKYYIHDFIPIEKYQESLYPIFMEGVGKPKIINSFT 829
Db 770 fieemknlnegeikwlrissvkkyyihdfipiekyqeslypifmegvgkpkilnsft 829
OY 830 QDDIEKHOSDAGLYVIVPIIISISSILLGLTLLISHQRMKLLFWEDEVNPKNCSNAQSLNF 889
Db 830 qddiekhsdaglyvivpiississillgltl lishqrmkllfwe devnpknscswaqslnf 889
OY 890 QK 891
Db 890 qk 891

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## RESULT 18

AAW38214  
ID AAW38214 standard; Protein; 958 AA.

XX AC AAW38214;

XX DT 11-JUN-1998 (first entry)

XX DE Human OB-R variant Form 1.

KW Detection; defective obese protein receptor; defective OB-R; human;

XX defective leptin receptor; variant Form 1; infertility.

OS Homo sapiens.

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PN WO9741263-A1.
XX
XX 06-NOV-1997.
PD
XX
XX 28-APR-1997; 97WO-US07676.
PF
XX
XX 29-APR-1996; 96US-0640389.
PR
XX
XX (PROG-) PROGENITOR INC.
PA
XX
XX Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;
PI
XX WPI; 1997-549757/50.
DR
XX N-PSDB; AAT95779.
DR
XX
PT Detecting defective obese protein or leptin receptor in reproductive
PT cells - using variant receptor gene specific probes
XX
XX Disclosure; Fig 3; 40pp; English.
PS
XX
XX The present sequence was used in the development of a novel method
CC for detecting a defective obese protein or leptin receptor (OB-R)
CC in cells. The method comprises contacting RNA extracted from a
CC cell population (preferably an ovary, prostate, testis, sperm, ova,
CC ovarian follicular or blood cell population) with an
CC oligonucleotide derived from a portion of the human OB-R variant
CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
CC associated with infertility, as they are unable to correctly
CC transduce signals from leptin binding. The detection method can be
CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
CC
XX
XX Sequence 958 AA;
SQ

```

Query Match 58.5%; Score 681; DB 18; length 958;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 110 TFVSTVNSLVFOQIDAMWNIQWLKGDCLKLFICYVESLEFKNLFERNYNYKVHLLVLEPEVL 169
Db 110 tfvstvnslvfqidamwniqcwlkgdclklficyveslfknlfrrnykvhllylpevl 169
OY 170 EDSPLVPKGSFOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPIMSV 229
Db 170 edsplvpqgsfomvhnscsvheccceclvpvptaklndtlmlclkitsgvifrsplmsv 229
OY 230 QPINMVKPDPPLGLHMETDDGNLKLISWSSPPLVPFLQYOVKYSNSTVTIREADKIVS 289
Db 230 qpinmvkppdplglhmetddgnlkliswsspplpvflqyqvkysenstlvireadkivs 289
OY 290 ATSLLDVSLPGSSYEVOYRGKRLDGPGLMSDMSTPRVFTTQDVIFPPKILTSVGSNVS 349
Db 290 atslldvslpgssyevyrgkrlldgpglmsdmsprvfttqdvifppkiltsvgsnvs 349
OY 350 FHCITYKKENKIVPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPNLNETKPRGKFTYDA 409
Db 350 fhciykenkivpskeivwmnlaeqipsgydvvsdhvskvtfpnlnetkprgkftйда 409
OY 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRS 469
Db 410 vycnehechhryaelvidvinniscetdgyltmtcrwststiqslaestlqrllyhrs 469
OY 470 SLVCS DIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCV 529
Db 470 slycsdipshipsepkdcylqsdgyfeci fqpifllsgytmwirinhs lsgldspptcv 529
OY 530 LPDSVVKPLPPSSVKAETINIGLKLISWEKVPFPENNLOQIIRYGLSGKEVQWKMEYV 589
Db 530 lpdsvvkplppssvkaetinigllkliswekvpfpennlqoiryglsgkevqwkmyevy 589

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Db 530 lpdsvvkplppssvkaetlnigllklswekpvfpennlqfgrlyglsqkevqwkmyevy 589  
QY 590 DAKSKSVSLPVDLCAYVAVQVRCRRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRII 649  
Db 590 daksksvsjlpdpdlcayvavqvrckridglgyswnsnpatyvmtdikvpmrgpefwrii 649  
QY 650 NGDTMKKEKNTVLLMKPLMKNDLSVQRYVINNHTSCNGTSEDVGNHTKFTFLMTEQA 709  
Db 650 ngdtmkkekntvllmkplmkndlsqsvqryvinhhtscngtsewdvgnhtkftflmtega 709  
QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIWSIISPSDYKLMY 769  
Db 710 htvvtlainsigasvanfnltfswpmksvniqslsayplnsscvivswiispsdyklymy 769  
QY 770 FIIWKNLNEDGEIKWLRISSSVKKYVYIHDPIPIEKYQFSLYPIFMEGVGKPKITNSFT 829  
Db 770 fiiwknlnedgeikwlrissvkkyyihdipiiekyqfslypifmegvgkpkitnsft 829  
QY 830 QDDIEKHQSDAGUVYVPIIISSTLLGTLTLLSHQRMKRLFWEVDVPPNPKNSWAQGLNF 889  
Db 830 qddiekhqsdaglyvivpiissslllgtlltllshqrmkrlfwevdvpnpknswaqglnf 889  
QY 890 QK 891  
Db 890 qk 891

RESULT 19

AAW31911  
ID AAW31911 standard; Protein; 958 AA.

AC AAW31911;

DT 02-FEB-1998 (first entry)

DE Human OB-R leptin receptor variant.

KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;

KV diagnosis; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 85 /note- "variation from published sequence"

FT Misc-difference 109 /note- "variation from published sequence"

FT Misc-difference 223 /note- "variation from published sequence"

FT Domain 845..862 /note- "variation from published sequence"

FT Misc-difference 892..958 /label- Transmembrane\_domain

FT /note- "divergence from published sequence"

PN WO9726370-A1.

PD 24-JUL-1997.

PF 17-JAN-1997; 97WO-US00570.

PR 18-JAN-1996; 96US-0588190.

PA (PROG-) PROGENITOR INC.

PI Cioffi J, Shafer AW, Snodgrass HR, Zupancic TJ;

DR WPI; 1997-385353/35.

DR N-PSDB; AAT89193.

PT Detecting defective leptin receptor by hybridisation assay - and  
PT treatment of obesity with agent that inhibits the defective  
PT receptor, also screening for compounds that supplement leptin  
PT activity

XX Claim 12; Fig 1A-E; 26pp; English.

PS This polypeptide comprises a variant of the human leptin receptor  
XX (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)  
CC derived from overlapping clones isolated from a human foetal liver  
CC library. The sequence shows near identity to a published OB-R  
CC sequence in the extracellular domain, with the exception of 3 amino  
CC acids, but there is extensive diversity in the intracellular  
CC cytoplasmic domain at the C-terminal end. A claimed method for  
CC detection of OB-R in cells comprises extraction of RNA and testing  
CC this for hybridisation to an oligonucleotide (I) derived from the  
CC OB-R variant gene, especially from the region beyond nucleotide  
CC 2770. Also claimed are methods of: (1) treating obesity by  
CC administration of an agent that inhibits expression of the OB-R  
CC variant gene; and (2) identification of a compound that can  
CC supplement activity of leptin by: (1) incubating cells expressing  
CC OB-R variant first with leptin and then with a test compound, and  
CC (11) comparing activation signals between cells treated and not  
CC treated with the test compound. Inhibition/down-regulation of the  
CC variant OB-R (found in obese people) improves response of cells to  
CC weight regulation by leptin. Replacing variant OB-R by gene therapy  
CC (in homozygous individuals) can be used to treat obesity. Labelled  
CC probes based on the gene can be used to isolate other variant forms  
CC of the receptor gene or to detect the variant gene (e.g. for  
CC determining predisposition to obesity), while the OB-R gene can be  
CC used to express recombinant OB-R (optionally as fusion protein) and  
CC in standard hybridisation assays. The OB-R gene can also be used  
CC therapeutically in cases of overexpression of functional OB-R  
CC (causing loss of appetite and hypermetabolic activity). Cells  
CC engineered to express variant receptor are used in method (2) to  
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate  
CC antibodies that competitively inhibit, neutralise or enhance activity  
CC of the variant receptor.

SO Sequence 958 AA;

Query Match 58.5%; Score 681; DB 18; length 958;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TRVSTVNSLVFQOIDANMNITQCLWLGDKLFCYVESLFRNLYNKKVHLVLPPEVL 169  
Db 110 trvstvnslvfqoidanmnitqclwlgdklfcyveslfrnlynkvhllvlppevl 169  
QY 170 EDSPLVPQKGSFQVWHCNCVHECCCLVPVPTAKLNDPLMLCKITSGGVIFQSPMLSV 229  
Db 170 edsplvpqkgsfvmwhcncsvheccclvpvptaklndplmlckitsggvifrsplmsv 229  
QY 230 QPINWVKPDPPLGLHMETTDGNNLKISWSSPPLVPFLOXYOVKXSENSTVIREADKIVS 289  
Db 230 qpimwvkpdpplglhmeitdgnnlkisswsspplvpfloyovkxsenstvirreadkivs 289  
QY 290 ATSLILDVSLPGSSYEVQVGRKRDGPGIWSDDSTPRVFTTQVYVFPKILTSVGSNVS 349  
Db 290 atslilvdslpgssyevqvrkrdpgiwsddstprvfttqvyyfppkiltsvgsnvs 349  
QY 350 FHCITYKKENKIYVPSKEIYVMMNLAEKIPQSOYDVSDHVSXVTFNNI.NETKPRGKFTYDA 409  
Db 350 fhcitykknkiyvpiskeiyvmmnlakipqsoydvshvskvtfnnlnetkprgkftlyda 409  
QY 410 YCCNEHECHHRYAELVIDVININISCEITDGYLTMTCRWSTSTIQSLAESTLQRLYHRS 469  
Db 410 yccnehechhryaelvidvininiscetdgyltmtcrwststrqslaestlqrlryhs 469  
QY 470 SLVCS DIPSIHIPISPKCYQSDGFYECIFQPIFLLSGYTMKIRINHSIGSLDSPPTCV 529  
Db 470 slvcsdipshpisepkdcyqsdgfyecifqpfllsgytmwirinhsigslsdspptcv 529  
QY 530 LPDSVVKPLPPSSVKAETITNIGLLKISWEKPVFPENNLOFOIYVGLSGKEVQWKMYEVY 589  
Db 530 lpdsvvkplppssvkaetitnigllklswekpvfpennlqfgrlyglsqkevqwkmyevy 589

OY 590 DAKSKSVLPVDPDLCAYAVQVRCRDLGIGYWSNMSNPATYVMDIKVPMRGPEFWRII 649  
Db 590 daksksvslpvpdlcayavqvrckrlidgigyswnsnnpaytvmldkvpmrpgefwrli 649  
OY 650 NGDTMKKENVTLMLKPLMKNDSLCSQVQRYVINHHTSCNGTWSDEVCNHTKFTFLWTEQA 709  
Db 650 ngdtmkkenvtllwklpmlkndslcsvqryvinhhtscngtwsedvgnhtkftflwtega 709  
OY 710 HTVTVLAINSIGASVAFNLTFSWPKSVNIVQSLAYPLNNSCVIVSWILSPSDYKLMY 769  
Db 710 htvvtlainsigasvanfntlfswpmkvniqvslisayplnsscviwswilspdyklimy 769  
OY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829  
Db 770 filewknlnedgelkwlri:sssvkkyihdhfipliekqfslpifmegvgkpkinsft 829  
OY 830 QDDIEKHQSDAGLYVIVPVISSSILGLTLLISHQRMKKLFWEDEVNPNKNCWAQGLNF 889  
Db 830 qddiekhqsdaglyvivpvlisslilgltilshqrmkklfwevdpnpkncswaqlnf 889  
OY 890 OK 891  
Db 890 qk 891

RESULT 20

AAW19535  
ID AAW19535 standard; Protein; 958 AA.

AC AAW19535;

DT 02-FEB-1998 (first entry)

DE Human OB-R leptin receptor variant.

KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;

OS diagnosis; human.

XX Homo sapiens.

Location/Qualifiers

FT Misc-difference 85 /note= "variation from published sequence"

FT Misc-difference 109 /note= "variation from published sequence"

FT Misc-difference 223 /note= "variation from published sequence"

FT Domain 845..862 /label= "Transmembrane\_domain"

FT Misc-difference 892..958 /note= "divergence from published sequence"

PN WO9726272-A1.

PD 24-JUL-1997.

PF 17-JAN-1997; 97WO-US00880.

PR 18-JAN-1996; 96US-0588189.

PA (PROG-) PROGENITOR INC.

PI Cloeffl J, Shafer AW, Snodgrass HR, Zupancic TJ;

DR WPI; 1997-385291/35.

DR P-PSDB; AAT72649.

XX Detecting defective form of leptin receptor by probing cellular RNA  
PT - with oligonucleotide derived from DNA of receptor variant, also  
PT treatment of obesity by inhibiting expression of variant receptor  
PT and screening for agents that increase leptin activity

PS Claim 12; Fig 1A-E; 26pp; English.

XX This polypeptide comprises a variant of the human leptin receptor  
CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT72649)  
CC derived from overlapping clones isolated from a human foetal liver  
CC library. The sequence shows near identity to a published OB-R  
CC sequence in the extracellular domain, with the exception of 3 amino  
CC acids, but there is extensive diversity in the intracellular  
CC cytoplasmic domain at the C-terminal end, suggesting alternative  
CC splicing of a common precursor mRNA. A claimed method for  
CC detection of OB-R in cells comprises extraction of RNA and testing  
CC this for hybridisation to an oligonucleotide (1) derived from the  
CC OB-R variant gene, especially from the region beyond nucleotide  
CC 2770. Also claimed are methods of: (1) treating obesity by  
CC administration of an agent that inhibits expression of the OB-R  
CC variant gene; and (2) identification of a compound that can  
CC supplement activity of leptin by: (1) incubating cells expressing  
CC OB-R variant first with leptin and then with a test compound, and  
CC (11) comparing activation signals between cells treated and not  
CC treated with the test compound. Inhibition/down-regulation of the  
CC variant OB-R (found in obese people) improves response of cells to  
CC weight regulation by leptin. Replacing variant OB-R by gene therapy  
CC (in homozygous individuals) can be used to treat obesity. Labelled  
CC probes based on the gene can be used to isolate other variant forms  
CC of the receptor gene or to detect the variant gene (e.g. for  
CC determining predisposition to obesity), while the OB-R gene can be  
CC used to express recombinant OB-R (optionally as fusion protein) and  
CC in standard hybridisation assays. The OB-R gene can also be used  
CC therapeutically in cases of overexpression of functional OB-R  
CC (causing loss of appetite and hypermetabolic activity). Cells  
CC engineered to express variant receptor are used in method (2) to  
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate  
CC antibodies that competitively inhibit, neutralise or enhance activity  
CC of the variant receptor.

SQ Sequence 958 AA;

Query Match 58.5%; Score 681; DB 18; Length 958;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 110 TFSVTNSLVFOQIDANWNIOCLKGLKLFCTCVESLEFKNLFRNRYNKHLLVLPVEL 169  
Db 110 tfsvtnslvfoqidanwnioclkwlgdklfctcveslefknlfrrnyknhllvlpvel 169  
OY 170 EDSPLVPQKGFQMYHNCNSVHECCELVVPYPTAKLNDTLMLCKITSGCIYFQSPPLMSV 229  
Db 170 edsplvpqkgsfqmynhcnsvhecceclvvpypjakindtlmclksqgyvifrspimsv 229  
OY 230 QPIMVKKPPPLGLHMEITDDGNLKISWSSPPLVPELOYQVKYSENSTVIREADKIVS 289  
Db 230 qpimvkkppplglhmeitddgnlkiswsspplvpfpqykvksenstvlreadkivs 289  
OY 290 ATSLVDSILPGSSYEVOVRGKRLDGPSTWSDSTPRVFTQVCTYFPPKILTSVGSNVS 349  
Db 290 atslvdsilpgssyevovrgkrlidgpgstwsdstprvftqdvlyfppkiltsvgsnvs 349  
OY 350 FHCITYKKENKIYFSKEIYVMMNLAEKIPQSOYDVVSDHVSKVTFNNLNETKPRGKFTYDA 409  
Db 350 fhciykkenkiyfskeiyvmmnlaekipqsgdyvvsdhvskvtfnnlnetkprgkftyda 409  
OY 410 VYCCNEHECHHRYAELVIDVININISCEFDGGLTKMTCRWSTSTIQSLAESTLQRLYHRS 469  
Db 410 vycnehechhryaelvidvininiscetdgytlkmtcrwststiqslaestliqlryhrs 469  
OY 470 SLYGSDIPSIHPISPEPKDCYLOSDFYECTFQPIFLLSGYTMWIRINHSGLSDSPPTCV 529  
Db 470 slygsdipsihpisepkdcylosdfyecfqpifllsgytmwirinhsldspsptcv 529  
OY 530 LPDSVVKPLPSSVKAETITINIGLKISMEKVPFPENNLOFQIRYGLSGKEVQMKMEYEV 589  
Db 530 lpdsvkvplpssvkaetitiniglkiswekvpfpennlqfdiryglsgkevqwmkyev 589

QY	590	D A K S K S V S L P V P D L C A V I Y A V O V C K R L D G L G T W S M N S P A Y I T V M D I K V P M R G E F F W R I I	649
Db	590	d a k s k s v s l p v p d l c a v i y a v o v c k r l d g l g t w s m n s p a y i t v m d i k v p m r g e f f w r i i	649
QY	650	N G D T M K K E K N V T L M K P L M K N D S L C S V Q R Y V I N H N T S C N G T W S E D Y C N H K F T F L W T E O A	709
Db	650	n g d t m k k e k n v t l m k p l m k n d s l c s v q r y v i n h n t s c n g t w s e d y c n h k f t f l w t e q a	709
QY	710	H T V T V L A I N S I G A S V A N F N L F S W P M S K V N I V O S L S A Y P L N S S C V I V S N I L S P S D Y K L M Y	769
Db	710	h t v t v l a i n s i g a s v a n f n l f s w p m s k v n i v o s l s a y p l n s s c v i v s n i l s p s d y k l m y	769
QY	770	F I I E W K N L N E D G E I K W L R I S S S V K K Y I I H D F I P I E K Y Q F S L P I F M E G Y G K P K I I N S F T	829
Db	770	f i i e w k n l n e d g e i k w l r i s s s v k k y i i h d f i p i e k y q f s l p i f m e g y g k p k i i n s f t	829
QY	830	Q D D I E K H Q S D A G L Y V I V P V I I S S I L L L G T L L I S H O R M K K L F W E D V P N P K N C S W A Q G L N F	889
Db	830	q d d i e k h q s d a g l y v i v p v i i s s i l l l g t l l i s h q r m k k l f w e d v p n p k n c s w a q g l n f	889
QY	890	Q K 891	
Db	890	q k 891	

OY 890 QK 891  
||  
Db 890 qk 891

RESULT 22

AAR88912

ID AAR88912 standard; Protein; 898 AA.

XX AAR88912;

DT 07-JUN-1996 (first entry)

DE Haematopoietin receptor Hu-B1.219 Form 3 protein.

KW Haematopoietin receptor; Hu-B1.129; probe; prenatal testing; cancer;

KM Leukemia; diagnosis; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 871..898

FT /label= Transmembrane\_domain

PN W09608510-A1.

XX 21-MAR-1996.

PF 30-AUG-1995; 95WO-US10965.

XX 14-DEC-1994; 94US-0355888.

PR 14-SEP-1994; 94US-0306231.

PA (PROG-) PROGENITOR INC.

XX Clöffl J, Shafer AW, Snodgrass RH, Zupancic TJ;

DR MPI; 1996-179901/18.

DR N-PSDB; AAT12913.

PT Human haematopoietin receptor Hu-B1.219 - useful in design of

XX molecular probes for prenatal testing and cancer diagnosis

PS Claim 26; Fig 3B; 67pp; English.

CC A novel haematopoietin receptor (AAR88912), HuB1.219 Form 3 protein,

CC is the product of a cDNA clone (AAT12913) isolated from a human

CC foetal liver library. 2 other forms of HuB1.219 (see AAR88910 and

CC AAR88911) have also been identified. The Hu-B1.219 protein, or a

CC portion of it, is pref. prepd. by culturing a host cell engineered

CC to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol.

CC form or expressed on the cell surface and opt. as part of a fusion

CC protein) is used to screen peptide libraries to identify ligands

CC of Hu-B1.219.

XX Sequence 898 AA;

Query Match 49.8%; Score 580; DB 17; Length 898;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 110 TFEVSTVNSLVEQQIDANWNIQCWLKGDLLFTCYVESLFPKNLFRNRYNYKVHLLVLPVEL 169

Db 112 tfvstvnslvfqidanwniqcwlkgdliklficyveslfknlfrrnykykhllvlpvel 171

OY 170 EDSPLVPQKGFQMVHNCNSVHECCLECLVPVPTAKLNDITLMLCKITSGGVIFQSPLMVS 229

Db 172 edsplvpqkgsfgmvhncnsvhecceclvpvptaklndtlmclkitsggvifrsplmsv 231

OY 230 QPINWVKPDPPLGLHMEITDDNLKISWSSPPLVPFPLOQYVKYSENSTVIREADKIVS 289

|||||

Db 232 qpimwvkpdpplglhmeitddgnlkiswssppilvpfpfqgvkysenstvtlireadkivs 291

OY 290 ATSLVDSILPGSSYEVOVRGKRDLDPGIVSDMSTPRVFTTQDVTFPPKILTSVGSNVS 349

Db 292 atslvdsilpgssyevqvrgrldgpgiwsdwtprvfttqdvtyfppkiltsvgsnvs 351

OY 350 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFPFLNETKPRGKFTYDA 409

Db 352 fhciykkkenkiypskeiymnmnlaekipqsdvdsdhvskvflfnlnetkprgkftyda 411

OY 410 VYCCNEHECHRYAELVIDVININISCTDGYLTMTCRWSTSTIOSIAESTLOLRHYRS 469

Db 412 vycnehechryaelvidvnlinscetdgyltmcrwststiosiaestlqirhyrs 471

OY 470 SLYCSDIPSIHPRISEPKDCYLQSDGFYECIFQPIELLSGYTMWIRIHNSLGLSDSPPTCV 529

Db 472 slycsdipslhprisepdkcyldgsdgyfeciqlpflilsgytmwirihnsiglsdspptcv 531

OY 530 LPDSVVKPLPPSSVKAETITINIGLTKISWEKVPFPENNLOFQIRYGSCKEVOQWMEVY 589

Db 532 lpdsvvkplppssvkaeititnigllkswekvpfpennlofqirysgkevqwmeyy 591

OY 590 DAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYSNWSNPNPAYTVVNDIKVPMRGPEFWRII 649

Db 592 daksksvslpvpdlcavyavvrckrlldglgysnwsnnpaytvvndikvpmrgpewrili 651

OY 650 NGDTMKKEKNTVLLMKPLMKNDLCSVQRYVINHTSCNGTWSSEVQVNHKTFTFLWTEQA 709

Db 652 ngdtmkkeknvllmkplmkndslcsvqrvyinhhtscngtwsedvqnhktftflwteqa 711

OY 710 HTVTVLAINSIGASVANENLFTSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMY 769

Db 712 htvvtlainsigasvanenlftswpmkvnivqslaysplnsscvivswilspdyklimy 771

OY 770 FIIEWKNLNEDEEIKWLRISSSVKKYVIHDFPIPIEKYQFSLYPRMEGVGKPKIINSFT 829

Db 772 fliewknlnedegelkwlri:ssvkkyyihdhfipiekqfslpymegvgkpkilnsft 831

OY 830 QDDIEKHQSDAGLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPNKNCWSAOGILNF 889

Db 832 qddiekhqsdaglyvivpvlisslillgltlshqrmkllfwedevnpnkncswaogilnf 891

OY 890 QK 891

||

Db 892 qk 893

RESULT 23

AAR88911

ID AAR88911 standard; Protein; 908 AA.

XX AAR88911;

DT 07-JUN-1996 (first entry)

DE Haematopoietin receptor Hu-B1.219 Form 2 protein.

KW Haematopoietin receptor; Hu-B1.129; probe; prenatal testing; cancer;

KM Leukemia; diagnosis; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 871..898

FT /label= Transmembrane\_domain

PN W09608510-A1.

XX 21-MAR-1996.

PF 30-AUG-1995; 95WO-US10965.

PR 14-DEC-1994; 94US-0355888.

PR 14-SEP-1994; 94US-0306231.  
XX  
PA (PROG-) PROGENITOR INC.  
XX  
PI Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;  
XX  
DR WPI; 1996-179901/18.  
DR N-PSDB; AAT12912.  
XX  
PT Human haematopoietin receptor Hu-B1.219 - useful in design of  
PT molecular probes for prenatal testing and cancer diagnosis  
XX  
PS Claim 25; Fig 3B; 67pp; English.  
XX  
CC A novel haematopoietin receptor (AAR88911), HuB1.219 Form 2 protein,  
CC is the product of a cDNA clone (AAT12912) isolated from a human  
CC foetal liver library. 2 Other forms of HuB1.219 (see AAR88910 and  
CC AAR88912) have also been identified. The Hu-B1.219 protein, or a  
CC portion of it, is pref. prepd. by culturing a host cell engineered  
CC to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol.  
CC form or expressed on the cell surface and opt. as part of a fusion  
CC protein) is used to screen peptide libraries to identify ligands  
CC of Hu-B1.219.  
XX  
SQ Sequence 908 AA;

Query Match 49.8%; Score 580; DB 17; Length 908;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 110 TFEVSTVNSLVFQOIDANWNICQWLKGDLEKLFICVESLEFKNLFRNRYNKVHLLVLEPEVL 169  
DB 112 tfvstvnslvfqgidanwniqcwlkgdleklicyveslfnlfrnykvhllvlepevl 171  
OY 170 EDSPLVPQKSFQWVHNCNSVHECECELVPEVPTAKLNDTLMLCLKITSGGVIFQSPIMSV 229  
DB 172 edsplvpqksgfqwmvncnsvehcececlvpyptaklndtlmlclkitsggvifrsplmsv 231  
OY 230 QPIMWKPDPPLGLHMEITDDGNLKISWSSPPLVPFLOQVKYSENSTYIREADKIVS 289  
DB 232 qpimwkpdpplglhmeitddgnlkiswsspplvpflogvksensltvireadkivs 291  
OY 290 ATSLVDSILPGSSYEYQVRGKRLDGPGLSDWSTPRVFTTODVYEPFKILTSVGSNVS 349  
DB 292 atslvdsilpgssyevqvrgrldgpglswdstprvfttdvlyfprkiltsvgsnvs 351  
OY 350 FHCITKKENKIYPSKEIWMWMLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDA 409  
DB 352 fhciykkenkiypskeiwmwmlaekipsgdyvsvdhvskvtfenlnetkprgkftyda 411  
OY 410 VYCCNEHECHHRYAELIYIDVININISCETDGLTKMTCRMSTSTIQSLAESTLDRYHRS 469  
DB 412 vycnehechhyaelyidvininiscetdgltkmtrcwststiqslaestlqlyrhys 471  
OY 470 SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLSDSPTCV 529  
DB 472 slycsdipslhipisepkdcylqsdgfyecifqpfllisgytmwirinhsigsldspctcv 531  
OY 530 LPDSVVKPLPSSVKAETINIGLKISWEKPYEPENNLOFOIRYGLSGKEVQWKMEYEV 589  
DB 532 lpdsvvkplpssvkaetiniglkiswekpyepennlofoiryglsgkevqwkmyevy 591  
OY 590 DAKSKSVSLPYDLCAYAVAVQVRCKRLDGLGYSWNSNPNATYTVMDIKVPMRGPEFWRII 649  
DB 592 daksksvslpydalcayavavqrckrldglgyswnsnpnatytvmidikvpmrgpewfwi 651  
OY 650 NGDTMKKEKNVTLMLKPLMKNDLSLSYQRYVINHHTSCNGTWSSEDEVGNHTKREFLWTEQA 709  
DB 652 ngdtmkkekvnllwplmkndslsycqryvinhhtscngtwsedvgnhtkreflwtega 711  
OY 710 HTVTVLAINSIGASVANENLTFSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMY 769  
HTVTVLAINSIGASVANENLTFSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMY 769

DB 712 htvvtlainsigasvanenlftswpmskvnivqslsayplnsscivswilspdyklymy 771  
OY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMGVGKPKRTINSFT 829  
DB 772 filewknlnedgetkwlrisssvkkyyihdhfipiekqfslpyifimegvqkpkrlinsft 831  
OY 830 QDDIEKHOSDAGLYVIVYIISSSILLGLTLISHQRMKLFWEDEVNPKNCSWAGCLNF 889  
DB 832 qddiekhsdaglyvvyvviissillgltlisngmklfwevdpnpkncswagqlnf 891  
OY 890 QK 891  
DB 892 qk 893

RESULT 24  
AAR88910  
ID AAR88910 standard; Protein; 960 AA.  
XX  
AC AAR88910;  
XX  
DT 07-JUN-1996 (first entry)  
XX  
DE Haematopoietin receptor Hu-B1.219 Form 1 protein.  
XX  
KW Haematopoietin receptor; Hu-B1.129; probe; prenatal testing; cancer;  
KW leukaemia; diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 871..898  
XX /label= Transmembrane\_domain  
PN W09608510-A1.  
XX  
PD 21-MAR-1996.  
XX  
PF 30-AUG-1995; 95WO-US10965.  
XX  
PR 14-DEC-1994; 94US-0355888.  
PR 14-SEP-1994; 94US-0306231.  
XX  
PA (PROG-) PROGENITOR INC.  
XX  
PI Cioffi J, Shafer AW, Snodgrass RH, Zupancic TJ;  
XX  
DR WPI; 1996-179901/18.  
DR N-PSDB; AAT12911.  
XX  
PT Human haematopoietin receptor Hu-B1.219 - useful in design of  
PT molecular probes for prenatal testing and cancer diagnosis  
XX  
PS Claim 24; page 35-38; 67pp; English.  
XX  
CC A novel haematopoietin receptor (AAR88910), HuB1.219 Form 1 protein,  
CC is the product of a cDNA clone (AAT12911) isolated from a human  
CC foetal liver library. 2 Other forms of HuB1.219 (see AAR88911 and  
CC AAR88912) have also been identified. The Hu-B1.219 protein, or a  
CC portion of it, is pref. prepd. by culturing a host cell engineered  
CC to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol.  
CC form or expressed on the cell surface and opt. as part of a fusion  
CC protein) is used to screen peptide libraries to identify ligands  
CC of Hu-B1.219.  
XX  
SQ Sequence 960 AA;

Query Match 49.8%; Score 580; DB 17; Length 960;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 110 TFEVSTVNSLVFQOIDANWNICQWLKGDLEKLFICVESLEFKNLFRNRYNKVHLLVLEPEVL 169



Db 112 tftvstvnslvfqgidanwniqcwkldkificyveslfknlfrnynkvhlllylpevl 171  
Qy 170 EDSPLVPQKGSFQMWHCNCSVHECCETVPVPTAKLNDTLMLCKITSGGVIFOSPLMSV 229  
Db 172 edsplvpqgsfgmwhcnscvhecceclvpyptaklndtlmlckltsqgvifrsplmsv 231  
Qy 230 QPINNVKPDPLPLGLHMEITDDGNLKISMSSSPLVPFLQYQVKYSENSTVIREADKIVS 289  
Db 232 qplnmvkpdpplglhmeitddgnlkiswssplvpflqyqvkysenstlvireadkivs 291  
Qy 290 ATSLVDSILLPGSSYEVQVRGKRLLDGGIWSDMSTPRVFTTQDVITFPFKILTSGSNVS 349  
Db 292 atsllyvdsillpgssyevqvrgrkrlldggpwwsdwstprvfttdvlyifppkiltsgsnvs 351  
Qy 350 FHCITKKENKIVPSKEIVMMNLAEKIPQSQYDVSDHVSKVTFPNNLNETKPRGKFTYDA 409  
Db 352 fhcllykknkivpskeiwmnlakekipqsqydvdsdhvskvtfnnlnektkprgkftyda 411  
Qy 410 VYCCNEHCHHRYAELVYIDVNNINISCTDGYLTMTCRWSTSTIQSLAESTLQRLYHRS 469  
Db 412 vycnehechhryaelvyidvnninscetdgyltkmtcrwststlqslaestlqlryhrs 471  
Qy 470 SLVCSPIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCV 529  
Db 472 slycsdipsihpisepkdcylqsdgfyecifqpfllsgytmwirinhsigsldspptcv 531  
Qy 530 LPDSVVKPLPPSSVKAETINIGLKISWEKRPVPENNLOQIRYGLSGKEVQWKMEYV 589  
Db 532 lpdsvvkplppssvkaeitiniglkiswekvpfennlqfiryglsgkevqwkmyevy 591  
Qy 590 DAKSKSVSLPVPDLCAYYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRI 649  
Db 592 daksksvslpvpdlcayyavqvrckrlldglgywsnwsnpaytlvmdikvpmrgpewrli 651  
Qy 650 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSGDNHTKFTFLWTEQA 709  
Db 652 ngdtmkkekntllmkplmkndslcsvqryvinnhhtscngtwsdvgnhkftflwteqa 711  
Qy 710 HTVTVLAINSIGASVANFNLTFSWPSKNVINQSLASAYPLNNSCVIVSWILSPSDYKLMY 769  
Db 712 htvtvlainSIGASVANfnltfswpsknvinqslasayplnnsCvIvswilspdyklmy 771  
Qy 770 FIEMKNLNEDEGEIKWLRISSSVKKYYIHDHFPIEKYOFSLYPIFMEGVGKPKIINSEFT 829  
Db 772 fllewknlnegeikwlrissvkkyyihdhfipiekyqfslypifmegvgkpklinseft 831  
Qy 830 QDDIEKHQSDAGLYIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNSWAGLNF 889  
Db 832 qddiekhqsdaglyivpviisssillgltllishqrmkklfwevdpnpknCswaglnf 891  
Qy 890 QK 891  
Db 892 qk 893

RESULT 25  
AAW62544  
ID AAW62544 standard; protein; 1221 AA.  
AC AAW62544;  
XX  
XX 12-OCT-1998 (first entry)  
DE Human ob-receptor replacement mutant.  
XX  
KW ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;  
KW anorexia; cachexia.  
XX  
OS Homo sapiens.  
XX  
PN WO9824881-A1.  
XX

PD 11-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US22165.  
XX  
PR 02-DEC-1996; 96US-0032367.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Huang RC, Van Der Ploeg L;  
XX  
DR WPI; 1998-333304/29.  
XX  
PI New mutant ob receptor(s) - used to develop products for drug  
PT screening and for gene therapy for weight control, e.g. obesity or  
PI anorexia  
XX  
PS Claim 6; Fig 2; 27pp; English.  
XX  
CC The ob-receptor (OB-R), a member of the cytokine receptor family is  
CC transcribed in the hypothalamus and is involved in obesity. The  
CC replacement mutant has had amino acids 420-496 the second CK-F3  
CC module in OB-R deleted and replaced by amino acids 500-632. The  
CC replacement mutant together with mutants lacking a functional first CK-F3  
CC module or a functional intracellular domain can be used in assays for the  
CC detection of ligands, agonists, antagonists and ligand mimetics. The  
CC leptin agonists identified can be used in situations where leptin  
CC insufficiency causes obesity, diabetes or infertility. The leptin  
CC antagonists identified can be used in the treatment of anorexia and  
CC cachexia. The mutant receptor nucleic acids can also be used in gene  
CC therapy for weight control, e.g. for treating obesity or anorexia.  
XX  
SQ Sequence 1221 AA:  
  
Query Match 48.8%; Score 568; DB 19; Length 1221;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 497 ECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPPSSVKAETINIGLKI 556  
Db 553 ecifqpfllsgytmwirinhsigsldspptcvlpdsvvpklppssvkaeitiniglkli 612  
Qy 557 SWEKRPVPENNLOQIRYGLSGKEVQWKMEYVDAKSKSVSLPVPDLCAYYAVQVRCKRL 616  
Db 613 swekvpfennlqfiryglsgkevqwkmyevydaksksvslpvpdlcayyavqvrckrl 672  
Qy 617 DGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLMKPLMKNDLSLCSV 676  
Db 673 dglgywsnwsnpaytlvmdikvpmrgpewrilingdtmkkekntllmkplmkndslcsv 732  
Qy 677 ORYVINNHTSCNGTWSGDNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMMS 736  
Db 733 qryvinnhhtscngtwsdvgnhkftflwteqahvtvtvlainSIGASVANfnltfswpms 792  
Qy 737 KVINVOGSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLNEDEGEIKWLRISSSVKKYY 796  
Db 793 knivgslsayplnnsCvIvswilspdyklmyfiemknlnedgelikwlrissvkkyy 852  
Qy 797 IHDHFPIEKYQFSLYPIFMEGVGKPKIINFTQDDIEKHQSDAGLYIVPVIISSSILL 856  
Db 853 ihdhfipiekyqfslypifmegvgkpklinftqddiekhqsdaglyivpviisssill 912  
Qy 857 LGTLISHQRMKKLFWEDEVNPNKNSWAGLNFQKPEFTEHFLFIKHTASVTCGPLLEPE 916  
Db 913 lgtllishqrmkklfwevdpnpknCswaglnfqkpetfehflfkhtasvtcgpilllepe 972  
Qy 917 TISEDIVDTSWKNKDEMPPTVVSLLSTTDLKGSVCISDQFNSVNFSEAGTEVTEYED 976  
Db 973 tisedivdtswknkdemptvvsllsttDLKGSvcISDQfnsVnfseagtevttyea 1032  
Qy 977 ESQRQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPLKDSFNSSSWEIEAQAF 1036  
Db 1033 esqrqpfvkYatIlnskpssetgeegqlnssvtkcfssknspLkdsfnsSweieaqaf 1092

QY 1037 FILSDQHPNISPHTFSEGLDELKLEGNPEENNDKSIYYLGVTSIKRESGLVLT 1096  
 |||  
 Db 1093 filsdqhpnlisphltfseglldelklegnpeenndksiylygvtsikresgvl 1152  
 QY 1097 KSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFASYPQFQTCSTQTHKIM 1156  
 |||  
 Db 1153 ksrsvscfpapclftdirvldqscshfvennlnlgtsskktffasypqfqtstqthkim 1212  
 QY 1157 ENKMCDLTV 1165  
 |||  
 Db 1213 enkmcldtv 1221

RESULT 26  
 AAW19536  
 ID AAW19536 standard; Protein; 908 AA.  
 XX AAW19536;  
 AC  
 XX 16-JAN-1998 (first entry)  
 DE Variant form of human leptin receptor OB-R.  
 XX  
 KM Variant; human leptin receptor; obesity receptor; obesity regulation;  
 KM ribozyme; triple helix; predisposition.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 87 /note- "different from previously published sequence"  
 FT Misc-difference 111 /note- "different from previously published sequence"  
 FT Misc-difference 125 /note- "different from previously published sequence"  
 FT Misc-difference 870..908 /note- "different from previously published sequence"  
 FT Misc-difference /note- "variant diverges both in length and  
 FT sequence composition from previously published  
 FT OB-R sequence"  
 XX  
 PN WO9726523-A2.  
 PD 24-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-US00881.  
 XX  
 PR 18-JAN-1996; 96US-0588526.  
 XX  
 PA (PROG-) PROGENITOR INC.  
 XX  
 PI Clotfi J, Shafer AW, Snodgrass HR, Zupancic TJ;  
 XX  
 DR MPI; 1997-385466/35.  
 DR N-PSDB; AAT74022.  
 XX  
 PT Detecting a variant form of human leptin receptor OB-R - for  
 PT diagnosis of predisposition to obesity, also treating obesity using  
 PT inhibitors of the variant receptor  
 PS  
 PS Disclosure; Pages 17-21; 35pp; English.  
 XX  
 CC The present sequence represents a new variant form of the human leptin  
 CC receptor, OB-R (obesity receptor). The sequence of the variant OB-R  
 CC differs structurally from a published human OB-R sequence (Tartaglia et  
 CC al., 1995, Cell 83: 1263-1271). There are 3 amino acid substitutions in  
 CC the extracellular domain and extensive diversity in the intracellular  
 CC cytoplasmic domain, ie. the region encoded by the sequence downstream of  
 CC nucleotide 2770. A new method for detecting a defective OB-R in cells  
 CC comprises (a) extracting RNA from a cell population; (b) contacting the  
 CC RNA with an oligonucleotide derived from nucleotide residue 2770 and  
 CC beyond of AAT74022; and (c) detecting hybridisation of the RNA with the  
 CC oligonucleotide. A new method for treating obesity consists of

CC administering an agent capable of inhibiting expression of the OB-R  
 CC variant gene. Preferred inhibitors are antisense molecules, ribozymes or  
 CC triple helix forming oligonucleotides. Also claimed is a method for  
 CC identifying a compound capable of supplementing the biological activity  
 CC of leptin.  
 CC  
 XX  
 SQ Sequence 908 AA;  
 QY 110 TFVSTVNSLVFQOIDANMNIQCMKLGDKLFCICYVESLEFKNLFRMYNKVHLLVLPVYL 169  
 |||  
 Db 112 tfvstvnslvfqoidanwniqcmwlgdklfcicyveslfknlfrynykvhllylvpvyl 171  
 QY 170 EDSPLVPQKGSFQMVHNCVSHCECECLVPVPTAKLNDTLMLCKITSGGVIFQSPMLMSV 229  
 |||  
 Db 172 edsplvpqkgsfvmvhnccsvhcececlvpvptaklndtlmlckitsggvifrspmmsv 231  
 QY 230 QPIMWVKPDPPLGLHMETIDGDNLKISWSSPPLVPFLOYOVKYSNSTVIREADKIVS 289  
 |||  
 Db 232 qpimwvkpdpplglhmeitddgnlkiswssplvpfplovykysnstvireadkivs 291  
 QY 290 ATSLVDSILPGSSYEVQVRGKRLDGPIMSDWSTPRVFTQDVYFPPKILTSGVSNVS 349  
 |||  
 Db 292 atslvdsilpgssyevqvrgrkldgpgiwsdstprvftqdvlyfppkiltsgvsnvs 351  
 QY 350 FHCTYKKENKIVPSKETVMMNLAEKIPQSOYDVSDHVSRYTFENLNETKPRGKFTYDA 409  
 |||  
 Db 352 fhctykkenki vpskeivmmnlaea k i p q s o y d v s d h v s r y t f e n l n e t k p r g k f t y d a 411  
 QY 410 VYCCNEHECHHRYAELVIDVNNINISCE TDGYLTMTCRMNSTIQSLAESTIQLRHRS 469  
 |||  
 Db 412 vycnehechhryaelvidvnniniscetdgyltmtcrmwstisqlaestlqlryhrs 471  
 QY 470 SLVCS DIPSTHPISEPKDCYQSDGFYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCV 529  
 |||  
 Db 472 slvcsdipsihpi sep k d c y q s d g f y e c i f q p i f l s g y t m i r i n h s l s g l s d s p p t c v 531  
 QY 530 LPDSVVKPLPPSSVKAETITNIGLKLISWEKVPFENNLOQIRYGLSGKEVOWKMYEYV 589  
 |||  
 Db 532 lpdsvvkplppssvkretitnigllklswekvpfennlqfiryglsgkevowkmyevy 591  
 QY 590 DAKSKSVSLVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRTI 649  
 |||  
 Db 592 daksksvslvpdlcavayavqvrckrldglgywsnwsnpaytvmdikvpmrgpewrti 651  
 QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTNSDEVGNHTKFTFLWTEQA 709  
 |||  
 Db 652 ngdtmkkekntllwkp lmkndslcsvqryvinhtscngtwsedvgnhtkftflwtega 711  
 QY 710 HVTYVLAINSIGASVANENLTFSPMSKVINIVQSLAYPLNSCIVYSWILSPSDYKLMY 769  
 |||  
 Db 712 hvtv la ins i g a s v a n e n l t f s p m s k v i n i v q s l a y p l n s c i v y s w i l s p s d y k l m y 771  
 QY 770 FILEWKNLNEDEIKWLRISSSVKYYIHDFIPIEKYOFSLPIFEGVGKPKIINFT 829  
 |||  
 Db 772 filewknlnedgelkwlrlsssvkyyihdfipiekyofslpifegvgkpkii n f t 831  
 QY 830 ODDIEKHQSDAGLYVIVPVIITSSILLGLTLISHQRMKRLFWEDVNPKNCSWAQG 886  
 |||  
 Db 832 oddiekhqsdaglyvivpvitssillgltlishqrmklfwdvnpknscswaqg 888

RESULT 27  
 AAW14841  
 ID AAW14841 standard; Protein; 896 AA.  
 XX AAW14841;  
 AC  
 XX 30-OCT-1997 (first entry)  
 DT

XX Human haemopoietin receptor NR2.  
DE  
XX  
KW Haemopoietin receptor; new receptor 2; NR2; leptin; human;  
KW autoimmune disease; nervous system; cerebral palsy;  
KW trauma induced paralysis; vascular ischaemia; stroke;  
KW neuronal tumour; motor neurone disease; Parkinson's disease;  
KW Huntington's disease; Alzheimer's disease; multiple sclerosis;  
KW peripheral neuropathy; heavy metal; alcohol; toxicity;  
KW kidney failure; infectious disease; herpes; rubella; measles;  
KW chicken pox; HIV; HTLV-1; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 223  
FT /note= "encoded by CRG"  
FT Misc-difference 687  
FT /note= "encoded by TSC"  
XX  
PN WO9712037-A1.  
XX  
PD 03-APR-1997.  
XX  
PF 26-SEP-1996; 96WO-AU00607.  
XX  
PR 26-SEP-1995; 95AU-0005641.  
XX  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Alexander WS, Gainsford T, Hilton DJ, Metcalf D,  
PI Ng A, Nicola NA, Willson C;  
XX  
DR WPI; 1997-212896/19.  
DR N-PSDB; AAT64442.  
XX  
PT Human haemopoietin receptor NR2, and corresponding DNA - used e.g.  
PT for treatment of autoimmune diseases  
XX  
PS Claim 11; Page 50-54; 96pp; English.  
XX  
CC Human haemopoietin receptor NR2 (AAW14841) interacts with leptin,  
CC and can be used to develop (ant)agonists, therapeutics and  
CC diagnostic reagents based on ligand interaction. Its amino acid  
CC sequence was deduced from an isolated DNA molecule (AAT64442).  
CC Recombinant NR2 can also be used in a claimed method to identify  
CC ligands capable of interacting with a haemopoietin receptor, and  
CC in a method for therapy of autoimmune diseases. Recombinant  
CC soluble NR2 polypeptides can be used in the treatment of disease,  
CC injury or abnormality in the nervous system, cerebral palsy, trauma  
CC induced paralysis, vascular ischaemia associated with stroke,  
CC neuronal tumours, motor neurone disease, Parkinson's disease,  
CC Huntington's disease, Alzheimer's disease, multiple sclerosis,  
CC peripheral neuropathies associated with diabetes, heavy metal or  
CC alcohol toxicity, renal failure and infectious diseases such as  
CC herpes, rubella, measles, chicken pox, HIV or HTLV-1.  
XX  
SQ Sequence 896 AA;

Query Match 33.3%; Score 388; DB 18; Length 896;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 588; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MICQKFCVLLHWEFIYITAFNLSTPITPWRFKLSMPNSTYDYFLPAGLSKNTS 60  
Db 1 micqkfcvllhwefiyitaflnsltpitpwrfklsmpnstydyflpagskntsns 60  
OY 61 NGHYETAPEPKFNSSGTHFSNLSKTTFHCFRSEQDRNCSLCADNIEGKTFVSTVNSIVF 120  
Db 61 nghyetapepkfnssgthfnskskttfhccfrseqdrncslcadniegrtlfvstvnslvf 120  
OY 121 QQIDANMNIOQWLKGLKLFICYVESLFKNLFRNRYNKVHLLYVLPEVLEDSPLVPQKGS 180

Db 121 qqidanmniocwlgdklficyveslfknlfrynnykvhllylpevledsplvpqkgs 180  
OY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGGVIFCSPLMSVQPINMVKRPDP 240  
Db 181 fgmvhcnscsvhecceclvpvptaklndtlmlcklitsgsvlfcsplmsvqpinmvrpdp 240  
OY 241 LGLHMETDDGNLKISWSSPPLVPFLOIOVKYSENSTTVIREAKIVSATSLLDVSLP 300  
Db 241 lglhmetddgnlkiswsspplvpfloykvysensttvireakivsatslldvslp 300  
OY 301 GSSYEYQVRGKRLDGPVWSWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
Db 301 gssyeqvtrgkrlpgvwsdstprvfttqdvlyfppkiltsvgsnvsfhclykckenki 360  
OY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVCCNEHECH 420  
Db 361 vpskeivwmnlakqipsoydvvsdhvskvtfenlnetkprgkftydavccnehech 420  
OY 421 RYAEIYVDVNNINISCEYDGYLTKMTCRWSSTSTQSLAESTLQRLRYHRSLSYCS DIPSIH 480  
Db 421 ryaelyvdivnniniscetdgyltkmtcrwststqlaestlqrlryhrslsycsdipsh 480  
OY 481 PISEPKDCYLQSDGFYECIFQPIFILSGYTMIRINHSLSGLDSPPCVLPDSVVKPLPP 540  
Db 481 pisepkdcylqsdgyfecifqipifilsgytmirinhslsgldspcclpdsvvkplpp 540  
OY 541 SSVKAETITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVD 590  
Db 541 ssvkaetitinigllkiswekpvfpennlofqirylsgkevqwkmyevyd 590

RESULT 28

AAG63999  
ID AAG63999 standard; protein; 213 AA.  
XX  
AC AAG63999;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE Amino acid sequence of human CRH.  
XX  
KW leptin; CRH-leptin receptor; weight loss; CRH;  
KW protein co-ordinate data.  
XX  
OS Homo sapiens.  
XX  
PN WO200166593-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 05-MAR-2001; 2001WO-JP01666.  
XX  
PR 07-MAR-2000; 2000JP-0062404.  
XX  
PA (BIOM-) BIOMOLECULAR ENG RES INST.  
XX  
PI Toh H, Hiroike T, Arltomi M, Kunishima N, Morikawa K;  
XX  
DR WPI; 2001-565574/63.  
XX  
PT New three-dimensional structural coordinate of a protein complex of  
PT leptin and its receptor binding domain, for identifying and designing  
PT leptin mutants with superior biological activity, or agonists and  
PT antagonists -  
XX  
PS Example 6; Page 676-677; 683pp; Japanese.  
XX  
CC The specification describes a three-dimensional (3D) structural  
CC coordinate of a complex formed from leptin and a binding domain of  
CC its receptor (CRH-leptin receptor). The 3D structural coordinate is  
CC applicable in identifying, searching, evaluating or designing leptin  
CC mutants with superior biological activity or its agonists and

CC antagonists after mutation or modification, particularly for providing  
CC effect on arcuate nuclei, and in inhibiting intake or reducing weight  
CC loss. The present sequence represents a human protein, designated CRH.  
CC The protein is used in the course of the invention.

XX  
SQ Sequence 213 AA;

Query Match 18.3%; Score 213; DB 22; Length 213;  
Best Local Similarity 100.0%; Pred. No. 2.3e-214;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 ELYVIDVININISCEITDGYLTMTCTRWSTSTIQSLAESTLQLRHRSLLYCS DIPSIHPIS 483  
|||||  
Db 1 elyvidvininiscedgytlmtcrwststlqslaestlqlyhrsslycsdipshpis 60

OY 484 EPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSLSPPTCVLPDSVVKPLPPSSV 543  
|||||  
Db 61 epkdcylqsdgyfeci fipfl lsgytmwirinhs lgsldspptcvlpds vvkplpps sv 120

OY 544 KAEITINIGLTKISWEKVPPENNIQOIRYGLSGKEVQWKMEVYDAKSKSVSLPVPDL 603  
|||||  
Db 121 kaeitinigl tkiswekvpfennlqfiryglsgkevqwkmyevdaksksvslpvpdl 180

OY 604 CAVYAVQVRCKRLDGLGYWSNWSNPATYVMDI 636  
|||||  
Db 181 cavyavqvrckrl dglgywsnwsnpaytvmd i 213

## RESULT 29

AAW62545  
ID AAW62545 standard; protein; 235 AA.

AC AAW62545;

DT 12-OCT-1998 (first entry)

DE Soluble leptin binding domain.

KW Ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;  
anorexia; cachexia.

OS Homo sapiens.

PN WO9824881-A1.

PD 11-JUN-1998.

PF 26-NOV-1997; 97WO-US22165.

PR 02-DEC-1996; 96US-0032367.

PA (MERI ) MERCK & CO INC.

PI Fong TM, Huang RC, Van Der Ploeg L;

DR WPI; 1998-333304/29.

PT New mutant ob receptor(s) - used to develop products for drug  
PT screening and for gene therapy for weight control, e.g. obesity or  
PT anorexia

PS Disclosure; Fig 5; 27pp; English.

CC The ob-receptor (OB-R), a member of the cytokine receptor family is  
CC transcribed in the hypothalamus and is involved in obesity. The  
CC soluble secreted form of leptin binding domain is used in the screening  
CC of OB-R ligands. The leptin agonists identified can be used in  
CC situations where leptin insufficiency causes obesity, diabetes or  
CC infertility. The leptin antagonists identified can be used in the  
CC treatment of anorexia and cachexia. The OB-R mutant receptor nucleic  
CC acids can also be used in gene therapy for weight control, e.g. for  
CC treating obesity or anorexia.

XX  
SQ Sequence 235 AA;

Query Match 18.3%; Score 213; DB 19; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-214;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 HRYAELVIDVININISCEITDGYLTMTCTRWSTSTIQSLAESTLQLRHRSLLYCS DIPSI 479  
|||||  
Db 23 hryaelvidvininiscedgytlmtcrwststlqslaestlqlyhrsslycsdipsi 82

OY 480 HPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSLSPPTCVLPDSVVKPLP 539  
|||||  
Db 83 hpisepdkcylqsdgyfeci fipfl lsgytmwirinhs lgsldspptcvlpds vvkplp 142

OY 540 PSSVKAETINIGLTKISWEKVPPENNIQOIRYGLSGKEVQWKMEVYDAKSKSVSLP 599  
|||||  
Db 143 pssvkaetinigl tkiswekvpfennlqfiryglsgkevqwkmyevdaksksvslp 202

OY 600 VPDLCAVYAVQVRCKRLDGLGYWSNWSNPATYV 632  
|||||  
Db 203 vpdlcavyavqvrckrl dglgywsnwsnpaytv 235

## RESULT 30

AAW22106  
ID AAW22106 standard; Protein; 805 AA.

AC AAW22106;

DT 16-MAR-1998 (first entry)

DE Murine leptin receptor splice variant OB-Re.

KW Murine; leptin receptor; OB-R; obesity; diabetes; high blood pressure;  
high cholesterol; body weight.

OS Mus musculus.

PN WO9726335-A1.

PD 24-JUL-1997.

PF 16-JAN-1997; 97WO-US01010.

PR 14-FEB-1996; 96US-0599974.

PR 16-JAN-1996; 96US-0586594.

PA (UYRQ ) UNIV ROCKEFELLER.

PI Friedman JM, Iofe E, Lee G, Proenca R;

DR WPI; 1997-385338/35.

DR N-PSDB; AAT75707.

PT Leptin receptor, OB-R, polypeptide - useful to treat obesity,  
PT optionally in conjunction with treatment for diabetes, high blood  
PT pressure and high cholesterol

PS Claim 16; Page 111-113; 171pp; English.

CC The present sequence represents a leptin receptor (OB-R) protein, OB-Re.  
CC The OB-R can be used to treat obesity, optionally in conjunction with  
CC a treatment for diabetes, high blood pressure and high cholesterol,  
CC or in cosmetic compositions for reducing body weight. It may also be  
CC used in agriculture to produce leaner food animals, e.g. beef cattle,  
CC swine poultry, sheep. An antibody specific for OB-R can be used to  
CC measure the presence of OB-R in a sample, optionally in vivo, while the  
CC nucleic acid molecule encoding OB-R can be used to detect defects in the  
CC OB-R polypeptide associated with obese phenotypes, or diagnostically to  
CC measure its encoded RNA and protein in nutritional disorders. The  
CC nucleic acid molecule can be used in gene therapy, or the antisense

CC nucleic acid molecule can be used to antagonise leptin activity. The  
CC nucleic acid molecule, or the antisense nucleic acid molecule, can be  
CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia  
CC nervosa.

XX Sequence 805 AA;

Query Match 3.6%; Score 42; DB 18; Length 805;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 500 FQPIFLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fqpfllsgytmwirinhsigslsdsptcvlpdsvkvplpps 539

RESULT 31

AAW22102 ID AAW22102 standard; Protein; 842 AA.

XX AC AAW22102;

XX DT 16-MAR-1998 (first entry)

XX DE Murine leptin receptor splice variant OB-Ra.

KW Murine; leptin receptor; OB-R; obesity; diabetes; high blood pressure;  
KW high cholesterol; body weight.

OS Mus musculus.

XX FH Key Location/Qualifiers

FT Misc-difference 29 /label= Stop\_codon  
FT /note= "encoded by TAG"

XX PN WO9726335-A1.

XX PD 24-JUL-1997.

XX PF 16-JAN-1997; 97WO-US01010.

XX PR 14-FEB-1996; 96US-0599974.

XX PR 16-JAN-1996; 96US-0586594.

XX PA (UYRQ ) UNIV ROCKEFELLER.

XX PI Friedman JM, Iofte E, Lee G, Proenca R;

XX DR WPI; 1997-385338/35.

XX DR N-PSDB; AAT75703.

XX PT Leptin receptor, OB-R, polypeptide - useful to treat obesity,  
PT optionally in conjunction with treatment for diabetes, high blood  
PT pressure and high cholesterol  
XX PS Disclosure; Page 95-97; 171pp; English.

CC The present sequence represents a leptin receptor (OB-R) protein, OB-Ra.  
CC The OB-R can be used to treat obesity, optionally in conjunction with  
CC a treatment for diabetes, high blood pressure and high cholesterol,  
CC or in cosmetic compositions for reducing body weight. It may also be  
CC used in agriculture to produce leaner food animals, e.g. beef cattle,  
CC swine poultry, sheep. An antibody specific for OB-R can be used to  
CC measure the presence of OB-R in a sample, optionally in vivo, while the  
CC nucleic acid molecule encoding OB-R can be used to detect defects in the  
CC OB-R polypeptide associated with obese phenotypes, or diagnostically to  
CC measure its encoded RNA and protein in nutritional disorders. The  
CC nucleic acid molecule can be used in gene therapy, or the antisense  
CC nucleic acid molecule can be used to antagonise leptin activity. The  
CC nucleic acid molecule, or the antisense nucleic acid molecule, can be  
CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia

CC nervosa.

XX Sequence 842 AA;

Query Match 3.6%; Score 42; DB 18; Length 842;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 500 FQPIFLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 446 fqpfllsgytmwirinhsigslsdsptcvlpdsvkvplpps 487

RESULT 32

AAW34260 ID AAW34260 standard; Protein; 892 AA.

XX AC AAW34260;

XX DT 11-MAY-1998 (first entry)

XX DE Rat ob receptor isoform c'.

XX KW Ob receptor isoform c'; obesity; leptin; ligand; rat.

XX OS Rattus sp.

XX PN WO9742340-A1.

XX PD 13-NOV-1997.

XX PF 02-MAY-1997; 97WO-US07521.

XX PR 24-MAY-1996; 96GB-0010995.

XX PR 06-MAY-1996; 96US-0016899.

XX PA (MERI ) MERCK & CO INC.

XX PI Caskey CT, Hess JW, Hey P, Phillips MS;

XX DR WPI; 1997-558993/51.

XX PT New isoform(s) of the Ob (leptin) receptor - used for identifying  
PT specific binding ligands, potentially useful for study, prevention  
PT and treatment of obesity  
XX PS Disclosure; Page -: 34pp; English.

CC This protein comprises isoform c' of the rat ob receptor. The ob  
CC receptor has numerous isoforms resulting from alternative splicing;  
CC 3 novel isoforms, designated f, g and c' are disclosed (see  
CC AAW34258-60). Isoform c' differs from the 1162-residue wild-type  
CC protein (see AAW34257) in that after Lys-889 there are only 3 amino  
CC acids. The c' isoform can be expressed in host cells, particularly  
CC E. coli, yeast or mammalian cells. It is used to identify specific  
CC binding ligands. Agonists, antagonists and ligand mimetics can be  
CC identified that are potentially useful in the study, prevention and  
CC treatment of obesity.  
CC (NB. the amino acid sequence of isoform c' was produced by  
CC adaptation of the wild-type ob receptor sequence provided in Fig 1  
CC of the specification).

XX SQ Sequence 892 AA;

Query Match 3.6%; Score 42; DB 18; Length 892;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fqpfllsgytmwirinhsigslsdsptcvlpdsvkvplpps 539



RESULT 33  
AAW37338  
ID AAW37338 standard; Protein; 894 AA.  
XX  
AC AAW37338;  
XX  
DT 07-MAY-1998 (first entry)  
XX  
DE Ob protein receptor.  
XX  
KW Ob protein receptor; obese phenotype detection; rat.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 805  
FT /note="encoded by TGT"  
XX  
PN WO9741217-A1.  
XX  
PD 06-NOV-1997.  
XX  
PF 24-APR-1997; 97WO-JP01470.  
XX  
PR 30-APR-1996; 96JP-0134422.  
XX  
PA (SAKA ) OTSUKA PHARM CO LTD.  
XX  
PI Iida M, Kodaira T, Murakami T, Shima K;  
XX  
DR WPI: 1997-549722/50.  
DR N-PSDB; AAT97156.  
XX  
PT Ob protein receptor gene and variant having cytosine at base 806 -  
PT for diagnosis of mutation(s) leading to development of obesity in  
PT animals  
XX  
PS Disclosure; Page 57-62; 71pp; Japanese.  
XX  
CC This sequence represents the obesity protein receptor of the  
CC invention. The gene sequence may be used for screening of warm blooded  
CC animals (such as rats) for spontaneous mutations resulting in the variant  
CC ob protein receptor gene which leads to animals having an obese  
CC phenotype. These are useful in the study of mechanisms of obesity and the  
CC development of anti-obesity drugs.  
XX  
SQ Sequence 894 AA;  
  
Query Match 3.6%; Score 42; DB 18; Length 894;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541  
Db 498 fqpfllsgytmwirinhsldspptcvlpdsvkvkplpps 539  
  
RESULT 34  
AAW37337  
ID AAW37337 standard; Protein; 894 AA.  
XX  
AC AAW37337;  
XX  
DT 07-MAY-1998 (first entry)  
XX  
DE Ob protein receptor.  
XX  
KW Ob protein receptor; obese phenotype detection; rat.  
XX  
OS Rattus sp.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 805  
FT /note="encoded by TGT"  
XX  
PN WO9741217-A1.  
XX  
PD 06-NOV-1997.  
XX  
PF 24-APR-1997; 97WO-JP01470.  
XX  
PR 30-APR-1996; 96JP-0134422.  
XX  
PA (SAKA ) OTSUKA PHARM CO LTD.  
XX  
PI Iida M, Kodaira T, Murakami T, Shima K;  
XX  
DR WPI: 1997-549722/50.  
DR N-PSDB; AAT97149.  
XX  
PT Ob protein receptor gene and variant having cytosine at base 806 -  
PT for diagnosis of mutation(s) leading to development of obesity in  
PT animals  
XX  
PS Claim 1; Page 49-54; 71pp; Japanese.  
XX  
CC This sequence represents the obesity protein receptor of the  
CC invention. The gene sequence may be used for screening of warm blooded  
CC animals (such as rats) for spontaneous mutations resulting in the variant  
CC ob protein receptor gene which leads to animals having an obese  
CC phenotype. These are useful in the study of mechanisms of obesity and the  
CC development of anti-obesity drugs.  
XX  
SQ Sequence 894 AA;  
  
Query Match 3.6%; Score 42; DB 18; Length 894;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 500 FQPIFLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541  
Db 498 fqpfllsgytmwirinhsldspptcvlpdsvkvkplpps 539  
  
RESULT 35  
AAW24064  
ID AAW24064 standard; Protein; 894 AA.  
XX  
AC AAW24064;  
XX  
DT 17-MAR-1998 (first entry)  
XX  
DE Murine WSX receptor.  
XX  
KW Murine; WSX receptor; mouse; identification; purification;  
KW ligand; activator; antibody; agonist; proliferation; obesity;  
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;  
KW Type II diabetes; polycystic ovarian disease;  
KW cardiovascular disease; osteoarthritis; dermatological disorder;  
KW hypertension; insulin resistance; hypercholesterolaemia;  
KW hypertriglyceridaemia; cancer; cholelithiasis.  
XX  
OS Mus sp.  
XX  
PN WO9725425-A1.  
XX  
PD 17-JUL-1997.  
XX  
PF 07-JAN-1997; 97WO-US00325.  
XX  
PR 20-JUN-1996; 96US-0667197.  
PR 08-JAN-1996; 96US-0585005.

XX (GETH ) GENENTECH INC.  
PA  
XX Bennett B, Carter PJ, Chiang NY, Kim RJ, Matthews W;  
PI Rodrigues ML;  
PI  
XX WPI; 1997-372864/34.  
DR  
XX  
PT WSX receptor and related antibodies and ligands - used to develop  
PT products for diagnosis and therapy, e.g. for improving  
PT haematopoiesis or for treating tumours  
XX  
PS Disclosure; Pages 124-127; 219pp; English.  
XX  
CC The present sequence is the murine WSX receptor, which can be used  
CC to identify and purify ligands and activators. An anti-WSX receptor  
CC antibody can be used as an agonist to activate the WSX receptor,  
CC leading to enhanced proliferation or differentiation of a cell  
CC expressing the WSX receptor. It can also be used to decrease body  
CC weight and/or fat-depot weight and/or food intake in an obese  
CC mammal. WSX receptor ligands can be used to enhance proliferation  
CC or differentiation of lymphoid, myeloid or erythroid blood cell  
CC lineages. This is useful when a mammal, especially a human, is  
CC suffering from decreased blood cell levels, i.e. anaemia, caused by  
CC chemotherapy, radiation therapy or bone marrow transplantation  
CC therapy. It can also be used to repopulate blood cells in a mammal.  
CC The products can also be used to treat, e.g. neoplastic disorders,  
CC arteriosclerosis, Type II diabetes, polycystic ovarian disease,  
CC cardiovascular diseases, osteoarthritis, dermatological disorders,  
CC hypertension, insulin resistance, hypercholesterolaemia,  
CC hypertriglyceridaemia, cancer and cholelithiasis.  
XX  
SQ Sequence 894 AA;  
  
Query Match 3.6%; Score 42; DB 18; Length 894;  
Best local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 500 EOPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPPS 541  
Db 498 Iqpfllslsgytmirinhslsgsdspptcvlpdsvkvkplpps 539  
  
RESULT 36  
AAW19114  
ID AAW19114 standard; Protein; 894 AA.  
XX  
AC AAW19114;  
XX  
DT 26-AUG-1997 (first entry)  
XX  
DE Murine short form Ob receptor.  
XX  
KW Ob receptor; ObR; cytokine receptor; signal transduction;  
KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;  
KW therapy.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= sig\_peptide  
FT 23..837  
FT Domain  
FT /label= ECD  
FT /note= "extracellular domain"  
FT 838..860  
FT /label= TMD  
FT /note= "transmembrane domain"  
FT 861..894  
FT /label= CD  
FT /note= "cytoplasmic domain"  
FT 317..321  
FT Peptide

FT /note= "motif conserved in class I cytokine  
FT receptors"  
FT Peptide 620..624  
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FT receptors"  
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FT Modified-site 686  
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XX  
PN W09719952-A1.  
XX  
PD 05-JUN-1997.  
XX  
PF 27-NOV-1996; 96WO-US19128.  
XX  
PR 03-SEP-1996; 96US-0708123.  
PR 27-NOV-1995; 95US-0562663.  
PR 04-DEC-1995; 95US-0566622.  
PR 08-DEC-1995; 95US-0569485.  
PR 11-DEC-1995; 95US-0570142.  
PR 28-DEC-1995; 95US-0583153.  
PR 22-JAN-1996; 96US-0599455.  
PR 26-APR-1996; 96US-0638524.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Culpepper JA, Tartaglia LA, Tepper RI, White DW;  
XX

DR WPI: 1997-310525/28.  
DR N-PSDB; AAT69590.  
XX  
PT Isolated Ob receptor genes and polypeptide(s) - useful to develop  
PT products for diagnosis or treatment of body weight disorders, e.g.  
PT obesity, cachexia, anorexia and bulimia  
XX  
PS Example; Fig 1; 265pp; English.  
XX  
CC The murine short form Ob receptor (OBR) (AAW19114) is associated with  
CC the obese phenotype in db/db mice. Its amino acid sequence was  
CC deduced from a cDNA clone (AAT69590) isolated from a choroid plexus  
CC cDNA expression library, and differs from long form OBR (AAW19115)  
CC in having a shorter cytoplasmic domain. Unlike long form OBR, the  
CC short form does not transduce signal mediated by the STAT pathway.  
CC The db mutant in db/db obese mice expresses an aberrantly spliced  
CC transcript that encodes a truncated OBR protein that is identical  
CC to short form OBR. OBR proteins, peptides, antibodies, agonists  
CC and antagonists can be used in the diagnosis and treatment of body  
CC weight disorders such as obesity, cachexia and anorexia.  
XX  
SQ Sequence 894 AA;

Query Match 3.6%; Score 42; DB 16; Length 894;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 EQPIFLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fqpifllsgytmwirinhsldspctcvlpdsvvrkplpps 539

RESULT 37  
AAE12608  
ID AAE12608 standard; Protein; 894 AA.  
XX  
AC AAE12608;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Murine short form Ob receptor (OBR) protein.  
XX  
KW Murine; obese receptor; OBR; anorectic; anabolic; body weight disorder;  
KW therapy; obesity; cachexia; anorexia.  
XX  
OS Mus sp.  
XX  
FH Key  
FT Peptide 1.22  
FT Protein /label- Signal\_peptide  
FT Domain 23.894  
FT /label- Murine\_mature\_short\_form\_OBR\_protein  
FT 23.837  
FT /label- Extracellular\_domain  
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FT Region 317.321  
FT /note- "Conserved motif of cytokine I receptor family"  
FT Modified-site 345.347  
FT /note- "Asn is N-glycosylated"  
FT Modified-site 431.433  
FT /note- "Asn is N-glycosylated"

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FT Modified-site 698.700  
FT /note- "Asn is N-glycosylated"  
FT Modified-site 726.728  
FT /note- "Asn is N-glycosylated"  
FT Domain 838.860  
FT /label- Transmembrane\_domain  
FT Domain 861.894  
FT /label- Cytoplasmic\_domain

US6287782-B1.

11-SEP-2001.

29-APR-1998; 98US-0069781.

27-NOV-1995; 95US-0562663.

04-DEC-1995; 95US-0566622.

08-DEC-1995; 95US-0569485.

11-DEC-1995; 95US-0570142.

28-DEC-1995; 95US-0583153.

22-JAN-1996; 96US-0599455.

26-APR-1996; 96US-0638524.

03-SEP-1996; 96US-0708123.

28-MAY-1997; 97US-0864564.

(MILL-) MILLENNIUM PHARM INC.

Tartaglia LA, Tepper RJ, Culpepper JA, White DW;

N-PSDB; AAD20508.

WPI: 2001-624489/72.

Identifying compounds for treating body weight disorder, e.g. obesity,

anorexia or cachexia, comprises contacting cell expressing mammalian Ob

receptor protein, JAK2 protein and mammalian SOCS-1 protein with test

compound

Example; Fig 1; 109pp; English.

The patent discloses obese receptor (OBR) proteins and nucleic acids

encoding them. OBR protein participates in the regulation of mammalian

body weight. The invention also relates to a method of identifying

therapeutic compounds for the treatment of a body weight disorder.

The method involves contacting a cell that expresses a mammalian OBR

protein, a JAK2 protein and a mammalian SOCS-1 protein with a test

compound. The method is useful for identifying compounds which modulate

OBR gene expression and gene product activity, which can be used as

agents to control body weight particularly as therapeutic-agents for

treating body weight disorders, including obesity, cachexia and anorexia.

The present sequence is short form OBR protein from murine.

Sequence 894 AA;

Query Match 3.6%; Score 42; DB 22; Length 894;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 EQPIFLSGYTMWIRINHSLSGSDSPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fqpifllsgytmwirinhsldspctcvlpdsvvrkplpps 539

```

RESULT 38
AAW34258
ID AAW34258 standard; Protein; 895 AA.
XX
AC AAW34258;
XX
DT 11-MAY-1998 (first entry)
XX
DE Rat ob receptor isoform f.
XX
KM Ob receptor isoform f; obesity; leptin; ligand; rat.
XX
OS Rattus sp.
XX
PN WO9742340-A1.
XX
PD 13-NOV-1997.
XX
PF 02-MAY-1997; 97WO-US07521.
XX
PR 24-MAY-1996; 96GB-0010995.
PR 06-MAY-1996; 96US-0016899.
XX
PA (MERL ) MERCK & CO INC.
XX
PI Caskey CT, Hess JW, Hey P, Phillips MS;
XX
DR WPI: 1997-558993/51.
DR N-PSDB; AAT93104.
XX
PT New isoform(s) of the Ob (leptin) receptor - used for identifying
PT specific binding ligands, potentially useful for study, prevention
PT and treatment of obesity
XX
PS Disclosure; Page -: 34pp; English.
XX
CC This protein comprises isoform f of the rat ob receptor. The ob
CC receptor has numerous isoforms resulting from alternative splicing;
CC 3 novel isoforms, designated f, g and c' are disclosed (see
CC AAW34258-60). Isoform f differs from the 1162-residue wild-type
CC protein (see AAW34257) in that after Lys-889 there are only 6 amino
CC acids. In the cDNA (see AAT93104), these codons are then followed by
CC a stop codon. The f isoform can be expressed in host cells,
CC particularly E. coli, yeast or mammalian cells. It is used to
CC identify specific binding ligands. Agonists, antagonists and
CC ligand mimetics can be identified that are potentially useful in
CC the study, prevention and treatment of obesity.
CC (NB. the amino acid sequence of isoform f was produced by
CC adaptation of the wild-type ob receptor sequence provided in Fig 1
CC of the specification).
XX
XX
SO Sequence 895 AA;

Query Match 3.6%; Score 42; DB 18; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.7e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db 498 fqpfifllsgytlmwlrlnhslgslspsptcvlpdsvkvkplpps 539

RESULT 39
AAW22105
ID AAW22105 standard; Protein; 900 AA.
XX
AC AAW22105;
XX
DT 16-MAR-1998 (first entry)
XX

```

```

DE Murine leptin receptor splice variant OB-Rd.
XX
XX Murine; leptin receptor; OB-R; obesity; diabetes; high blood pressure;
KM high cholesterol; body weight.
XX
XX Mus musculus.
OS
XX
XX WO9726335-A1.
PN
XX
XX 24-JUL-1997.
PD
XX
XX 16-JAN-1997; 97WO-US01010.
PF
XX
XX 14-FEB-1996; 96US-0599974.
PR 16-JAN-1996; 96US-0586594.
XX
XX (UVRQ ) UNIV ROCKEFELLER.
PA
XX
XX Friedman JM, Iofte E, Lee G, Proenca R;
PI
XX
XX WPI; 1997-385338/35.
DR N-PSDB; AAT75706.
XX
XX Leptin receptor, OB-R, polypeptide - useful to treat obesity,
PT optionally in conjunction with treatment for diabetes, high blood
PT pressure and high cholesterol
XX
XX Disclosure; Page 105-109; 171pp; English.
PS
XX
XX The present sequence represents a leptin receptor (OB-R) protein, OB-Rd.
CC The OB-R can be used to treat obesity, optionally in conjunction with
CC a treatment for diabetes, high blood pressure and high cholesterol,
CC or in cosmetic compositions for reducing body weight. It may also be
CC used in agriculture to produce leaner food animals, e.g. beef cattle,
CC swine poultry, sheep. An antibody specific for OB-R can be used to
CC measure the presence of OB-R in a sample, optionally in vivo, while the
CC nucleic acid molecule encoding OB-R can be used to detect defects in the
CC OB-R polypeptide associated with obese phenotypes, or diagnostically to
CC measure its encoded RNA and protein in nutritional disorders. The
CC nucleic acid molecule can be used in gene therapy, or the antisense
CC nucleic acid molecule can be used to antagonise leptin activity. The
CC nucleic acid molecule, or the antisense nucleic acid molecule, can be
CC used to treat weight loss e.g. associated with AIDS, cancer or anorexia
CC nervosa.
XX
XX
XX Sequence 900 AA;
SQ

```

PD 13-NOV-1997.  
XX  
PI Caskey CT, Hess JW, Hey P, Phillips MS;  
XX  
DR WPI; 1997-558993/51.  
XX  
PT New isoform(s) of the Ob (leptin) receptor - used for identifying  
PT specific binding ligands, potentially useful for study, prevention  
PT and treatment of obesity  
XX  
PS Disclosure; Page -, 34pp; English.  
XX  
CC This protein comprises isoform g of the rat ob receptor. The ob  
CC receptor has numerous isoforms resulting from alternative splicing;  
CC 3 novel isoforms, designated f, g and c' are disclosed (see  
CC AAW34258-60). Isoform g is much shorter than the 1162-residue  
CC wild-type sequence (see AAW34257). 18 N-terminal amino acids are  
CC spliced to a large fragment of the wild-type molecule, beginning at  
CC Pro-166. The isoform then extends for the remainder of wild-type  
CC ob receptor molecule. Alternatively, it could contain another  
CC isoform variation, such as isoform a, b, c, d, e or f. The g  
CC isoform can be expressed in host cells, particularly E. coli, yeast  
CC or mammalian cells. It is used to identify specific binding  
CC ligands. Agonists, antagonists and ligand mimetics can be  
CC identified that are potentially useful in the study, prevention and  
CC treatment of obesity.  
CC (NB. the amino acid sequence of isoform g was produced by  
CC adaptation of the wild-type ob receptor sequence provided in Fig 1  
CC of the specification).  
XX  
XX Sequence 1015 AA;  
SO

Query Match 3.6%; Score 42; DB 18; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 351 fgplfllsgyltmwirinhsigslspsptcvlpdsvkvklpps 392

RESULT 41  
AAW34257  
ID AAW34257 standard; Protein; 1162 AA.  
XX  
AC AAW34257;  
XX  
DT 11-MAY-1998 (first entry)  
XX  
DE Rat wild-type ob receptor.  
XX  
KW Ob receptor; obesity; leptin; isoform; ligand; rat;  
XX  
OS Rattus sp.  
XX  
PN WO9742340-A1.  
XX  
PD 13-NOV-1997.  
XX  
PE 02-MAY-1997; 97WO-US07521.  
XX  
PR 24-MAY-1996; 96GB-0010995.  
PR 06-MAY-1996; 96US-0016899.  
XX  
PA (MERI ) MERCK & CO INC.

XX  
PI Caskey CT, Hess JW, Hey P, Phillips MS;  
XX  
DR WPI; 1997-558993/51.  
DR N-PSDB; AAT93103.  
XX  
PT New isoform(s) of the Ob (leptin) receptor - used for identifying  
PT specific binding ligands, potentially useful for study, prevention  
PT and treatment of obesity  
XX  
PS Disclosure; Fig 1; 34pp; English.  
XX  
CC This protein sequence comprises wild-type (lean) rat ob receptor.  
CC The ob receptor has numerous isoforms resulting from alternative  
CC splicing; 3 novel isoforms, designated f, g and c' are disclosed  
CC (see AAW34258-60). These isoforms also apply to mouse and human ob  
CC receptors. The isoforms can be expressed in host cells,  
CC particularly E. coli, yeast or mammalian cells. They are used to  
CC identify specific binding ligands. Agonists, antagonists and  
CC ligand mimetics can be identified that are potentially useful in  
CC the study, prevention and treatment of obesity.  
XX  
SO Sequence 1162 AA;

Query Match 3.6%; Score 42; DB 18; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSIGSLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fgplfllsgyltmwirinhsigslspsptcvlpdsvkvklpps 539

RESULT 42  
AAW23399  
ID AAW23399 standard; Protein; 1162 AA.  
XX  
AC AAW23399;  
XX  
DT 23-FEB-1998 (first entry)  
XX  
DE Rat ob receptor (fa mutant).  
XX  
KW Ob receptor; obesity; leptin; rat; rodent; animal model; ligand;  
KW fatty; fa mutation; therapy.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FH Peptide 1..28  
FT /label= Sig\_peptide  
FT Protein 29..1162  
FT /label= Mat\_protein  
FT Domain 29..830  
FT /label= Extracellular\_domain  
FT Domain 839..860  
FT /label= Transmembrane\_domain  
FT /note= "6"  
FT Domain 860..1162  
FT /label= Cytoplasmic\_domain  
FT Misc-difference 269  
FT /note= "residue 269 is Gln in wild-type OB-R"  
XX  
PN WO9731015-A1.  
XX  
PD 28-AUG-1997.  
XX  
PE 18-FEB-1997; 97WO-US02397.  
XX  
PR 25-APR-1996; 96GB-0008473.  
PR 22-FEB-1996; 96US-0090405.  
PR 22-MAR-1996; 96US-0013969.



```
XX PA (MERI ) MERCK & CO INC.
XX PI Caskey CT, Hess JW, Liu Q, Phillips MS;
XX DR WPI: 1997-435085/40.
XX DR N-PSDB; AAT64962.
XX PT Rat wild-type and mutant ob receptor protein - useful in
XX PT identification of new ligands for prevention and treatment of
XX PT obesity
XX PS Claim 4; Page -: 35pp; English.
XX CC This protein comprises the rat fatty (fa) mutant ob receptor
XX CC (OB-R). Its amino acid sequence was deduced from a cDNA sequence
XX CC (see AAT64962) obtained by PCR amplifications. The sequence differs
XX CC at only 1 position from the wild-type (i.e. lean) OB-R sequence;
XX CC the fa OB-R mutant receptor has proline at amino acid 269 rather
XX CC than glutamine (see AAW23398). This is a result of an A to C
XX CC transversion in the fa OB-R gene (see AAT64962). Every tissue
XX CC examined in an fa/fa Zucker rat was homozygous for this mutation.
XX CC The wild-type and mutant OB-R can be expressed in prokaryotic or
XX CC eukaryotic host cells. They are useful in assays to identify
XX CC putative ligands, which may be receptor agonists or antagonists or
XX CC bind with little effect, and which may be useful in understanding
XX CC obesity and for its prevention and treatment.
XX CC (NB. the sequence for the fa OB-R was obtained by adapting the
XX CC sequence of wild-type OB-R provided in Fig 1 of the specification).
XX SQ Sequence 1162 AA:

Query Match 3.6%; Score 42; DB 18; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPPS 541
Db 498 fqpfllsgytmwlrlnhsllsldspptcvlpdsrvkplpps 539

RESULT 43
AAW23398
ID AAW23398 standard; Protein; 1162 AA.
XX AC AAW23398;
XX DT 23-FEB-1998 (first entry)
XX DE Rat ob receptor (wild-type).
XX KW Ob receptor; obesity; leptin; rat; rodent; animal model; ligand;
XX KW fatty; fa mutation; therapy.
XX OS Rattus sp.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..28
XX FT Protein /label= Slg-peptide
XX FT /label= Mat_protein
XX FT Domain 29..830
XX FT /label= Extracellular_domain
XX FT /label= Transmembrane_domain
XX FT /note= "6"
XX FT Domain 860..1162
XX FT /label= Cytoplasmic_domain
XX FT Misc-difference 269
XX FT /note= "site of mutation in fa OB-R"
XX PN W09731015-A1.
```

```
XX PD 28-AUG-1997.
XX PF 18-FEB-1997; 97WO-US02397.
XX PR 25-APR-1996; 96GB-0008473.
XX PR 22-FEB-1996; 96US-0090405.
XX PR 22-MAR-1996; 96US-0013969.
XX PA (MERI ) MERCK & CO INC.
XX PI Caskey CT, Hess JW, Liu Q, Phillips MS;
XX DR WPI: 1997-435085/40.
XX DR N-PSDB; AAT64961.
XX PT Rat wild-type and mutant ob receptor protein - useful in
XX PT identification of new ligands for prevention and treatment of
XX PT obesity
XX PS Claim 5; Fig 1A-1B; 35pp; English.
XX CC This protein comprises rat wild-type (i.e. lean) ob receptor
XX CC (OB-R). Its amino acid sequence was deduced from a cDNA sequence
XX CC (see AAT64961) obtained by PCR amplifications. The sequence differs
XX CC at only 1 position from the OB-R sequence from rats with a fatty
XX CC (fa) mutation; the fa OB-R mutant receptor has proline at amino
XX CC acid 269 rather than glutamine (see AAW23398). This is a result of
XX CC an A to C transversion in the fa OB-R gene (see AAT64962). Every
XX CC tissue examined in an fa/fa Zucker rat was homozygous for this
XX CC mutation. The wild-type and mutant OB-R can be expressed in
XX CC prokaryotic or eukaryotic host cells. They are useful in assays to
XX CC identify putative ligands, which may be receptor agonists or
XX CC antagonists or bind with little effect, and which may be useful in
XX CC understanding obesity and for its prevention and treatment.
XX SQ Sequence 1162 AA:

Query Match 3.6%; Score 42; DB 18; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPPS 541
Db 498 fqpfllsgytmwlrlnhsllsldspptcvlpdsrvkplpps 539

RESULT 44
AAW19115
ID AAW19115 standard; Protein; 1162 AA.
XX AC AAW19115;
XX DT 26-AUG-1997 (first entry)
XX DE Murine long form Ob receptor.
XX KW Ob receptor; OBR; cytokine receptor; signal transduction;
XX KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;
XX KW therapy.
XX OS Mus musculus.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..22
XX FT Protein /label= Slg-peptide
XX FT /label= ECD
XX FT Domain 23..837
XX FT /note= "extracellular domain"
XX FT /label= TMD
XX FT /note= "transmembrane domain"
XX PN W09731015-A1.
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FT	Domain	861..1162
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FT	/note= "cytoplasmic domain"	
FT	Peptide	317..321
FT	/note= "motif conserved in class I cytokine receptors"	
FT	Peptide	620..624
FT	/note= "motif conserved in class I cytokine receptors"	
FT	Modified-site	41
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FT	/note= "potential N-linked glycosylation site"	
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XX	PN	WO9719952-A1.
XX	PD	05-JUN-1997.
XX	PF	27-NOV-1996;
XX	PR	03-SEP-1996;
XX	PR	27-NOV-1995;
XX	PR	04-DEC-1995;
XX	PR	08-DEC-1995;
XX	PR	11-DEC-1995;
XX	PR	28-DEC-1995;
XX	PR	22-JAN-1996;
XX	PR	26-APR-1996;
XX		96US-0638524.
XX		96US-0708123.
XX		96US-052663.
XX		96US-0566622.
XX		96US-0569485.
XX		96US-0570142.
XX		96US-0583153.
XX		96US-059455.
XX		96US-0638524.

PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Culpepper JA, Tartaglia LA, Tepper RI, White DW;
XX	
DR	WPI; 1997-310525/28.
DR	N-PSDB; AAT69591.
XX	
PT	isolated Ob receptor genes and polypeptide(s) - useful to develop
PT	products for diagnosis or treatment of body weight disorders, e.g.
PT	obesity, cachexia, anorexia and bulimia
XX	
PS	Example; Page 205-213; 265pp; English.
XX	
CC	The murine long form Ob receptor (OBR) (AAW19115) is a novel
CC	polypeptide that participates in the control of body weight and
CC	which is involved in signal transduction triggered by the binding
CC	of its natural ligand, Ob (leptin). It is a member of the class I
CC	cytokine receptor family and is predominantly expressed in the
CC	hypothalamus. Its amino acid sequence was deduced from a
CC	hypothalamus cDNA clone (AAT69591). A short form (AAW19114) of murine
CC	OBR, expressed in the choroid plexus, is associated with the obese
CC	phenotype in db/db mice. The 2 forms differ in the length of the
CC	cytoplasmic domain. OBR proteins, peptides, antibodies, agonists
CC	and antagonists can be used in the diagnosis and treatment of body
CC	weight disorders such as obesity, cachexia and anorexia.
XX	
SQ	Sequence 1162 AA;
	Query Match 3.6%; Score 42; DB 18; Length 1162;
	Best Local Similarity 100.0%; Pred. No. 2.2e-34;
	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	500 FQPIFLSGYTMWIRINHSLSGSDSPCTCVLPDSVVKPLPPS 541       Db 498 fgqiflslsgyltmwirinhslgsidspsptcvlpdsvkvplpps 539
RESULT 45	
AAY13473	
ID	AAY13473 standard; Protein; 1162 AA.
XX	
AC	AAY13473;
XX	
DT	26-JUL-1999 (first entry)
XX	
DE	Peptide Seq ID No: 2 of W09923493;
XX	
KW	Leptin: phosphorylated leptin receptor; tyrosine phosphatase 1D; PTP-1D;
KW	modulator; drug; weight loss; adiposity; hypertension;; heart disease;
KW	type II diabetes; cancer; AIDS; agriculture.
XX	
OS	Mus musculus.
XX	
PN	W09923493-A1.
XX	
PD	14-MAY-1999.
XX	
Pf	27-OCT-1998; 98WO-US22797.
XX	
PR	26-OCT-1998; 98US-0178691.
PR	31-OCT-1997; 97US-0961809.
XX	
PA	(UYRQ ) UNIT ROCKEFELLER.
XX	
PI	Friedman JM, Li C;
XX	
DR	WPI; 1999-327025/27.
DR	N-PSDB; AAX55587.
XX	
PT	Identifying modulators agents that modulate leptin activity
XX	
PS	Disclosure; Page 67-74; 96pp; English.

XX The invention provides a method for identifying modulators of binding of  
CC a phosphorylated leptin receptor with tyrosine phosphatase 1D (PTP-1D).  
CC The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin  
CC receptor or its phosphorylated fragment with protein PTP-1D or its  
CC fragment in the presence and absence of a candidate agent under  
CC conditions in which the absence of the agent the binding of the  
CC phosphorylated leptin receptor or fragment with PTP-1D or its fragment  
CC can be detected; and (b) detecting the binding of the phosphorylated  
CC leptin receptor and PTP 1D; where an increase in binding detected in the  
CC presence of the agent, indicates that the agent enhances binding, and a  
CC decrease in binding in the presence of the agent indicates that the agent  
CC is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin  
CC receptor-dependent PTP-1D phosphorylation are useful as drugs in weight  
CC loss diet regimens. The drugs identified can regulate adiposity and fat  
CC content of animals, particularly in mammals. Disorders that can be  
CC treated by PTP-1D modulators include obesity and its associated diseases,  
CC e.g. hypertension, heart disease and type II diabetes, and weight loss  
CC associated with cancer and AIDS. Additionally the agents identified may  
CC be useful in agriculture where body weight of domestic animals can be  
CC modulated.

SO Sequence 1162 AA;

Query Match 3.6%; Score 42; DB 20; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSGLDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 fqpfllsgytmwirinhslgsldspptcvlpdsrvkplpps 539

## RESULT 46

AAE12615 AAE12615 standard; Protein; 1162 AA.

XX AAE12615;

DT 03-JAN-2002 (first entry)

DE Murine long form Ob receptor (Obr) protein.

KW Murine; obese receptor; Obr; anorectic; anabolic; body weight disorder;  
KW therapy; obesity; cachexia; anorexia.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..22 /label= Signal\_peptide

FT Protein 23..1162 /label= Murine\_mature\_short\_form\_Obr\_protein

FT Domain 23..837 /label= Extracellular\_domain

FT Domain 838..860 /label= Transmembrane\_domain

FT Domain 861..1162 /label= Cytoplasmic\_domain

XX US6287782-B1.

XX 11-SEP-2001.

XX 29-APR-1998; 98US-0069781.

XX 27-NOV-1995; 95US-0562663.

XX 04-DEC-1995; 95US-0566622.

XX 08-DEC-1995; 95US-0569485.

XX 11-DEC-1995; 95US-0570142.

XX 28-DEC-1995; 95US-0583153.

XX 22-JAN-1996; 96US-0599455.

PR 26-APR-1996; 96US-0638524.  
PR 03-SEP-1996; 96US-0708123.  
PR 28-MAY-1997; 97US-0864564.  
XX

PA (MILL-) MILLENNIUM PHARM INC.

PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;

DR WPI; 2001-624489/72.

DR N-PSDB; AAD20541.

XX

PT Identifying compounds for treating body weight disorder, e.g. obesity,

PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob

PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test

PT compound

XX

PS Disclosure; Fig 6; 109pp; English;

XX

CC The patent discloses obese receptor (Obr) proteins and nucleic acids

CC encoding them. Obr protein participates in the regulation of mammalian

CC body weight. The invention also relates to a method of identifying

CC therapeutic compounds for the treatment of a body weight disorder.

CC The method involves contacting a cell that expresses a mammalian Obr

CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test

CC compound. The method is useful for identifying compounds which modulate

CC Obr gene expression and gene product activity, which can be used as

CC agents to control body weight particularly as therapeutic agents for

CC treating body weight disorders, including obesity, cachexia and anorexia.

XX The present sequence is murine long form Obr protein.

SO Sequence 1162 AA;

Query Match 3.6%; Score 42; DB 22; Length 1162;

Best Local Similarity 100.0%; Pred. No. 2.2e-34;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 500 FQPIFLSGYTMWIRINHSGLDSPPTCVLPDSVVKPLPPS 541  
|||||

Db 498 fqpfllsgytmwirinhslgsldspptcvlpdsrvkplpps 539

## RESULT 47

AAW24054 AAW24054 standard; Protein; 783 AA.

XX AAW24054;

DT 17-MAR-1998 (first entry)

DE Murine WSX receptor extracellular domain.

KW Murine; WSX receptor; mouse; identification; purification;

KW ligand; activator; antibody; agonist; proliferation; obesity;

KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;

KW Type II diabetes; polycystic ovarian disease;

KW cardiovascular disease; osteoarthritis; dermatological disorder;

KW hypertension; insulin resistance; hypercholesterolaemia;

KW hypertriglyceridaemia; cancer; cholelithiasis.

XX Mus sp.

XX WO9725425-A1.

XX 17-JUL-1997.

XX 07-JAN-1997; 97WO-US00325.

XX 20-JUN-1996; 96US-0667197.

XX 08-JAN-1996; 96US-0585005.

XX (GETH ) GENENTECH INC.

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;  
 PI Rodrigues ML;  
 XX  
 DR WPI: 1997-372864/34.  
 DR N-PSDB: AAT85578.  
 XX  
 PT WSX receptor and related antibodies and ligands - used to develop  
 PT products for diagnosis and therapy, e.g. for improving  
 PT haematopoiesis or for treating tumours  
 PS  
 XX Example 7; Pages 98-101; 219pp; English.  
 CC The present sequence is the murine WSX receptor extracellular  
 CC domain, which can be used to identify and purify ligands and  
 CC activators. An anti-WSX receptor antibody can be used as an agonist  
 CC to activate the WSX receptor, leading to enhanced proliferation or  
 CC differentiation of a cell expressing the WSX receptor. It can also  
 CC be used to decrease body weight and/or fat-depot weight and/or food  
 CC intake in an obese mammal. WSX receptor ligands can be used to  
 CC enhance proliferation or differentiation of lymphoid, myeloid or  
 CC erythroid blood cell lineages. This is useful when a mammal,  
 CC especially a human, is suffering from decreased blood cell levels,  
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone  
 CC marrow transplantation therapy. It can also be used to repopulate  
 CC blood cells in a mammal. The products can also be used to treat,  
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,  
 CC polycystic ovarian disease, cardiovascular diseases,  
 CC osteoarthritis, dermatological disorders, hypertension, insulin  
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer  
 CC and cholelithiasis.  
 CC  
 SQ Sequence 783 AA;  
 XX  
 Query Match 2.8%; Score 33; DB 18; Length 783;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 418 CHHRYAELLYVIDVNINISCEWIDGYLTMTGRWS 450  
 ||||||||||||||||||||||||||||||||||||  
 Db 416 chhryaelyvidvniniscetdgyltkmtcrws 448

RESULT 48  
 AAB48723  
 ID AAB48723 standard; peptide; 25 AA.  
 XX  
 AC AAB48723;  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Human leptin receptor (OBR) CRM2 E-F loop.  
 XX  
 KW Haematopoietic growth factor receptor; cytokine receptor; subunit;  
 KW CR domain; CRD; CRD3; h-beta-c subunit; GM-CSF receptor; IL-3 receptor;  
 KW IL-5 receptor; agonist; antagonist; myeloid leukaemia; cancer; human;  
 KW lymphocyte leukaemia; non-haematopoietic tumour; inflammatory disease;  
 KW asthma; rheumatoid arthritis; atherosclerosis; CR module; CRM; E-F loop.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20006632-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PE 01-MAY-2000; 2000WO-AU00394.  
 XX  
 PR 29-APR-1999; 99AU-0000053.  
 XX  
 PA (MEDV-) MEDVET SCI PTY LTD.  
 XX  
 PI D'Andrea R, Bagley C, Vadas MA;  
 XX

DR WPI: 2001-049688/06.  
 XX  
 PT New agonists or antagonists of haematopoietic growth factors for treating  
 PT myeloid and lymphocyte leukemias, tumors and acute and chronic  
 PT inflammation such as asthma, rheumatoid arthritis and atherosclerosis -  
 XX  
 PS Disclosure; Fig 6; 35pp; English.  
 XX  
 CC The invention relates to a novel agonist or antagonist of a haematopoietic  
 CC growth factor which is capable of binding a region of the CRD3 (cytokine  
 CC receptor domain 3) of the human GM-CSF receptor/IL-3R/IL-5R shared  
 CC subunit h-beta-c, or an equivalent CRD in a different haematopoietic  
 CC growth factor receptor or other cytokine receptor. Binding of the  
 CC agonist or antagonist has an effect on the interaction between CDR3 and  
 CC CDR4 (or analogous domains) which mediates the agonist or antagonist  
 CC property. In particular, the agonist or antagonist binds to the A-B loop  
 CC or the E-F loop of CRD3 or its equivalent. The invention also relates to  
 CC a method for screening and isolating a haematopoietic growth factor agonist  
 CC or antagonist, and pharmaceutical compositions containing an agonist or  
 CC antagonist. The agonists are used for treating conditions currently  
 CC treated by GM-CSF (granulocyte macrophage-colony stimulating factor),  
 CC IL-3 (interleukin-3), IL-5, and other members of the family of  
 CC haematopoietic growth factors. Haematopoietic growth factor antagonists are  
 CC useful for treating diseases such as myeloid and lymphocyte leukaemias,  
 CC tumours of non-haematopoietic origin and acute and chronic inflammatory  
 CC conditions (e.g., asthma, rheumatoid arthritis and atherosclerosis).  
 CC Sequences AAB48717-B48723 represent the E-F loops of a variety of human  
 CC cytokine receptor subunits.  
 CC  
 SQ Sequence 25 AA;  
 XX  
 Query Match 2.1%; Score 25; DB 22; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-18;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 493 DGFYECIFQPIFLLSGYTMWRINH 517  
 ||||||||||||||||||||||||||||||||  
 Db 1 dgfyecifqipifllsgytmwrinh 25

RESULT 49  
 AAW32073  
 ID AAW32073 standard; peptide; 23 AA.  
 XX  
 AC AAW32073;  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Leptin internalisation sequence receptor fragment.  
 XX  
 KW Human; leptin; receptor;  
 KW internalisation sequence; screening; treatment; NIDDM;  
 KW non-insulin dependent diabetes mellitus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9732899-A1.  
 XX  
 PD 12-SEP-1997.  
 XX  
 PF 07-MAR-1997; 97WO-US03549.  
 XX  
 PR 23-JAN-1997; 97US-0788820.  
 PR 08-MAR-1996; 96US-0612999.  
 PR 22-AUG-1996; 96US-0701382.  
 XX  
 PA (RECE-) RECEPTRON.  
 XX  
 PI Navrenda T, Olsson L;  
 XX  
 DR WPI: 1997-457487/42.  
 XX

PT Peptide(s) derived from a cell surface receptor extracellular domain  
PT - correspond to the internalisation sequence, modulate  
PT internalisation of cell surface receptors, for treating disease with  
PT reduced hormone sensitivity  
XX  
PS Claim 12; Page 23; 37pp; English.  
XX  
CC The present leptin internalisation sequence receptor fragment, was  
CC used in the preparation of a novel oligopeptide. The oligopeptide  
CC comprises an internalisation domain of 8-40 amino acids having a  
CC sequence corresponding to the extracellular domain of a cell  
CC surface receptor, where the oligopeptide enhances the effect of  
CC ligand binding to the receptor expressed by a cell. The  
CC oligopeptide and cell can be used to screen for bioactive agents  
CC capable of modulating the internalisation of a cell surface  
CC receptor. Internalisation sequences of the extracellular domains of  
CC receptor inhibit internalisation of the receptor, but do not affect  
CC binding of the ligand. Inhibition of receptor internalisation  
CC results in more receptors at the cell surface to bind the ligand,  
CC i.e. an increase in ligand binding effectiveness. The increase in  
CC ligand signalling is useful for treating diseases where hormone  
CC sensitivity is reduced, e.g. non-insulin dependent diabetes  
CC mellitus (NIDDM).  
XX  
SQ Sequence 23 AA;

Query Match 2.0%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.9e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 KKENKIYPSKEIYWMNLAEKIP 377  
Db 1 kkenkiypskeiywmnlaekip 23

## RESULT 50

ID AAY39406 standard; peptide; 23 AA.

XX AAY39406;

DT 30-NOV-1999 (first entry)

DE Human leptin receptor-derived activation peptide.

KW Leptin; receptor; activation; internalisation; obesity.

OS Synthetic.

OS Homo sapiens.

PN WO9942127-A2.

PD 26-AUG-1999.

PF 23-FEB-1999; 99WO-US03910.

PR 24-FEB-1998; 98US-0028938.

PA (RECE-) RECEPTRON INC.

PI Olsson L, Naranda T;

DR WPI; 1999-527422/44.

PT Modulating activity of type-2 cell surface receptors used in treatment

PT of, e.g. obesity

PS Claim 8; Page 17; 92pp; English.

CC This sequence represents a peptide derived from the extracellular

CC activation sequence of the human leptin receptor.

CC Activation sequences are involved in modulation of receptor

CC responses and are separate from the ligand binding site. Activation  
CC sequences are important in two distinct ways: in the modulation of  
CC receptor internalisation; and/or in the modulation of activation of the  
CC receptor. Use of peptides corresponding to the activation sequence of a  
CC receptor can retard or inhibit receptor internalisation, thereby  
CC increasing or stabilising the steady-state number of active receptors on  
CC the cell surface. This has the effect of increasing signalling per unit  
CC of ligand. In addition, the receptor is classed as a type 2 cell surface  
CC receptor, meaning that such peptides can actually replace the requirement  
CC for the ligand, causing ligand-independent activation. This activation is  
CC probably brought about by a dimerisation mechanism in which one peptide  
CC molecule is bound by two receptors, mimicking the dimerisation and  
CC subsequent activation that occurs when two receptors bind one ligand.  
CC This peptide could be used to treat disorders involving an inadequate  
CC or inappropriate response from its corresponding receptor e.g., obesity.

Query Match 2.0%; Score 23; DB 20; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.9e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 KKENKIYPSKEIYWMNLAEKIP 377  
Db 1 kkenkiypskeiywmnlaekip 23

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Job time: 532 sec





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:02:01 ; Search time 124.34 Seconds  
(without alignments)  
3297.872 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVLLHMEFIYIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 3502263 seqs, 351980561 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1165	100.0	1165	9	US-08-583-153A-4
3	1165	100.0	1165	9	US-08-585-005-2
4	1165	100.0	1165	10	US-08-638-524B-4
5	1165	100.0	1165	10	US-08-667-197-2
6	1165	100.0	1165	11	US-08-708-123D-4
7	1165	100.0	1165	11	US-08-779-457-2

8	1165	100.0	1165	11	US-08-780-562-2	Sequence 2, Appli
9	1165	100.0	1165	14	US-09-094-410-4	Sequence 4, Appli
10	1165	100.0	1165	15	US-09-137-132-4	Sequence 4, Appli
11	1165	100.0	1165	23	US-09-950-149-4	Sequence 4, Appli
12	1165	100.0	1216	11	US-08-774-414-7	Sequence 7, Appli
13	1165	100.0	1216	20	US-09-671-049-7	Sequence 7, Appli
14	1064	91.3	1165	9	US-08-599-974C-56	Sequence 56, Appli
15	1064	91.3	1165	11	US-08-713-296-11	Sequence 11, Appli
16	1064	91.3	1165	13	US-08-961-809-4	Sequence 4, Appli
17	1064	91.3	1165	15	US-09-178-691-4	Sequence 4, Appli
18	1064	91.3	1165	21	US-09-700-813-10	Sequence 10, Appli
19	1064	91.3	1165	23	US-09-948-933-256	Sequence 256, App
20	1064	91.3	1165	23	US-09-948-947-73	Sequence 73, Appli
21	1064	91.3	1165	24	US-10-095-929-11	Sequence 11, Appli
22	963	82.7	1165	9	US-08-583-153-4	Sequence 4, Appli
23	963	82.7	1165	9	US-08-599-455A-4	Sequence 4, Appli
24	963	82.7	1165	10	US-08-638-524A-4	Sequence 4, Appli
25	963	82.7	1165	11	US-08-708-123C-4	Sequence 4, Appli
26	963	82.7	1165	12	US-08-864-564A-4	Sequence 4, Appli
27	963	82.7	1165	24	US-10-079-625-4	Sequence 284, App
28	963	82.7	1167	23	US-09-948-933-284	Sequence 87, Appli
29	963	82.7	1167	23	US-09-948-947-87	Sequence 4, Appli
30	962	82.6	1165	9	US-08-570-142B-4	Sequence 4, Appli
31	962	82.6	1165	9	US-08-570-142C-4	Sequence 4, Appli
32	891	76.5	896	9	US-08-582-825-1	Sequence 1, Appli
33	891	76.5	896	9	US-08-582-825A-1	Sequence 1, Appli
34	891	76.5	896	9	US-08-585-005-3	Sequence 3, Appli
35	891	76.5	896	10	US-08-667-197-3	Sequence 3, Appli
36	891	76.5	896	11	US-08-779-457-3	Sequence 3, Appli
37	891	76.5	896	11	US-08-780-562-3	Sequence 3, Appli
38	891	76.5	923	9	US-08-585-005-4	Sequence 4, Appli
39	891	76.5	923	10	US-08-667-197-4	Sequence 4, Appli
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47	891	76.5	969	11	US-08-774-414-6	Sequence 6, Appli
48	891	76.5	969	20	US-09-671-049-5	Sequence 5, Appli
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50	891	76.5	995	9	US-08-582-825-3	Sequence 3, Appli
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52	891	76.5	995	11	US-08-774-414-3	Sequence 3, Appli
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54	839	72.0	839	11	US-08-774-414-10	Sequence 10, Appli
55	839	72.0	839	20	US-09-671-049-10	Sequence 10, Appli
56	811	69.6	1137	9	US-08-569-485-4	Sequence 4, Appli
57	798	68.5	804	11	US-08-774-414-13	Sequence 13, Appli
58	798	68.5	804	15	US-09-116-676-10	Sequence 10, Appli
59	798	68.5	804	20	US-09-671-049-13	Sequence 13, Appli
60	742	63.7	883	13	US-08-982-430-1	Sequence 1, Appli
61	735	63.1	841	9	US-08-565-405-2	Sequence 2, Appli
62	681	58.5	896	11	US-08-713-296-10	Sequence 10, Appli
63	681	58.5	896	17	US-09-357-914-33	Sequence 33, Appli
64	681	58.5	896	24	US-10-095-929-10	Sequence 10, Appli
65	681	58.5	906	11	US-08-713-296-9	Sequence 9, Appli
66	681	58.5	906	17	US-09-357-914-32	Sequence 32, Appli
67	681	58.5	906	24	US-10-095-929-9	Sequence 9, Appli
68	681	58.5	958	11	US-08-713-296-8	Sequence 8, Appli
69	681	58.5	958	24	US-10-095-929-8	Sequence 8, Appli
70	681	58.5	960	9	US-08-589-915A-3	Sequence 3, Appli
71	681	58.5	960	17	US-09-357-914-8	Sequence 8, Appli
72	580	49.8	960	11	US-08-713-296-3	Sequence 3, Appli
73	580	49.8	960	24	US-10-095-929-3	Sequence 3, Appli
74	568	48.8	1221	13	US-08-982-430-2	Sequence 2, Appli
75	474	40.7	898	9	US-08-588-189-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-08-570-142D-4  
: Sequence 4, Application US/08570142D  
: GENERAL INFORMATION:  
: APPLICANT: Tartaglia, Louis A.  
: APPLICANT: Tepper, Robert I.  
: APPLICANT: Culpepper, Janice A.  
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
: TITLE OF INVENTION: OBESITY AND CACHEXIA  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fish & Richardson, P.C.  
: STREET: 225 Franklin Street  
: CITY: Boston  
: STATE: MA  
: COUNTRY: US  
: ZIP: 02110-2804  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: Windows95  
: SOFTWARE: FASTSEQ for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/570,142D  
: FILING DATE: 11-DEC-1995  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/569,485  
: FILING DATE: 08-DEC-1995  
: APPLICATION NUMBER: 08/566,622  
: FILING DATE: 04-DEC-1995  
: APPLICATION NUMBER: 08/562,663  
: FILING DATE: 27-NOV-1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Meiklejohn, Ph.D., Anita L.  
: REGISTRATION NUMBER: 35,283  
: REFERENCE/DOCKET NUMBER: 07334/014001  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 617-542-5070  
: TELEFAX: 617-542-8906  
: TELEX: 200154  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1165 amino acids  
: TYPE: amino acid  
: TOPOLOGY: unknown  
: MOLECULE TYPE: protein  
: FRAGMENT TYPE: Internal  
: US-08-570-142D-4

Query Match 100.0%; Score 1165; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNSTVDYFLLPAGLSKNTSNS 60  
|||  
DB 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNSTVDYFLLPAGLSKNTSNS 60  
|||

QY 61 NGHYETAVERKFNSSGTHFSNLSKTFHCFCRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
|||  
DB 61 NGHYETAVERKFNSSGTHFSNLSKTFHCFCRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
|||

QY 121 QOIDANMNIOQWLKGLKLFICYVESLEKFLFRNYKVVHLVLEPEVLEDSPLVPQKGS 180  
|||  
DB 121 QOIDANMNIOQWLKGLKLFICYVESLEKFLFRNYKVVHLVLEPEVLEDSPLVPQKGS 180  
|||

QY 181 FQMVHNCVSHCECECLVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
|||  
DB 181 FQMVHNCVSHCECECLVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
|||

QY 241 LGLHMEITDDGNLKISWSSPLVPFLQYQVXSENSTTVIREADKIVSATSLVDLSILP 300  
|||

DB 241 LGLHMEITDDGNLKISWSSPLVPFLQYQVXSENSTTVIREADKIVSATSLVDLSILP 300  
QY 301 GSSYEVQVRGRRLDGPIMSDWSTPRVFETQDYIYEPKILTSVGSNVSFHCYKKNKI 360  
|||  
DB 301 GSSYEVQVRGRRLDGPIMSDWSTPRVFETQDYIYEPKILTSVGSNVSFHCYKKNKI 360  
|||

QY 361 VPSKEIVMMNLAEKIPQSDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECH 420  
|||  
DB 361 VPSKEIVMMNLAEKIPQSDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHECH 420  
|||

QY 421 RYAEIYIDVNNINISCETDGYLTMTCRWSTSTIOSLAESTLQLRHRSLLYCSIDPSIH 480  
|||  
DB 421 RYAEIYIDVNNINISCETDGYLTMTCRWSTSTIOSLAESTLQLRHRSLLYCSIDPSIH 480  
|||

QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
|||  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
|||

QY 541 SSVKAEITINIGLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
|||  
DB 541 SSVKAEITINIGLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
|||

QY 601 PDLCAVYAVQVRGRRLDGLGYSNWSNPATVYMDIKVPMRGPPEFRIINGDTMKKEKNV 660  
|||  
DB 601 PDLCAVYAVQVRGRRLDGLGYSNWSNPATVYMDIKVPMRGPPEFRIINGDTMKKEKNV 660  
|||

QY 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
|||  
DB 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720  
|||

QY 721 GASVANFNLTFSWPMKSVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
|||  
DB 721 GASVANFNLTFSWPMKSVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
|||

QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLPIFMEGVGPKIINSTQDDIEKHQSDA 840  
|||  
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLPIFMEGVGPKIINSTQDDIEKHQSDA 840  
|||

QY 841 GLYVIVPVISSILLGLTLLISHORMKLEWEDVPNPKNCWAQGLNFQKPEFHEHFI 900  
|||  
DB 841 GLYVIVPVISSILLGLTLLISHORMKLEWEDVPNPKNCWAQGLNFQKPEFHEHFI 900  
|||

QY 901 KHTASVTCGPLLEPETISEDISVDTSNKNDEMPPTTVVSLSTPDLKGSVCISDOFN 960  
|||  
DB 901 KHTASVTCGPLLEPETISEDISVDTSNKNDEMPPTTVVSLSTPDLKGSVCISDOFN 960  
|||

QY 961 SVNFSEAGTEVYEDESQROPFVKYATILSNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
|||  
DB 961 SVNFSEAGTEVYEDESQROPFVKYATILSNSKPSSETGEEGLINSVTKCFSSKNSPL 1020  
|||

QY 1021 KDSFSSNWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1080  
|||  
DB 1021 KDSFSSNWEIEAQAFFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNDKKSIIYL 1080  
|||

QY 1081 GVTISIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
|||  
DB 1081 GVTISIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
|||

QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
|||  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
|||

RESULT 2  
US-08-583-153A-4  
: Sequence 4, Application US/08583153A  
: GENERAL INFORMATION:  
: APPLICANT: Tartaglia, Louis A.  
: APPLICANT: Tepper, Robert I.  
: APPLICANT: Culpepper, Janice A.  
: TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
: TITLE OF INVENTION: OBESITY AND CACHEXIA

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melklejohn, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-583-153A-4

Query Match 100.0%; Score 1165; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYF 120  
DB 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLYF 120  
QY 121 QOIDANWNIQCWLKGLKLFICYVESLFFKNLFRNRYKVHLLVLPVLEDSPLYVQKGS 180  
DB 121 QOIDANWNIQCWLKGLKLFICYVESLFFKNLFRNRYKVHLLVLPVLEDSPLYVQKGS 180  
QY 181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMCLKITSGGVIFQSPILMSVOPINNVKRPDP 240  
DB 181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMCLKITSGGVIFQSPILMSVOPINNVKRPDP 240  
QY 241 LGLHMEITDDGNLKISNSPPLVPFPLQYQVKSSENSTTVIREADKIVATSLSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISNSPPLVPFPLQYQVKSSENSTTVIREADKIVATSLSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPGLMSDSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREKI 360  
DB 301 GSSYEYQVRGKRLDGPGLMSDSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREKI 360  
QY 361 VPSKEIWMNMLAEKIPQSQYDVSDHVSQVTFNINLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIWMNMLAEKIPQSQYDVSDHVSQVTFNINLNETKPRGKFTYDAVYCCNEHECHH 420

DB 361 VPSKEIWMNMLAEKIPQSQYDVSDHVSQVTFNINLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCEFTDGLTKMTCRWSTSTIQSLAESTLQLRHRSSLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNINISCEFTDGLTKMTCRWSTSTIQSLAESTLQLRHRSSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDGFYECLIFQPIFLLSGYTMWIRINSLGSLNSPPTCVLPDSVYKPLPP 540  
DB 481 PISEPKDCYLOSDGFYECLIFQPIFLLSGYTMWIRINSLGSLNSPPTCVLPDSVYKPLPP 540  
QY 541 SSVKAEITINIGLKISWEKVPPEPNLQFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKISWEKVPPEPNLQFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPENRTINGDTMKKEKNV 660  
DB 601 PDLCAVYAVOVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPENRTINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSQVGNHTKFTFLTEQAHVTVLAINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSQVGNHTKFTFLTEQAHVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIYSWILSPSDYKLMFYIIEWKNLNE 780  
DB 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIYSWILSPSDYKLMFYIIEWKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKYYIHDFPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVIVPVTISSILLGLTLLSHQRMKLPWEDVPNPKNSWAQGLNFQKPTFEHLFI 900  
DB 841 GLYIVIVPVTISSILLGLTLLSHQRMKLPWEDVPNPKNSWAQGLNFQKPTFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDSVDTSMKNKDEMPPTVVSILSTDLKESVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDSVDTSMKNKDEMPPTVVSILSTDLKESVCISDQFN 960  
QY 961 SVNFEAEGTEVTEYEDSQRQPFYKATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFEAEGTEVTEYEDSQRQPFYKATLISNSKPSSETGEGGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTISIKKRESGVLLTDKSRVSCPEPPAPCLFTDIRVLQDSCSHVENNINLGTSSKKTFS 1140  
DB 1081 GVTISIKKRESGVLLTDKSRVSCPEPPAPCLFTDIRVLQDSCSHVENNINLGTSSKKTFS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
RESULT 3  
US-08-585-005-2  
; Sequence 2, Application US/08585005  
; GENERAL INFORMATION:  
; APPLICANT: Matthews, William  
; APPLICANT: Bennett, Brian  
; TITLE OF INVENTION: WSX RECEPTOR  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,005  
FILING DATE: 08-Jan-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-585-005-2

Query Match 100.0%; Score 1165; DB 9; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHWEIYVITAFNLSTPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCGRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
DB 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCGRSEODRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANMNIQCWLKGLDLKFLICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180  
DB 121 QQIDANMNIQCWLKGLDLKFLICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180  
QY 181 FOMVHCNSVHECCCLVPTAKLNDTLMLCKITSGVIFQSPMLSVQPINMVKPDP 240  
DB 181 FOMVHCNSVHECCCLVPTAKLNDTLMLCKITSGVIFQSPMLSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKLISWSSPLVFPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMETDDGNLKLISWSSPLVFPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOYRGKRLDGPGLSDMSTPRVFTTQDYIYFPFKILTSGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVOYRGKRLDGPGLSDMSTPRVFTTQDYIYFPFKILTSGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDYNINISCEITDGYLTMTGCRWSTSTQSLAESTLQIRYHRSLSLYCSDIPSIH 480  
DB 421 RYAEIYVIDYNINISCEITDGYLTMTGCRWSTSTQSLAESTLQIRYHRSLSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPTCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLQOIRYGLSGKEVQMKMYEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLQOIRYGLSGKEVQMKMYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATVVMIDIKVPMRGPFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYSWMSNPATVVMIDIKVPMRGPFWRIINGDTMKKEKNV 660  
QY 661 TLHMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLMTEQAHVTVLAINSI 720  
DB 661 TLHMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLMTEQAHVTVLAINSI 720

QY 721 GASVANFLTFSPMSKVINIVOSLSAYPLNNSCVIVSWILSPSDYKIMYFIEMKNLNE 780  
DB 721 GASVANFLTFSPMSKVINIVOSLSAYPLNNSCVIVSWILSPSDYKIMYFIEMKNLNE 780  
QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKITNSFTODDIEKHOSDA 840  
DB 781 GEIKWLRISSVKKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKITNSFTODDIEKHOSDA 840  
QY 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMSAQGLNFQKPEFELHFI 900  
DB 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMSAQGLNFQKPEFELHFI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTTVVSLSTTDLEKGSVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTTVVSLSTTDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETEYTESQROPEVKYATLLISNSKPSSETGEEQGLINSSVTCKFSSKNSPL 1020  
DB 961 SVNFSEAEGETEYTESQROPEVKYATLLISNSKPSSETGEEQGLINSSVTCKFSSKNSPL 1020  
QY 1021 KDSFNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
DB 1021 KDSFNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPACUFTDIRVLQDSCSHEVENNINLGTSSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPFPACUFTDIRVLQDSCSHEVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

#### RESULT 4

US-08-638-524B-4

Sequence 4, Application US/08638524B

#### GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

TITLE OF INVENTION: CACHEXIA

CORRESPONDENCE ADDRESS: 50

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

FILING DATE: 26-APR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/018001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-638-524B-4

Query Match 100.0%; Score 1165; DB 10; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVTAFLNLSYPTIPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVTAFLNLSYPTIPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQWLKGLDKLFICYVESLFLKFLFRNYNKVHLLVLPVLEDSPLVPQKS 180  
Db 121 QOIDANMNIOQWLKGLDKLFICYVESLFLKFLFRNYNKVHLLVLPVLEDSPLVPQKS 180  
QY 181 FQMVHCNCSVHECCCLVYPYPAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMKPDP 240  
Db 181 FQMVHCNCSVHECCCLVYPYPAKLNDTLMLCLKITSQGVIFQSPILMSVQPINMKPDP 240  
QY 241 LGLHMEITDDGNLKSWSPPLPVFPLOYQVYSENSTVIREADKIVSATSLVDILP 300  
Db 241 LGLHMEITDDGNLKSWSPPLPVFPLOYQVYSENSTVIREADKIVSATSLVDILP 300  
QY 301 GSSYEVOVRGKRLDGPISDMSPTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKENK 360  
Db 301 GSSYEVOVRGKRLDGPISDMSPTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKENK 360  
QY 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFENLNKTRGKFTYDAVYCCNEHECH 420  
Db 361 VPSKEIWMNMNLAEKIPQSQDYVSDHVSQVTFENLNKTRGKFTYDAVYCCNEHECH 420  
QY 421 RYALYVIDVNINISCEITDGLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSH 480  
Db 421 RYALYVIDVNINISCEITDGLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSH 480  
QY 481 PISEPKDCYLQSDGFYECIFQIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFYECIFQIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHHSTSCNGTWSQEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDLSQVQRYVINHHSTSCNGTWSQEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780

Db 721 GASVANFNLTFSWPMKSVNIQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMGEVGRKINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMGEVGRKINSFTQDDIEKHQSDA 840  
QY 841 GLYIVPVITISSILLGLTLISHQRMKLFMEDVNPKNCSWAQGLNFQKPFTEFHELF 900  
Db 841 GLYIVPVITISSILLGLTLISHQRMKLFMEDVNPKNCSWAQGLNFQKPFTEFHELF 900  
QY 901 KHTASVTCGPLLEPETISEDIVTSWKKNKDEMPPTVVSLSLSTDLKSGVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDIVTSWKKNKDEMPPTVVSLSLSTDLKSGVCISDQFN 960  
QY 961 SVNFESEAGTEVTYEDESQROPVRYAULISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020  
Db 961 SVNFESEAGTEVTYEDESQROPVRYAULISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSSEGLDELKLEGNFPEENNDKSIYYL 1080  
Db 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTSTIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSTIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 5  
US-08-667-197-2  
Sequence 2, Application US/08667197  
GENERAL INFORMATION:  
APPLICANT: Matthews, William  
TITLE OF INVENTION: USES FOR WSX LIGANDS  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/667,197  
FILING DATE: 20-Jun-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: P-40,378  
REFERENCE/DOCKET NUMBER: P0986P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-667-197-2

Query Match 100.0%; Score 1165; DB 10; Length 1165;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVALLHMEFIYVITAENLSYPIEWRKLSCMPNSTYDYFLLPAGLSKNTSNS 60  
 DB 1 MICQFCVALLHMEFIYVITAFNLSTYPIEWRKLSCMPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHYETAVEPKENSSGTHFSNLSKTIHFCRSEQDRNCSLCADNIEGTFVSTVNSLVE 120  
 DB 61 NGHYETAVEPKENSSGTHFSNLSKTIHFCRSEQDRNCSLCADNIEGTFVSTVNSLVE 120

QY 121 QOIDANMNIOCMWLGDKLFLICYVESLTFKLNFRNRYKHLLYLPEVLEDSPLVPQKS 180  
 DB 121 QOIDANMNIOCMWLGDKLFLICYVESLTFKLNFRNRYKHLLYLPEVLEDSPLVPQKS 180

QY 181 FQMVHCNCSVHECCCLVPTAKLNDITLMCLKITSGVIFQSPILMSVQPINMVKPDP 240  
 DB 181 FQMVHCNCSVHECCCLVPTAKLNDITLMCLKITSGVIFQSPILMSVQPINMVKPDP 240

QY 241 LGLHMETDDGNLKISWSSPPLVPFLOQVYKXSENSTVIREADKIYSAFSLVDSILP 300  
 DB 241 LGLHMETDDGNLKISWSSPPLVPFLOQVYKXSENSTVIREADKIYSAFSLVDSILP 300

QY 301 GSSYEVQVRGKRLDGPWSDWSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360  
 DB 301 GSSYEVQVRGKRLDGPWSDWSTPRVFTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360

QY 361 VPSKEIWMWMLAEKIPQSOYDVSDHVSATFENLNETKPRGKFTYDAVYCCNEHECHH 420  
 DB 361 VPSKEIWMWMLAEKIPQSOYDVSDHVSATFENLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVNMNISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
 DB 421 RYAEIYVIDVNMNISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480

QY 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMWIRINHSLSGLSDSPFCVLPDSVVKPLRP 540  
 DB 481 PISEPKDCYLOSDGFYECIFOPIFLLSGYTMWIRINHSLSGLSDSPFCVLPDSVVKPLRP 540

QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 600  
 DB 541 SSVKAEITINIGLKLISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDKAKSKSVSLPV 600

QY 601 PDLCAVYAVQYRCKRLDGLGYWSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
 DB 601 PDLCAVYAVQYRCKRLDGLGYWSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTLAINSI 720  
 DB 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVGNHTKFTFLWTEQAHTVTLAINSI 720

QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780  
 DB 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780

QY 781 GEIKMLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
 DB 781 GEIKMLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVIISSIIILGLTLLISHQRMKLLFEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
 DB 841 GLYVIVPVIISSIIILGLTLLISHQRMKLLFEDVNPKNCSWAQGLNFQKPETFEHLFI 900

QY 901 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPPTVSVSLSTDLEKGSVCISDQFN 960  
 DB 901 KHTASVTCGPLEPETISEDISVDTSMKNKDEMPPTVSVSLSTDLEKGSVCISDQFN 960

QY 961 SVNFSEAGTEVYDEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
 DB 961 SVNFSEAGTEVYDEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020

QY 1021 KDSFNSNSWEIEAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNFPEENNDKKSIYYL 1080

DB 1021 KDSFNSNSWEIEAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNFPEENNDKKSIYYL 1080

QY 1081 GVTISKKRESGYLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
 DB 1081 GVTISKKRESGYLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
 DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 6  
 US-08-708-123D-4  
 ; Sequence 4, Application US/08708123D  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis A.  
 ; APPLICANT: Tepper, Robert I.  
 ; APPLICANT: Culpepper, Janice A.  
 ; APPLICANT: White, David W.  
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
 ; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/708,123D  
 ; FILING DATE: 03-SEP-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/638,524  
 ; FILING DATE: 26-APR-1996  
 ; APPLICATION NUMBER: 08/599,455  
 ; FILING DATE: 22-JAN-1996  
 ; APPLICATION NUMBER: 08/583,153  
 ; FILING DATE: 28-DEC-1995  
 ; APPLICATION NUMBER: 08/570,142  
 ; FILING DATE: 11-DEC-1995  
 ; APPLICATION NUMBER: 08/569,485  
 ; FILING DATE: 08-DEC-1995  
 ; APPLICATION NUMBER: 08/566,622  
 ; FILING DATE: 04-DEC-1995  
 ; APPLICATION NUMBER: 08/562,663  
 ; FILING DATE: 27-NOV-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.  
 ; REGISTRATION NUMBER: 35,283  
 ; REFERENCE/DOCKET NUMBER: 07334/019001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-542-5070  
 ; TELEFAX: 617-542-8906  
 ; TELELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1165 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-708-123D-4

Query Match 100.0%; Score 1165; DB 11; Length 1165;

	Best Local Similarity	100.0%;	Pred. No. 0;	
	Matches 1165;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MICQKFCVLLHWEFIYVTAENLSYPITPWREKLSGCMPPNNTYDYFLLPAGLSKNTSNS	60	
Db	1	MICQKFCVLLHWEFIYVTAENLSYPITPWREKLSGCMPPNNTYDYFLLPAGLSKNTSNS	60	
QY	61	NGHYETAVEPKFNSSGTHFSNLSKTEFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120	
Db	61	NGHYETAVEPKFNSSGTHFSNLSKTEFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120	
QY	121	QOIDANMNIOCLWKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS	180	
Db	121	QOIDANMNIOCLWKGDCLKFICVYESLFKNLFRNRYNKVHLLYLPEVLEDSPLVPQKGS	180	
QY	181	FQMVHCNCVHECCCECLVPVPTAKLNDLLMCLKITSGGVIFQSPMSVOPINMVKPPDP	240	
Db	181	FQMVHCNCVHECCCECLVPVPTAKLNDLLMCLKITSGGVIFQSPMSVOPINMVKPPDP	240	
QY	241	LGLHMEITDDGNLKISWSSPPLVPEPLQYQVYKSENSTTVIREADKIVSATSLLVDSILP	300	
Db	241	LGLHMEITDDGNLKISWSSPPLVPEPLQYQVYKSENSTTVIREADKIVSATSLLVDSILP	300	
QY	301	GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI	360	
Db	301	GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKENKI	360	
QY	361	VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH	420	
Db	361	VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH	420	
QY	421	RYAELLYVDNININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH	480	
Db	421	RYAELLYVDNININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH	480	
QY	481	PISEPKDCYLQSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCYLPDSVYKKPLPP	540	
Db	481	PISEPKDCYLQSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCYLPDSVYKKPLPP	540	
QY	541	SSVKAIEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMEYVDAKSKSVSLPV	600	
Db	541	SSVKAIEITINIGLLKISWEKPVFPENNLOQOIRYGLSGKEVQWKMEYVDAKSKSVSLPV	600	
QY	601	PDLCAVYAVQVRCKRLDGLGIYSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV	660	
Db	601	PDLCAVYAVQVRCKRLDGLGIYSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV	660	
QY	661	TLMKPPLMKNDLSLCSVQRYVINHHTSCNGTWSEDOVGNHTKFTFLWTEQAHVTVLAINSI	720	
Db	661	TLMKPPLMKNDLSLCSVQRYVINHHTSCNGTWSEDOVGNHTKFTFLWTEQAHVTVLAINSI	720	
QY	721	GASVANFNLTFSWPMKSVNIQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED	780	
Db	721	GASVANFNLTFSWPMKSVNIQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED	780	
QY	781	GEIKMLRISSSVKKYIHDHFPIEKKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA	840	
Db	781	GEIKMLRISSSVKKYIHDHFPIEKKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA	840	
QY	841	GLYIVVPIIISSTILLGLTLLISHQMKKLFMEDVPPNPKNCSWAOGLEFQKPETFEHLFI	900	
Db	841	GLYIVVPIIISSTILLGLTLLISHQMKKLFMEDVPPNPKNCSWAOGLEFQKPETFEHLFI	900	
QY	901	KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTTVVSLSTTDLEKGSVCISDOFN	960	
Db	901	KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTTVVSLSTTDLEKGSVCISDOFN	960	
QY	961	SVNFEAEGETEVTYEDESQROPFVKAATLISNSKPSETGEEQGLINSVYTKCFSSKNSPL	1020	
Db	961	SVNFEAEGETEVTYEDESQROPFVKAATLISNSKPSETGEEQGLINSVYTKCFSSKNSPL	1020	
QY	1021	KDSEFNSSWEIEAOAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDRKSIYYL	1080	
Db	1021	KDSEFNSSWEIEAOAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDRKSIYYL	1080	

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Db      1021 KDFSNSSWEIEAOAFILSDQHPNIIISPHLTFSEGLDELLKLGONFPEENNDKKSIIYYL 1080
QY      1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
        |||||||
Db      1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY      1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
        |||||||
Db      1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT      7
US-08-779-457-2
: Sequence 2, Application US/08779457
: GENERAL INFORMATION:
:   APPLICANT: Carter, Paul J.
:   APPLICANT: Chiang, Nancy Y.
:   APPLICANT: Kyung, Jin Kim
:   APPLICANT: Matthews, William
:   APPLICANT: Rodrigues, Maria L.
:   TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
:   NUMBER OF SEQUENCES: 51
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Genentech, Inc.
:     STREET: 460 Point San Bruno Blvd
:     CITY: South San Francisco
:     STATE: California
:     COUNTRY: USA
:     ZIP: 94080
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: WinpatIn (Genentech)
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/779,457
:     FILING DATE:
:     CLASSIFICATION: 435
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: 08/667197
:       FILING DATE: 06/20/96
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: 08/585005
:       FILING DATE: 01/08/96
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Lee, Wendy M.
:       REGISTRATION NUMBER: 40,378
:       REFERENCE/DOCKET NUMBER: P0986P2
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: 415/225-1994
:       TELEFAX: 415/952-9881
:       TELEX: 910/371-7168
:     INFORMATION FOR SEQ ID NO: 2:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 1165 amino acids
:         TYPE: Amino Acid
:         TOPOLOGY: linear
:
US-08-779-457-2

Query Match      100.0%; Score 1165; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSCMPNStYDYFLLPAGLSKNTSNS 60
        |||||||
Db      1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSCMPNStYDYFLLPAGLSKNTSNS 60
QY      61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNI EGKTFVSTVNSLVF 120
        |||||||
Db      61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNI EGKTFVSTVNSLVF 120
QY      121 QQIDANMNIOQWLKGLDKLFICIVESLEFKNLFRNRYNKVHLLYVLPVLEDSPLVPQKGS 180

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Db 121 QOIDANWNIQCWLKGDCLKLFCYVESLEFKNLFRNRYNKVHLTYLPEVLEDSPLVPOKGS 180
Qy 181 FQMVHNCVSHECCCLVVPVPTAKNDTLLMCLKITSGVIFQSPILMSVOPINMVKPDP 240
Db 181 FQMVHNCVSHECCCLVVPVPTAKNDTLLMCLKITSGVIFQSPILMSVOPINMVKPDP 240
Qy 241 LGLHMETDDGNLKISWSSPPLVPPLOQYQVKYSENSTTVIREADKIVATSLSLVDSILP 300
Db 241 LGLHMETDDGNLKISWSSPPLVPPLOQYQVKYSENSTTVIREADKIVATSLSLVDSILP 300
Qy 301 GSSYEVOVRGKRLLDGPGLMSDMSVTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEVOVRGKRLLDGPGLMSDMSVTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Qy 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAEIYVIDVNNINISCEITDGYLTMTCTRWSTSTIQSLAESTLQIRYHRSLSYCSDDIPSIH 480
Db 421 RYAEIYVIDVNNINISCEITDGYLTMTCTRWSTSTIQSLAESTLQIRYHRSLSYCSDDIPSIH 480
Qy 481 PISEPKCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKCYLQSDGFYECIFQPIFLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Qy 541 SSVKAEITINIGLKLKISWEKVPFENNLOFOIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKLKISWEKVPFENNLOFOIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600
Qy 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Qy 661 TLLMKPLMKNDSLCSVQRYVINNHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 661 TLLMKPLMKNDSLCSVQRYVINNHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVLAINSI 720
Qy 721 GASVANFNLFWSMPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 721 GASVANFNLFWSMPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Qy 781 GEIKMLRISSSVKYYIHDFPIEYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKYYIHDFPIEYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Qy 841 GLVYIVPVISSSILLGLTLLSHORMKLLFWEDEVNPNKNCNAOGLNFQKPEFELHFI 900
Db 841 GLVYIVPVISSSILLGLTLLSHORMKLLFWEDEVNPNKNCNAOGLNFQKPEFELHFI 900
Qy 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDIVDTSWKNKDEMPPTVVSLLSTTDLEKGSVCISDQFN 960
Qy 961 SVNFESEAGTEVTEDESQROPYKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFESEAGTEVTEDESQROPYKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSSSWEIEAQAFILSDOHNIIISPHLTFSEGLDELKLEGNFPEENNDKRSIYYL 1080
Db 1021 KDSFNSSSWEIEAQAFILSDOHNIIISPHLTFSEGLDELKLEGNFPEENNDKRSIYYL 1080
Qy 1081 GVTSLIKKRESGLVLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSLIKKRESGLVLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
```

RESULT 8

```
US-08-780-562-2
: Sequence 2, Application US/08780562
: GENERAL INFORMATION:
: APPLICANT: Matthews, William
: APPLICANT: Bennett, Brian
: TITLE OF INVENTION: MSX RECEPTOR
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/780,562
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/585005
: FILING DATE: 01/08/97
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/
: FILING DATE: 01/08/97
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0986R1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/952-9881
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1165 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
US-08-780-562-2

Query Match 100.0%; Score 1165; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MICQKFCVYLLHWEFIYVITAENLSYPTTPWRKFLKSCMPNPNSTYDVFLLPAGLSKNTSNS 60
Db 1 MICQKFCVYLLHWEFIYVITAENLSYPTTPWRKFLKSCMPNPNSTYDVFLLPAGLSKNTSNS 60
Qy 61 NGHYTEAVEPKFNSSGTHFSNLSKTFTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKTFTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Qy 121 QOIDANWNIQCWLKGDCLKLFCYVESLEFKNLFRNRYNKVHLTYLPEVLEDSPLVPOKGS 180
Db 121 QOIDANWNIQCWLKGDCLKLFCYVESLEFKNLFRNRYNKVHLTYLPEVLEDSPLVPOKGS 180
Qy 181 FQMVHNCVSHECCCLVVPVPTAKNDTLLMCLKITSGVIFQSPILMSVOPINMVKPDP 240
Db 181 FQMVHNCVSHECCCLVVPVPTAKNDTLLMCLKITSGVIFQSPILMSVOPINMVKPDP 240
Qy 241 LGLHMETDDGNLKISWSSPPLVPPLOQYQVKYSENSTTVIREADKIVATSLSLVDSILP 300
Db 241 LGLHMETDDGNLKISWSSPPLVPPLOQYQVKYSENSTTVIREADKIVATSLSLVDSILP 300
Qy 301 GSSYEVOVRGKRLLDGPGLMSDMSVTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEVOVRGKRLLDGPGLMSDMSVTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
```



```

QY 361 VPSKEIWMNMNLAETIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
    |||||||
Db 361 VPSKEIWMNMNLAETIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDNINISCTEDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
    |||||||
Db 421 RYAEIYVIDNINISCTEDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDFIECIHQPIFLSLGYTMWIRINSLGSLDSPPTCVLPDSVYKPLRP 540
    |||||||
Db 481 PISEPKDCYLOSDFIECIHQPIFLSLGYTMWIRINSLGSLDSPPTCVLPDSVYKPLRP 540
QY 541 SSVKAEITINIGLKISWEKPVPEENNLOQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKISWEKPVPEENNLOQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVOVRCKRLDGLGYWSNMSNPAYTVMDIKYPMRGPEFWRRIINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVOVRCKRLDGLGYWSNMSNPAYTVMDIKYPMRGPEFWRRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSQYRYVINHTSCNGTWSQVGNHTKFTFLWTEQAHVTVLAINSI 720
    |||||||
Db 661 TLLMKPLMKNDLSQYRYVINHTSCNGTWSQVGNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCAIVSNLSPSDYKLMFTIEKKNED 780
    |||||||
Db 721 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCAIVSNLSPSDYKLMFTIEKKNED 780
QY 781 GEIKWLRISSVKKYIHHFPIPIEKYQSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
    |||||||
Db 781 GEIKWLRISSVKKYIHHFPIPIEKYQSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKCSWAQGLNFQKPEFHEHPI 900
    |||||||
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKCSWAQGLNFQKPEFHEHPI 900
QY 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
    |||||||
Db 901 KHTASVTCGPLLEPETISEDIVDTSMKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
QY 961 SYNFEAEGTEVTEDESQRPVFKYATLLISNSKPSSETGHEOGLINSSVTKCFSSKN SPL 1020
    |||||||
Db 961 SYNFEAEGTEVTEDESQRPVFKYATLLISNSKPSSETGHEOGLINSSVTKCFSSKN SPL 1020
QY 1021 KDSFNSNSWEIEAQAFILSDOHPNIIISPHLTFSEGLDELKLEGNFPEENNNDKKSIIYL 1080
    |||||||
Db 1021 KDSFNSNSWEIEAQAFILSDOHPNIIISPHLTFSEGLDELKLEGNFPEENNNDKKSIIYL 1080
QY 1081 GYTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCHFEVNNINLGTSSKKTFFAS 1140
    |||||||
Db 1081 GYTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCHFEVNNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
    |||||||
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

```

```

; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,410
; FILING DATE: 09-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-094-410-4

Query Match 100.0%; Score 1165; DB 14; length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKECVLLHMEFIYVITAFNLISYPITPWRFKLSQMPNNTYDYFLPAGLSKNTSNS 60
    |||||||
Db 1 MICOKECVLLHMEFIYVITAFNLISYPITPWRFKLSQMPNNTYDYFLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
    |||||||
Db 61 NGHETAVEPKFNSSGTHFSNLSTKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLKLFCTIVESLEFKNLFRNRYKXVHLIYVLPVELEDSPLVPQKS 180
    |||||||
Db 121 QQIDANWNIQCWLKGLKLFCTIVESLEFKNLFRNRYKXVHLIYVLPVELEDSPLVPQKS 180
QY 181 FQWVHCNCSVHECCCLVPPVPTAKINDTLMLCKITSGVIFQSPLMISVQPINMKRDPDP 240
    |||||||
Db 181 FQWVHCNCSVHECCCLVPPVPTAKINDTLMLCKITSGVIFQSPLMISVQPINMKRDPDP 240
QY 241 LGHMEITDDGNLKISWSSPPLVPFPLOYOVKYSSENSTVIREADKIVSATSLVDSILP 300
    |||||||
Db 241 LGHMEITDDGNLKISWSSPPLVPFPLOYOVKYSSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLNSDMSTPRVFTTQDVITYFPKILTSVGSNVSFHCIVKKNKI 360

```

Db 301 GSSYEVQVRGKRDLGPGIWSDMSTPRVFTQVITYFPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIWMWMLAEKIPQSOYDVSDHVSKEYFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMWMLAEKIPQSOYDVSDHVSKEYFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCEITDGYLTMTKCRNSTSIQSLAESTLQLRHRSLLYCSDIPSIH 480  
Db 421 RYAEIYVIDVNNISCEITDGYLTMTKCRNSTSIQSLAESTLQLRHRSLLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDSPPTCYLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDSPPTCYLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINDTMMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVMDIKVPMRGPEFWRIINDTMMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSQVRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSQVRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSNPSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSNPSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDA 840  
Db 781 GEIKWLRISSSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDA 840  
QY 841 GLYVIVPVITSSSILLGLTLLISHQRMKKLEWEDVYPNPKNSWAQGLNFQKPEFHEHLEI 900  
Db 841 GLYVIVPVITSSSILLGLTLLISHQRMKKLEWEDVYPNPKNSWAQGLNFQKPEFHEHLEI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNDEMPITVSLSTTDLKGSVCISDOFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNDEMPITVSLSTTDLKGSVCISDOFN 960  
QY 961 SVNFSEAGTEVYEDESQROPFVKYATLLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAGTEVYEDESQROPFVKYATLLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 10  
US-09-137-132-4  
; Sequence 4, Application US/09137132  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,132  
FILING DATE: 18-AUG-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MelkleJohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-137-132-4

Query Match 100.0%; Score 1165; DB 15; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPIYPAWFKLSKMPNNTYDIFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHMEFIYVITAFNLSYPIYPAWFKLSKMPNNTYDIFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERKNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERKNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANWNIOQWLKGLKLFICYVESLFXNLFERNYNYKVHLLYYLPEVLEDSPLVPQKS 180  
Db 121 QOIDANWNIOQWLKGLKLFICYVESLFXNLFERNYNYKVHLLYYLPEVLEDSPLVPQKS 180  
QY 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
Db 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMETDDCNLKSWSPPPLVPFLOYKYSENSTVITREADKIVSATSLLVDSILP 300  
Db 241 LGLHMETDDCNLKSWSPPPLVPFLOYKYSENSTVITREADKIVSATSLLVDSILP 300

Db 241 LGLHMETDDGNLKIWSSPPLVPEPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRDLDPGIMSDMSTPRVFTTQDVITYFPFKILTVSGSNVSFHCITYKKENKI 360  
Db 301 GSSYEYQVRGKRDLDPGIMSDMSTPRVFTTQDVITYFPFKILTVSGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYIDVNNINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYIDVNNINISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIPLLSGYTMMIRINHSLSGSDSPPCTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIPLLSGYTMMIRINHSLSGSDSPPCTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKPVPEENNLOQIRYGLSGKEVOMKYEYVDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISWEKPVPEENNLOQIRYGLSGKEVOMKYEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAQVRCKRLDGLGYWSMNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAQVRCKRLDGLGYWSMNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSEDEVGNHTKFTFLMTEQAHTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSEDEVGNHTKFTFLMTEQAHTVLAINSI 720  
QY 721 GASVANFNLFESWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780  
Db 721 GASVANFNLFESWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPLEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPLEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
QY 841 GLVYIVPVIISSSILLGLTLLISHQRMKLFWEDEVNPNKNSMAOGLNFQKPEFHEHLEFI 900  
Db 841 GLVYIVPVIISSSILLGLTLLISHQRMKLFWEDEVNPNKNSMAOGLNFQKPEFHEHLEFI 900  
QY 901 KHTASVTCGPLLLEPETISEDIVDSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLLEPETISEDIVDSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETEVTYEDESQROPEYKATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETEVTYEDESQROPEYKATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAOAFILSDQHNIIISPHLTFSEGLDELLEKGNFPEENNDDKSIYYL 1080  
Db 1021 KDSFNSSSWEIEAOAFILSDQHNIIISPHLTFSEGLDELLEKGNFPEENNDDKSIYYL 1080  
QY 1081 GVTSLKKRESGLVLTDKSRVSCPAPCLFTDIRVLAQSDCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSLKKRESGLVLTDKSRVSCPAPCLFTDIRVLAQSDCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTY 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTY 1165

RESULT 11  
US-09-950-149-4  
; Sequence 4, Application US/09950149  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; ; Tepper, Robert I.  
; ; Culpepper, Janice A.  
; ; White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

NUMBER OF SEQUENCES: 50 INCLUDING OBESITY AND CACHEXIA  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/950,149  
FILING DATE: 10-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,781  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: US 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: US 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: US 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: US 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: US 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: US 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: US 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-950-149-4

Query Match 100.0%; Score 1165; DB 23; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTPWREKLSGMPNPNSTYVFLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSYPTPWREKLSGMPNPNSTYVFLPAGLSKNTSNS 60  
QY 61 NGHYETAPEKFNSSGTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAPEKFNSSGTHFSNLSKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANNIQCWLKGDLLFCIYVESLFEKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 180  
Db 121 QQIDANNIQCWLKGDLLFCIYVESLFEKNLFRNRYNKVHLVYLPEVLEDSPLVPQKGS 180  
QY 181 FQMVHCNSVHECCGLVPVPTAKNDTFLMCLKITSGGVIFQSPIMSVQPINMKPDDP 240  
Db 181 FQMVHCNSVHECCGLVPVPTAKNDTFLMCLKITSGGVIFQSPIMSVQPINMKPDDP 240

Db 181 FQMVHNCNSVHECCCLVVPVPTAKLNDTLMLCLKITSGGVIPOSPLMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYALYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
Db 421 RYALYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSVDGNHTKFTFLWTEQAHTVTLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSVDGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANFLTFSPWMSKVINIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANFLTFSPWMSKVINIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKMLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKYYIHDHFIPRIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYIVIPVLISSSILLGLTLISHQRMKLFENEDVNPKNCSWAQGLNFQKPFTEHFLI 900  
Db 841 GLYIVIPVLISSSILLGLTLISHQRMKLFENEDVNPKNCSWAQGLNFQKPFTEHFLI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVSVSLSTDLKGSVCISDOFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVSVSLSTDLKGSVCISDOFN 960  
QY 961 SVNFSEAGTEVTEYEDSQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAGTEVTEYEDSQROPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080  
QY 1081 GYTSIKKRESGYLLDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
Db 1081 GYTSIKKRESGYLLDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 12  
US-08-774-414-7  
; Sequence 7, Application US/08774414  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; APPLICANT: WELCHER, ANDREW A.

; APPLICANT: FLETCHER, FREDERICK A.  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; NUMBER OF INVENTIONS: COMPOSITIONS AND METHODS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,414  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pesslin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382-A  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1216 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-774-414-7

Query Match 100.0%; Score 1165; DB 11: Length 1216;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHNEFIYVITAFNLSTPIFPWRFKLSMPNNTYVYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHNEFIYVITAFNLSTPIFPWRFKLSMPNNTYVYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNI:GKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPKNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNI:GKTFVSTVNSLVF 120  
QY 121 QQIDANMNIOQWLGKDLKLFICYVESLFKNLFRNRYKVVHLLVYLPVLEDSPLVPKGS 180  
Db 121 QQIDANMNIOQWLGKDLKLFICYVESLFKNLFRNRYKVVHLLVYLPVLEDSPLVPKGS 180  
QY 181 FQMVHNCNSVHECCCLVVPVPTAKLNDTLMLCLKITSGGVIPOSPLMSVQPINMVKPDP 240  
Db 181 FQMVHNCNSVHECCCLVVPVPTAKLNDTLMLCLKITSGGVIPOSPLMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYALYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
Db 421 RYALYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKVPFPENNIOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKVPFPENNIOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVAVQVRCRRLDGLGYSNWSNPAATVYMDIKVPMRGPEFNRITNGDTMKKEKNV 660  
DB 601 PDLCAVAVQVRCRRLDGLGYSNWSNPAATVYMDIKVPMRGPEFNRITNGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFHEHLP 900  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFHEHLP 900  
QY 901 KHTASVTCGPILLPEPITISEDISVDTSKKNKDEMPPTVVSLLSTIDLEKGSVCISDQFN 960  
DB 901 KHTASVTCGPILLPEPITISEDISVDTSKKNKDEMPPTVVSLLSTIDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETVYEDSQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAEGETVYEDSQRQPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKSIYYL 1080  
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLTLDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
DB 1081 GVTSIKKRESGVLTLDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 13  
US-09-671-049-7  
: Sequence 7, Application US/09671049  
: GENERAL INFORMATION:  
: APPLICANT: CHANG, MING-SHI  
: WELCHER, ANDREW A.  
: FLETCHER, FREDERICK A.  
: TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
: COMPOSITIONS AND METHODS  
: NUMBER OF SEQUENCES: 33  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Amgen Inc.  
: STREET: 1840 Dehavilland Drive  
: CITY: Thousand Oaks  
: STATE: California  
: COUNTRY: USA  
: ZIP: 91320  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/671,049  
: FILING DATE: 27-Sep-2000  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/774,414  
: FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Pessin, Karol M.  
REFERENCE/DOCKET NUMBER: A-362-A  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1216 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-671-049-7

Query Match 100.0%; Score 1165; DB 20; Length 1216;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMEFIYVITAFNLSTYPTPWRFKLSCMPNSIYVFLPAGLSKNTSNS 60  
DB 1 MICQKFCVVLHMEFIYVITAFNLSTYPTPWRFKLSCMPNSIYVFLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVERPNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANWNIDGKLDKLFICYVESLFKMEFRNRYKVHLLYVLEVEDSPLVPQGS 180  
DB 121 QOIDANWNIDGKLDKLFICYVESLFKMEFRNRYKVHLLYVLEVEDSPLVPQGS 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMCLKITSGVIFQSPLMVQPINMVKPDP 240  
DB 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMCLKITSGVIFQSPLMVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPLVPFPLQYQKXSENSTTVIREADKIYATSLLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPLVPFPLQYQKXSENSTTVIREADKIYATSLLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPQIWSDWSTPRVFTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVQVRGKRLDGPQIWSDWSTPRVFTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQYTFNLETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQYTFNLETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCEFDGYLTMTQCRWSTSTIOSLAESTLQRLRYHRSLLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNNISCEFDGYLTMTQCRWSTSTIOSLAESTLQRLRYHRSLLYCSDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCYLPDSVVKPLRP 540  
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCYLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISWEKVPFPENNIOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKVPFPENNIOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVAVQVRCRRLDGLGYSNWSNPAATVYMDIKVPMRGPEFNRITNGDTMKKEKNV 660  
DB 601 PDLCAVAVQVRCRRLDGLGYSNWSNPAATVYMDIKVPMRGPEFNRITNGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840



```

OY 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNFQKPTFEHLFI 900
DB 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNFQKPTFEHLFI 900
OY 901 KHTASVTCGPLLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTDLKSGSVCSIDQFN 960
DB 901 KHTASVTCGPLLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTDLKSGSVCSIDQFN 960
OY 961 SVNFSEAGTEVTEYDESOQROPFVKYATLISNSKPSGTGEEOGLINSSVTKCFSSKNSPL 1020
DB 961 SVNFSEAGTEVTEYDESOQROPFVKYATLISNSKPSGTGEEOGLINSSVTKCFSSKNSPL 1020
OY 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080
DB 1021 KDSFSNSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKKSITYL 1080
OY 1081 GVTSIKKRESGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
DB 1081 GVTSIKKRESGVLLTDKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
OY 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKCDLTV 1165

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RESULT 14
US-08-599-974C-56
; Sequence 56, Application US/08599974C
; GENERAL INFORMATION:
; APPLICANT: Friedman, Jeffrey M.
; APPLICANT: Lee, Gwo-Hua
; APPLICANT: Proenca, Ricardo
; TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,974C
; FILING DATE: 14-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,594
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-162 CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:

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; ORGANISM: Homo sapiens
US-08-599-974C-56
Query Match 91.3%; Score 1064; DB 9; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MICQFCVLLHWEFTVITAENLSTPITPWRKLSGMPNSTYDVFLLPAGLSKNTS 60
DB 1 MICQFCVLLHWEFTVITAENLSTPITPWRKLSGMPNSTYDVFLLPAGLSKNTS 60
OY 61 NGHYETAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTEVSTVNSLVF 120
DB 61 NGHYETAVEPKFNSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTEVSTVNSLVF 120
OY 121 QCIDANWNIQCWLKGDLEKLFICYVESLFKNLFRNRYKVHLVLPVLEDSPLVPQGS 180
DB 121 QCIDANWNIQCWLKGDLEKLFICYVESLFKNLFRNRYKVHLVLPVLEDSPLVPQGS 180
OY 181 FQMVHNCNVHECCLELVPVPTAKLNDTLMLCLKITSQGVIFOSPLMSVOPINMYKPDPP 240
DB 181 FQMVHNCNVHECCLELVPVPTAKLNDTLMLCLKITSQGVIFOSPLMSVOPINMYKPDPP 240
OY 241 LGLHMEITDDGNLKRISMSPLVPPLQYQVKSSENSTTVIREADKIVSATSLVDSTLP 300
DB 241 LGLHMEITDDGNLKRISMSPLVPPLQYQVKSSENSTTVIREADKIVSATSLVDSTLP 300
OY 301 GSSYEVQVRGKRLDGEIWSDMSTPRVFTTQDVYTFPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEVQVRGKRLDGEIWSDMSTPRVFTTQDVYTFPPKILTSVGSNVSFHCITYKKENKI 360
OY 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
OY 421 RYAEIYVIDVININISCTDGYLTMTGRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
DB 421 RYAEIYVIDVININISCTDGYLTMTGRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
OY 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
OY 541 SSVKAEITINIGLKRISMEKVPFENNLOFQIRGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLKRISMEKVPFENNLOFQIRGLSGKEVQWKMEYVDAKSKSVSLPV 600
OY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPPEFWRIINDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPPEFWRIINDTMKKEKNV 660
OY 661 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLMKPLMKNDLSGVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
OY 721 GASVANFLTFWPMNSKVNIVOSLSAYPLNSGVIYSWILSPSDYKLMYFIEMKNLNE 780
DB 721 GASVANFLTFWPMNSKVNIVOSLSAYPLNSGVIYSWILSPSDYKLMYFIEMKNLNE 780
OY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
OY 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNFQKPTFEHLFI 900
DB 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCMAOGLNFQKPTFEHLFI 900
OY 901 KHTASVTCGPLLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTDLKSGSVCSIDQFN 960
DB 901 KHTASVTCGPLLLEPETISEDISVDTSMKNKDEMPPTVVSLLSTDLKSGSVCSIDQFN 960
OY 961 SVNFSEAGTEVTEYDESOQROPFVKYATLISNSKPSGTGEEOGLINSSVTKCFSSKNSPL 1020

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|||||  
Db 961 SVNFSEAEGETEVTYEAESOROPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKKSIIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKKSIIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
RESULT 15  
US-08-713-296-11  
: Sequence 11, Application US/08713296  
: GENERAL INFORMATION:  
: APPLICANT: Snodgrass, H. Ralph  
: APPLICANT: Cioffi, Joseph  
: APPLICANT: Zupancic, Thomas Joel  
: APPLICANT: Shafer, Alan Wayne  
: APPLICANT: Mikhail, Adel A.  
: APPLICANT: Barut, Bruce A.  
: TITLE OF INVENTION: METHODS FOR USING THE OBESE  
: TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
: NUMBER OF SEQUENCES: 30  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Pennie & Edmonds  
: STREET: 1155 Avenue of The Americas  
: CITY: New York  
: STATE: NY  
: COUNTRY: USA  
: ZIP: 10036-2811  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/713,296  
: FILING DATE: 13-SEP-1996  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Polissant, Brian M.  
: REGISTRATION NUMBER: 28,462  
: REFERENCE/DOCKET NUMBER: 008907-0039-999  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 650-493-4935  
: TELEFAX: 650-493-5556  
: TELEX: 66141 PENNIE  
: INFORMATION FOR SEQ ID NO: 11:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1165 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-713-296-11  
Query Match 91.3%; Score 1064; DB 11: Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MICQKFCVLLHMEFIYVITAFNLSTPTTPWRKLSKMPNPNSTYDYLPLAGLSKNTSNS 60  
QY 61 NGHYETAVERKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERKENSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOQWLKGLDLKLFICYVESLFLKLFNRYNYKVHLLVLYLEVELEDSPVLPQKGS 180  
Db 121 QOIDANMNIOQWLKGLDLKLFICYVESLFLKLFNRYNYKVHLLVLYLEVELEDSPVLPQKGS 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFCSPLNSVQPINMKPDPP 240  
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFCSPLNSVQPINMKPDPP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQVKSSENSTVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQVKSSENSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTODVITYFPKILTVSGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPGLMSDMSPTPRVFTTODVITYFPKILTVSGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEPLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFEPLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVINISCEITDGYLTMTCRNSTFIQSLAESTLQLRHRSGLYCSIDIPSIH 480  
Db 421 RYAEIYVIDVINISCEITDGYLTMTCRNSTFIQSLAESTLQLRHRSGLYCSIDIPSIH 480  
QY 481 PISEPKDCYQSDGFYECIFOPIFILSGTYMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYQSDGFYECIFOPIFILSGTYMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAATVYMDIKVPMRGEFWRILNGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAATVYMDIKVPMRGEFWRILNGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSDEVGNHTKFTFLTECAHTVTVALINSI 720  
Db 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSDEVGNHTKFTFLTECAHTVTVALINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLASAPLNSSCVIVSWILSPSDYKLMYFIIEKMLNED 780  
Db 721 GASVANENLTFSPMSKVNIVQSLASAPLNSSCVIVSWILSPSDYKLMYFIIEKMLNED 780  
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHORMKLEWEDVPNPKNSWAGLNFQKPEFELHFI 900  
Db 841 GLYVIVPVISSSILLGLTLLISHORMKLEWEDVPNPKNSWAGLNFQKPEFELHFI 900  
QY 901 KHTASVTCGPLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETEVTYEAESOROPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETEVTYEAESOROPVKYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKKSIIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNPEENNNDKKSIIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 16

US-08-961-809-4  
; Sequence 4, Application US/08961809  
; GENERAL INFORMATION:  
; APPLICANT: Li, Cai  
; APPLICANT: Friedman, Jeffrey M.  
; TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT  
; TITLE OF INVENTION: MODULATE LEPTIN ACTIVITY  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue, 4th Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,809  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-961-809-4

Query Match 91.3%; Score 1064; DB 13; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPWRPKLSCMPNSTYDYELLFAGLSKNTSNS 60  
Db 1 MICQKFCVLLHMEFIYVITAFNLSTPTPWRPKLSCMPNSTYDYELLFAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCGRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCGRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QOIDANWNIOQWLKGDULKFCYVESLFFKMLFRNRYNYKVHLVYLPVELEDSPVPOKGS 180  
Db 121 QOIDANWNIOQWLKGDULKFCYVESLFFKMLFRNRYNYKVHLVYLPVELEDSPVPOKGS 180  
QY 181 FQMVHCNCSVHECCCECIVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
Db 181 FQMVHCNCSVHECCCECIVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVFPPLQYQVXSENSTTVIREADKIVSATSLVDSILP 300

Db 241 LGLHMEITDDGNLKISWSSPPLVFPPLQYQVXSENSTTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFETQVLYFPFKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFETQVLYFPFKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAERIPQSOYDVSDHVSQVTFENLNETKPRGKFYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAERIPQSOYDVSDHVSQVTFENLNETKPRGKFYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNINISCEITDGYLTMTCRMSTSTIOSLAESTLQLRHYRSSLYCSDIPSII 480  
Db 421 RYAEIYVIDVNNINISCEITDGYLTMTCRMSTSTIOSLAESTLQLRHYRSSLYCSDIPSII 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPICVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPICVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKLISWEKVPPENNLOFOIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKVPPENNLOFOIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600  
QY 601 PDLCAVAVQVRCKRLDGLGYSWMSNPAYVYMDIKVPMRGPETWRLNGDTMKKEKNV 660  
Db 601 PDLCAVAVQVRCKRLDGLGYSWMSNPAYVYMDIKVPMRGPETWRLNGDTMKKEKNV 660  
QY 661 TLLWPKLKNDSLSQVRYVINHTSCNGTWEEDVGNHTKFTFLWTEQAHTVTLAINSI 720  
Db 661 TLLWPKLKNDSLSQVRYVINHTSCNGTWEEDVGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANFNLTFSWMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSVAKYIYIHDHFIPIEKYQSLPIFMEGVGPKIINSTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSVAKYIYIHDHFIPIEKYQSLPIFMEGVGPKIINSTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSILLGLTLISHQRMKLEWEDVNPKNCSWAQGLNEQKPEFEHLFI 900  
Db 841 GLYVIVPVISSILLGLTLISHQRMKLEWEDVNPKNCSWAQGLNEQKPEFEHLFI 900  
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVVSLSLTFDEKGSVCISDOFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVVSLSLTFDEKGSVCISDOFN 960  
QY 961 SVNFSEAEGETVYIYEAESQROPFVKYATLISNSKPSSETGEEQGLINSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAEGETVYIYEAESQROPFVKYATLISNSKPSSETGEEQGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFFILSDOHPNIIISPHLTFSEGLDELKLEGNPEENNNDKSIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFFILSDOHPNIIISPHLTFSEGLDELKLEGNPEENNNDKSIYYL 1080  
QY 1081 GVTISIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140  
Db 1081 GVTISIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 17  
US-09-178-691-4  
; Sequence 4, Application US/09178691  
; GENERAL INFORMATION:  
; APPLICANT: Li, Cai  
; APPLICANT: Friedman, Jeffrey M.  
; TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS THAT MODULATE LEPTIN  
; TITLE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 600-1-205 N

; CURRENT APPLICATION NUMBER: US/09/178,691
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-691-4

Query Match 91.3%; Score 1064; DB 15; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
QY 121 QOIDANMNIOQWLKGDCLKFLICYVESLEFKNLFRNRYNKVHLVLPVLEDSPLVPQKGS 180
Db 121 QOIDANMNIOQWLKGDCLKFLICYVESLEFKNLFRNRYNKVHLVLPVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPPLMSVQPINMVKPDP 240
Db 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKSWSPLVPPLOQYQVYKSENSTVIYREADKIVATSLSLVDSTLP 300
Db 241 LGLHMEITDDGNLKSWSPLVPPLOQYQVYKSENSTVIYREADKIVATSLSLVDSTLP 300
QY 301 GSSYEYQVGRKRLDGPGLMSDSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVGRKRLDGPGLMSDSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTEFNLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTEFNLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RYAEIYVIDVNNINISCEITDGLTKMTCRMSTSTIOSLAESTLQRYHRSLSYCSIDPIS 480
Db 421 RYAEIYVIDVNNINISCEITDGLTKMTCRMSTSTIOSLAESTLQRYHRSLSYCSIDPIS 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLKSISWEKPPVPPENNLQFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKSISWEKPPVPPENNLQFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSMWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSMWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMPLMKNDLSQVQRYVINHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720
Db 661 TLLMPLMKNDLSQVQRYVINHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQVSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 GASVANFNLTFSWPMKSVNIQVSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
QY 781 GEIKMLRISSSVKKYIYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYIYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCWSAOGLNFOKPETFEHLFI 900

Db 841 GLYVIVPVIISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCWSAOGLNFOKPETFEHLFI 900
QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVYSLSTDLKSGVCSIDQFN 960
QY 961 SVNFEAEGTEVTYEAESQRPVKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020
Db 961 SVNFEAEGTEVTYEAESQRPVKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSWEIEAOAFILSDQHPNIIISPHLTSEGLDELLKLEGNFPEENNDKKSIVYL 1080
Db 1021 KDSFNSSWEIEAOAFILSDQHPNIIISPHLTSEGLDELLKLEGNFPEENNDKKSIVYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140
QY 1141 YMPQOTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQOTCSTQTHKIMENKMDLTV 1165

RESULT 18
US-09-700-813-10
; Sequence 10, Application US/09700813
; GENERAL INFORMATION:
; APPLICANT: SIERRA-HONIGMANN, Rocio
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND WOUND HEALING
; FILE REFERENCE: 044574-5029
; CURRENT APPLICATION NUMBER: US/09/700,813
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/US99/11209
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 60/086,354
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-700-813-10

Query Match 91.3%; Score 1064; DB 21; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
QY 121 QOIDANMNIOQWLKGDCLKFLICYVESLEFKNLFRNRYNKVHLVLPVLEDSPLVPQKGS 180
Db 121 QOIDANMNIOQWLKGDCLKFLICYVESLEFKNLFRNRYNKVHLVLPVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPPLMSVQPINMVKPDP 240
Db 181 FQWVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSQGVTFQSPPLMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKSWSPLVPPLOQYQVYKSENSTVIYREADKIVATSLSLVDSTLP 300
Db 241 LGLHMEITDDGNLKSWSPLVPPLOQYQVYKSENSTVIYREADKIVATSLSLVDSTLP 300
QY 301 GSSYEYQVGRKRLDGPGLMSDSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360
Db 301 GSSYEYQVGRKRLDGPGLMSDSTPRVFTTQDVITYFPKILTSVGSNVSFHCITYKKENKI 360

QY 361 VPSKEIWMNNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMNNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIIH 480  
Db 421 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIIH 480  
QY 481 PISEPKDCYLQSDGFEYCIFQPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFEYCIFQPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
Db 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
QY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLEWEDVPNPKNCSWAOGLNFOKPEFHEHLFI 900  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLEWEDVPNPKNCSWAOGLNFOKPEFHEHLFI 900  
QY 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDOFN 960  
Db 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDOFN 960  
QY 961 SVNFSEAGTEVYEDESOROPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFSEAGTEVYEDESOROPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDDKSIYYL 1080  
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNFPEENNDDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLEFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLEFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 19  
US-09-948-933-256  
; Sequence 256, Application US/09948933  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO00787  
; CURRENT APPLICATION NUMBER: US/09/948, 933  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,399  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 6404  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 256

; LENGTH: 1165  
; TYPE: PRT  
; ORGANISM: Human  
US-09-948-933-256

Query Match 91.3%; Score 1064; DB 23; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPIPTMRFKLSCMPNSTYIYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPIPTMRFKLSCMPNSTYIYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCISCADNIEGTFVSTVNSLVF 120  
Db 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCISCADNIEGTFVSTVNSLVF 120  
QY 121 QOIDANMNIOCNLKGDKLFCICYVESLFKNLFRRNRYKVHLLVLPVLELDSPLVPQKGS 180  
Db 121 QOIDANMNIOCNLKGDKLFCICYVESLFKNLFRRNRYKVHLLVLPVLELDSPLVPQKGS 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPPLMSVOPINMVKPDP 240  
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPPLMSVOPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYKYSNSTVIREADKIYSAISLVDISLP 300  
Db 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYKYSNSTVIREADKIYSAISLVDISLP 300  
QY 301 GSSYEVQVRGKRLDGPIMSDWSTPRVFTQDVIYFPKKILTSVGSNVSFHCYKKEKNI 360  
Db 301 GSSYEVQVRGKRLDGPIMSDWSTPRVFTQDVIYFPKKILTSVGSNVSFHCYKKEKNI 360  
QY 361 VPSKEIWMNNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMNNLAEKIPQSQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIIH 480  
Db 421 RYAEIYVIDVNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIIH 480  
QY 481 PISEPKDCYLQSDGFEYCIFQPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540  
Db 481 PISEPKDCYLQSDGFEYCIFQPIFLLSGYTMIRINHSLSGLSDSPPTCYLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
Db 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
QY 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLEWEDVPNPKNCSWAOGLNFOKPEFHEHLFI 900  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLEWEDVPNPKNCSWAOGLNFOKPEFHEHLFI 900  
QY 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDOFN 960  
Db 901 KHTASVTCGPLLPEPTISEDISVDTSMKNKDEMPPTVVSLLSTTDLEKGSVCISDOFN 960



OY	961	SVNFEAEGETEVTVEDEDSQROPEVKYATLISNSKPSETGEEGLINSSVTKCFSSKRN SPL	1020
Db	961	SVNFEAEGETEVTVEAESQRQPFVKYATLISNSKPSETGEEGLINSSVTKCFSSKRN SPL	1020
OY	1021	KDSFNSSSWEIEAQAFILISDQHNIISPHLTFSEGLDELKLEGNPPEENNDRKS IYYL	1080
Db	1021	KDSFNSSSWEIEAQAFILISDQHNIISPHLTFSEGLDELKLEGNPPEENNDRKS IYYL	1080
OY	1081	GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTS SKRTFAS	1140
Db	1081	GVTSIKKRESGVLLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTS SKRTFAS	1140
OY	1141	YMPQFOTCSTQTTHKIMENKMCDLT V 1165	
Db	1141	YMPQFOTCSTQTTHKIMENKMCDLT V 1165	

```

RESULT 20
US-09-948-947-73
: Sequence 73, Application US/09948947
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL000786
: CURRENT APPLICATION NUMBER: US/09/948,947
: CURRENT FILING DATE: 2001-09-10
: PRIOR APPLICATION NUMBER: 60/231,397
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 2172
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 73
: LENGTH: 1165
: TYPE: PRT
: ORGANISM: Human
US-09-948-947-73

```

Query Match	91.38;	Score 1064;	DB 23;	length 1165;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 1164;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
QY 1	MICOKECVLLHWEFIYVITAFNLSYPTTPWRFKLSGMPNSTDYFLLPAGLSKNTSNS	60		
Db 1	MICOKECVLLHWEFIYVITAFNLSYPTTPWRFKLSGMPNSTDYFLLPAGLSKNTSNS	60		
QY 61	NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF	120		
Db 61	NGHYETAVERPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF	120		
QY 121	QOIDANWNIQCWLKGDCLKFICVYESLFKNLFRNYNYKVHLLYVLEVEDSPVLPQKGS	180		
Db 121	QOIDANWNIQCWLKGDCLKFICVYESLFKNLFRNYNYKVHLLYVLEVEDSPVLPQKGS	180		
QY 181	FQMVHCNCSVHECCCECLVPVPFAKLNLTLLMCLKITSGGVIFQSPMSVOPINMVKPDP	240		
Db 181	FQMVHCNCSVHECCCECLVPVPFAKLNLTLLMCLKITSGGVIFQSPMSVOPINMVKPDP	240		
QY 241	LGTHMEITDDGNLKISWSSPPLVPEPLQYQVKYSENSTVIREADKIVSATSLLVDSILP	300		
Db 241	LGTHMEITDDGNLKISWSSPPLVPEPLQYQVKYSENSTVIREADKIVSATSLLVDSILP	300		
QY 301	GSSYEYQVRGKRLLDGPGISWDSMPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI	360		
Db 301	GSSYEYQVRGKRLLDGPGISWDSMPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI	360		
QY 361	VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH	420		
Db 361	VPSKEIVMMNLAEKIPQSQDYVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH	420		
QY 421	RAELLYVIDVNNINISCEITDGLTKTKCRWSTSTIOSLAESTLOLRHRSSLYCSDIPSIH	480		

Db	421	RAELIYDIVNINISCEIYGLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIPSIH	480
QY	481	PISEPKDCYLQSDGFYECEIYQPIFLLSGYTMWIRINHSLGSLUSPTCVLPDSVYKPLPP	540
Db	481	PISEPKDCYLQSDGFYECEIYQPIFLLSGYTMWIRINHSLGSLUSPTCVLPDSVYKPLPP	540
QY	541	SSVKAETITINIGLKLISWEKPEVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV	600
Db	541	SSVKAETITINIGLKLISWEKPEVFPENNLOFOIRYGLSGKEVQWKMEYVDKSKSVSLPV	600
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	601	PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
QY	661	TLIMKPLMKNDLSLCSVQRYVINHHTSCNGTWSEDEVGNHTKFTFLWTEQAHTVTLAINSI	720
Db	661	TLIMKPLMKNDLSLCSVQRYVINHHTSCNGTWSEDEVGNHTKFTFLWTEQAHTVTLAINSI	720
QY	721	GASVANENLTFSPMPSKVNIYQSLSAYPLNSSCVIYSNLTSPSDYKLMYFIIEKNLNE	780
Db	721	GASVANENLTFSPMPSKVNIYQSLSAYPLNSSCVIYSNLTSPSDYKLMYFIIEKNLNE	780
QY	781	GETKMLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSDA	840
Db	781	GETKMLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSDA	840
QY	841	GLYIVIVPVISSSILLGLTLLISHQRMKKLFMEDVDPNPKNCWSAQGLNFQKPETEHILFI	900
Db	841	GLYIVIVPVISSSILLGLTLLISHQRMKKLFMEDVDPNPKNCWSAQGLNFQKPETEHILFI	900
QY	901	KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPITYVSLSTDLKSGVCSIDQFN	960
Db	901	KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPITYVSLSTDLKSGVCSIDQFN	960
QY	961	SVNPEAEGETEVTYEDESQROPVKYATLISNSKPSETGEQGLINSSVTKCFSSKNSPL	1020
Db	961	SVNPEAEGETEVTYEAESQROPVKYATLISNSKPSETGEQGLINSSVTKCFSSKNSPL	1020
QY	1021	KDSFNSNSSWEIEAQAFILSDQHNIISPHLTSEGLDELILKLEGNFPEENNDRKSIYYL	1080
Db	1021	KDSFNSNSSWEIEAQAFILSDQHNIISPHLTSEGLDELILKLEGNFPEENNDRKSIYYL	1080
QY	1081	GVTSIKKRESGVLLTDKSRVSGPFPAPCLFTDIRVLQSDCSHFVNNINLGTSSKRTFAS	1140
Db	1081	GVTSIKKRESGVLLTDKSRVSGPFPAPCLFTDIRVLQSDCSHFVNNINLGTSSKRTFAS	1140
QY	1141	YMPQFQTCSTQTHKIMENKMDLTV 1165	
Db	1141	YMPQFQTCSTQTHKIMENKMDLTV 1165	

RESULT 21  
 US-10-095-929-11  
 ; Sequence 11, Application US/10095929  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Snodgrass, H. Ralph  
 ; Cioffi, Joseph  
 ; Zupancic, Thomas Joel  
 ; Shafer, Alan Wayne  
 ;  
 ; TITLE OF INVENTION: METHODS FOR USING THE OBEBE  
 ; GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
 ; DEVELOPMENT  
 ;  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of The Americas  
 ; CITY: New York  
 ; STATE: NY  
 ;  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette



COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/095,929  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,957  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 008907-0033-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-095-929-11

Query Match 91.3%; Score 1064; DB 24; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVALLHMEFIYVITAFNLSYPTPWRKLSKMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVALLHMEFIYVITAFNLSYPTPWRKLSKMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTNSLV 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTNSLV 120  
QY 121 QOIDANMNIDCMKGLKLFICYVESLEFKNLFERNYKVVHLLVLPVLEDSPLVPQKGS 180  
DB 121 QOIDANMNIDCMKGLKLFICYVESLEFKNLFERNYKVVHLLVLPVLEDSPLVPQKGS 180  
QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDPLMLCKITSGVTFQSPMLSVQPINVKKPDP 240  
DB 181 FOMVHCNCSVHECCCLVPVPTAKLNDPLMLCKITSGVTFQSPMLSVQPINVKKPDP 240  
QY 241 LGLHMEITDDGKLSWSSPPLVPFPIQYQVKSSENSTVIREADKIYATSLLVDSILP 300  
DB 241 LGLHMEITDDGKLSWSSPPLVPFPIQYQVKSSENSTVIREADKIYATSLLVDSILP 300  
QY 301 GSSYEYQVRKRLDGPIMSDMSTPRVFTTQDVIYFPKILTSVGSNVSFHCILYKKENKI 360  
DB 301 GSSYEYQVRKRLDGPIMSDMSTPRVFTTQDVIYFPKILTSVGSNVSFHCILYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIVMMNLAEKIPQSQYDVVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCEITDGYLTMTKCRNSTSTIOSLAESTLOLRHRSLSLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNNISCEITDGYLTMTKCRNSTSTIOSLAESTLOLRHRSLSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLRP 540  
DB 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEYQWKMYEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEYQWKMYEYDAKSKSVSLPV 600

QY 601 PDLCAVYAVQYRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEIRNLIINGDTMKKENY 660  
DB 601 PDLCAVYAVQYRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEIRNLIINGDTMKKENY 660  
QY 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLVTEQAHTVTLAINSI 720  
DB 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLVTEQAHTVTLAINSI 720  
QY 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSSCVTVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLFSPMSKVNIVOSLSAYPLNSSCVTVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIEMGVGPKIINFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIEMGVGPKIINFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVITSSILLSTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFELFI 900  
DB 841 GLYVIVPVITSSILLSTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFELFI 900  
QY 901 KHTASVTCGPIILEPETISEDISVDTSMKNKDEMPTTVVSLSTTDEKGSVCISDQFN 960  
DB 901 KHTASVTCGPIILEPETISEDISVDTSMKNKDEMPTTVVSLSTTDEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETEYVEDESQROPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAEGETEYVEDESQROPFVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEQAFFILSDQHPNIIISPHLTFSEGLDELLKLEKNPBEENNDKSIYYL 1080  
DB 1021 KDSFSSNSWEIEQAFFILSDQHPNIIISPHLTFSEGLDELLKLEKNPBEENNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVNNINLGTSSKKTFFAS 1140  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 22  
US-08-583-153-4  
Sequence 4, Application US/08583153  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
NUMBER OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153  
FILING DATE: 28-DEC-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-050  
TELECOMMUNICATION INFORMATION:



MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-599-455A-4

Query Match 82.7%; Score 963; DB 9; Length 1165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMERIYVITAFNLSTPTPMPREKLSCMPNSTYDYFLPAGLSKNTSNS 60  
DB 1 MICQKFCVVLHMERIYVITAFNLSTPTPMPREKLSCMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIQCWLKGDCLKFICYVESLFEKNLFRNYKVHLLVLPVELEDSPLVPQKGS 180  
DB 121 QOIDANMNIQCWLKGDCLKFICYVESLFEKNLFRNYKVHLLVLPVELEDSPLVPQKGS 180  
QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPIMSVOPINMYKPDPP 240  
DB 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSQGVIFQSPIMSVOPINMYKPDPP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTVIREADKIYSAATSLVDLILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTVIREADKIYSAATSLVDLILP 300  
QY 301 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360  
DB 301 GSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNISCEITDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480  
DB 421 RYAEIYVIDVNNISCEITDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQYRCKRLDGLGWSNMSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQYRCKRLDGLGWSNMSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
DB 721 GASVANENLTFSPMSKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNEED 780  
QY 781 GEIKWLRISSSVYKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVYKYYIHDHFIPIEKYQPSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVYIISSSILLGLTLISHQRMKLFMEDVYVNPKNCSWAQGLNFQKPETFEHLFI 900  
DB 841 GLYVIVPVYIISSSILLGLTLISHQRMKLFMEDVYVNPKNCSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTGGLLEPETISEDISVDTSWKNKDEMPPTVVSLSSTDIEKGSVCISDQFN 960  
DB 901 KHTASVTGGLLEPETISEDISVDTSWKNKDEMPPTVVSLSSTDIEKGSVCISDQFN 960

QY 961 SVNFESEAGTEVTEDESQROPFVKYATLISNSKPSGTGEEQGLNSSVTCKCFSSKNSPL 1020  
DB 961 SVNFESEAGTEVTEDESQROPFVKYATLISNSKPSGTGEEQGLNSSVTCKCFSSKNSPL 1020  
QY 1021 KDSFSSSWEIEAQAFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDRKSIYYL 1080  
DB 1021 KDSFSSSWEIEAQAFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDRKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDRKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
DB 1081 GVTSIKKRESGVLLTDRKSRVSCPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

## RESULT 24

US-08-638-524A-4

Sequence 4, Application US/08638524A

## GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING

NUMBER OF SEQUENCES: 50

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 021001-2804

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect (Version 5.1)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/638,524A

FILING DATE: 26-APR-1996

CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,455

FILING DATE: 22-JAN-1996

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/583,153

FILING DATE: 28-DEC-1995

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/570,142

FILING DATE: 11-DEC-1995

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/569,485

FILING DATE: 08-DEC-1995

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/566,622

FILING DATE: 04-DEC-1995

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/562,663

FILING DATE: 27-NOV-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/018001

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acids

TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-638-524A-4

Query Match 82.7%; Score 963; DB 10; Length 1165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHMEFIYVITAFNLSTYPTWRFKLSCLMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHMEFIYVITAFNLSTYPTWRFKLSCLMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSTFHCFCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVEPKFNSSGTHFSNLSTFHCFCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANMNIOQWLKGLDLKFLICYESLFLKNLFRNYKVHLLYLPEVLEDSPLVPQKGS 180
Db 121 QQIDANMNIOQWLKGLDLKFLICYESLFLKNLFRNYKVHLLYLPEVLEDSPLVPQKGS 180
QY 181 FQMVHNCVSHECCCECLVPVPAPAKNDTLMLCLKITSGGVTFQSPILMSVQPINMKPPDP 240
Db 181 FQMVHNCVSHECCCECLVPVPAPAKNDTLMLCLKITSGGVTFQSPILMSVQPINMKPPDP 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPPLOYQVYKSENSTVIREADKIVSATSLVDLSLP 300
Db 241 LGLHMEITDDGNLKSWSPPPLVPPLOYQVYKSENSTVIREADKIVSATSLVDLSLP 300
QY 301 GSSYEYQVGRKRLDGPVMSDWTSPRVETTQDVIYFPKILTSVGSNVSPHCYKKENKI 360
Db 301 GSSYEYQVGRKRLDGPVMSDWTSPRVETTQDVIYFPKILTSVGSNVSPHCYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKETYDAVCCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKETYDAVCCNEHECHH 420
QY 421 RYAEIYVIDVININISCTDGYLTKMTCRMSTSTIOSLAESTLOLRHRSLLYCSIDIPSIH 480
Db 421 RYAEIYVIDVININISCTDGYLTKMTCRMSTSTIOSLAESTLOLRHRSLLYCSIDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540
QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLKLISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVORYVINHFTSCNGTWSERVEDVGNHTKFTFLMTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSVORYVINHFTSCNGTWSERVEDVGNHTKFTFLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIQVSLSAVPLNSSCVIVSWIILSPDYKLMYFIIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSVNIQVSLSAVPLNSSCVIVSWIILSPDYKLMYFIIEWKNLNED 780
QY 781 GEIKMLRISSSVKKYIYIHDHFIPIEKQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKMLRISSSVKKYIYIHDHFIPIEKQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVYIISSSILLGLTLLISHQMKLLFWEDVNPKNCSWAQGLNFQKPEFHEHFT 900
Db 841 GLYVIVPVYIISSSILLGLTLLISHQMKLLFWEDVNPKNCSWAQGLNFQKPEFHEHFT 900
QY 901 KHTASVTCGPLEPETISEDIVDTSMKNKDEMPPTTVVSLSTDLDEKGSVCISDQFN 960
Db 901 KHTASVTCGPLEPETISEDIVDTSMKNKDEMPPTTVVSLSTDLDEKGSVCISDQFN 960
```

```
QY 961 SVNFSEAGTEVTEDESQROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020
Db 961 SVNFSEAGTEVTEDESQROPFVKYATLISNSKPSSETGEEGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWETEAQAFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080
Db 1021 KDSFNSNSWETEAQAFILSDQHPNITSPHLTFSEGLDELKLEGNFPEENNKKSIYYL 1080
QY 1081 GVTISIKKREGSVLLTDKSRVSCFPAPCLFTDIRVLODSCSHFVENNINLTSSKKTFFAS 1140
Db 1081 GVTISIKKREGSVLLTDKSRVSCFPAPCLFTDIRVLODSCSHFVENNINLTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 25
US-08-708-123C-4
; Sequence 4, Application US/08708123C
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHOD FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708,123C
; FILING DATE: 03-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
```

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-708-123C-4

Query Match 82.7%; Score 963; DB 11; Length 1165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQFCVLLHMEFIYVITAFLNLSYPTPWREKLSMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQFCVLLHMEFIYVITAFLNLSYPTPWREKLSMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSGTHFSNLSKTYTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVERPKFNSGTHFSNLSKTYTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIQCWLKGLKFLICYVESLFFKNLFRNRYKVVHLLVYLPEVLEDSPLVPQKGS 180  
DB 121 QOIDANMNIQCWLKGLKFLICYVESLFFKNLFRNRYKVVHLLVYLPEVLEDSPLVPQKGS 180  
QY 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINMVKRDPDP 240  
DB 181 FQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINMVKRDPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPPLQYQKYSNSTTVIREADKIVASATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPPLQYQKYSNSTTVIREADKIVASATSLVDSILP 300  
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVETTDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
DB 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVETTDVYIFPPKILTSVGSNVSFHCYKKEKNI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSKEVFFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
DB 421 RYAEIYVIDVNINISCTDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDLPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRKRLDGLGYWSMNSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVQVRKRLDGLGYWSMNSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTMSDVGNTKFTFLMTEQAHTVTVLAINSI 720  
DB 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTMSDVGNTKFTFLMTEQAHTVTVLAINSI 720  
QY 721 GASVANENLTFSPMMSKVNIVQSLASAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANENLTFSPMMSKVNIVQSLASAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISISSVAKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISISSVAKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVLISSILLGLLISHQRMKLEWEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
DB 841 GLYVIVPVLISSILLGLLISHQRMKLEWEDVNPKNCSWAQGLNFQKPETFEHLFI 900  
QY 901 KHTASVTCGPILEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960  
DB 901 KHTASVTCGPILEPETISEDIVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDQFN 960

QY 961 SVNFEAEGETEYTEDESORQPFVKYATLISNSKPSPTGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFEAEGETEYTEDESORQPFVKYATLISNSKPSPTGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAQAFFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKSTIYLL 1080  
DB 1021 KDSFNSSSWEIEAQAFFILSDQHNPNIISPHLTFSEGLDELLKLEGNFPEENNDKSTIYLL 1080  
QY 1081 GVTSIKKRESGYLLTDKSRVSCFPAPCLFTDIRVLDQSCSHFVENNINLGTSSKRTFAS 1140  
DB 1081 GVTSIKKRESGYLLTDKSRVSCFPAPCLFTDIRVLDQSCSHFVENNINLGTSSKRTFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 26  
US-08-864-564A-4  
Sequence 4, Application US/08864564A  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,564A  
FILING DATE: 28-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids







; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-079-625-4

Query Match 82.7%; Score 963; DB 24; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIOQWLKGDCLKFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
DB 121 QOIDANWNIOQWLKGDCLKFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMCLKITSGGVIFOSPILMSVOPINMVKPDP 240
DB 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMCLKITSGGVIFOSPILMSVOPINMVKPDP 240
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSISWSSPPLVPFPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAERIPQSQDYDVSDHVSQVTFPNNLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAERIPQSQDYDVSDHVSQVTFPNNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLRYHRSSLCYSDIPSIIH 480
DB 421 RYAEIYVIDVNNINISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLRYHRSSLCYSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCYLBDPSVVKPLP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDLPPTCYLBDPSVVKPLP 540
QY 541 SSVKAEITINIGLIKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
DB 541 SSVKAEITINIGLIKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEYVDKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDSLCSQORYVINHTSCNGTSEDEVGNHTKFTFLMTQEAHTVTLAINSI 720
DB 661 TLLMKPLMKNDSLCSQORYVINHTSCNGTSEDEVGNHTKFTFLMTQEAHTVTLAINSI 720
QY 721 GASVANFNLTFSMPSKVNIVQSLSATPLNSSCVIYSWILSPSDYKLMYFIEMKNLNE 780
DB 721 GASVANFNLTFSMPSKVNIVQSLSATPLNSSCVIYSWILSPSDYKLMYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVIVPVISSILLGLTLLISHQRMKLFMEDVPPNPKNCSWAQLNEQKPETFEHLFI 900
DB 841 GLYIVIVPVISSILLGLTLLISHQRMKLFMEDVPPNPKNCSWAQLNEQKPETFEHLFI 900

QY 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTTDLEKGSVCISDQFN 960
DB 901 KHTASVTCGPLLEPETISEDISVDTSMKNKDEMPPTVYSLSTTDLEKGSVCISDQFN 960
QY 961 SVNFEAEGTEVTEDESOROPFVKYATLISNSKPSSTGEEQGLINSSVTKCFSSKNSPL 1020
DB 961 SVNFEAEGTEVTEDESOROPFVKYATLISNSKPSSTGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNEPEENNDRKSIYYL 1080
DB 1021 KDSFSSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNEPEENNDRKSIYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVNNINLGTSSKRTFAS 1140
DB 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVNNINLGTSSKRTFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 28
US-09-948-933-284
; Sequence 284, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
US-09-948-933-284

Query Match 82.7%; Score 963; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHMEFIYVITAFNLSTPITPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 62
QY 61 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 63 NGHYETAVEPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANWNIOQWLKGDCLKFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 180
DB 123 QOIDANWNIOQWLKGDCLKFICYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKGS 182
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMCLKITSGGVIFOSPILMSVOPINMVKPDP 240
DB 183 FQMVHCNCSVHECCGLVPVPTAKLNDTLMCLKITSGGVIFOSPILMSVOPINMVKPDP 242
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300
DB 243 LGLHMEITDDGNLKSISWSSPPLVPFPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 360
DB 303 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKENKI 362
QY 361 VPSKEIYVMMNLAERIPQSQDYDVSDHVSQVTFPNNLNETKPRGKFTYDAVYCCNEHECHH 420

```
|||||
Db 363 VPSKEIYWMNLAEKIPQSOYDVVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVININISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVININISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
Db 543 SSVAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 663 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 723 GASVANFNLTFSWPMKVNIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 782
QY 781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVITISSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFQKPEFELHFI 900
Db 843 GLYVIVPVITISSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFQKPEFELHFI 902
QY 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLSLSTTDLLEKGSVCISDOFN 960
Db 903 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLSLSTTDLLEKGSVCISDOFN 962
QY 961 SVNFSEABGEVTEYDESOQROPFYKATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
Db 963 SVNFSEABGEVTEYDESOQROPFYKATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1022
QY 1021 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNPPEENNDKSIYYL 1080
Db 1023 KDSFNSSSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNPPEENNDKSIYYL 1082
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1083 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1142
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQFQTCSTQTHKIMENKMDLTV 1167

RESULT 29
US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/09/948,947
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1167
```

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TYPE: PRT
ORGANISM: Human
US-09-948-947-87

Query Match      82.7%; Score 963; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMEFIYVITAFNLSTPTPRMREKLSKMPNSTYOVFLPAGLSKNTSNS 60
Db 3 MICQKFCVVLHMEFIYVITAFNLSTPTPRMREKLSKMPNSTYOVFLPAGLSKNTSNS 62
QY 61 NGHYETAVERFNSSGTHFSNLSKTFHCGRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHYETAVERFNSSGTHFSNLSKTFHCGRSEQDRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QQIDANNIQCWLKGDCLKFICYVESLEFKNLFRNYKYVHLVLPVELEDSPLVPQKGS 180
Db 123 QQIDANNIQCWLKGDCLKFICYVESLEFKNLFRNYKYVHLVLPVELEDSPLVPQKGS 182
QY 181 FQMVHCNCSYHECCCLVPVPTAKLNDTLMLCKITSGGVIPOSLPMSYQPINMVKPDP 240
Db 183 FQMVHCNCSYHECCCLVPVPTAKLNDTLMLCKITSGGVIPOSLPMSYQPINMVKPDP 242
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 300
Db 243 LGLHMEITDDGNLKISWSSPPLVPFLOQYKYSNSTVIREADKIVSATSLVDSILP 302
QY 301 GSSYEVQVRGRDGPQIWSDWSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKKEKNI 360
Db 303 GSSYEVQVRGRDGPQIWSDWSTPRVFTQDVIYFPKILTSVGSNVSFHCITYKKEKNI 362
QY 361 VPSKEIYWMNLAEKIPQSOYDVVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYWMNLAEKIPQSOYDVVSDHVSKEYTFENLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVININISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVININISCEITDGYLTMTKCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
Db 543 SSVAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 663 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db 723 GASVANFNLTFSWPMKVNIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIEMKNLNE 782
QY 781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVITISSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFQKPEFELHFI 900
Db 843 GLYVIVPVITISSILLGLTLLISHORMKLFMEDVNPKNCSWAQGLNFQKPEFELHFI 902
QY 901 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLSLSTTDLLEKGSVCISDOFN 960
Db 903 KHTASVTCGPLLLEPETISEDIVDTSMKNKDEMPPTVVSLSLSTTDLLEKGSVCISDOFN 962
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QY 961 SVNFSEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTCKCFSSKNSPL 1020  
Db 963 SVNFSEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTCKCFSSKNSPL 1022  
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
Db 1023 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1082  
QY 1081 GVTSIKKRESGVLITDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1140  
Db 1083 GVTSIKKRESGVLITDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1142  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
Db 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

RESULT 30  
US-08-570-142B-4  
Sequence 4, Application US/08570142B  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS  
TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,142B  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-570-142B-4

Query Match 82.6%; Score 962; DB 9; Length 1165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTTPWRFKLSGMPNPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHMEFIYVITAFNLSYPTTPWRFKLSGMPNPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAPEPKFNSSGTHSNNLSKTFHCCFRSEQDRNCSLCAONIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAPEPKFNSSGTHSNNLSKTFHCCFRSEQDRNCSLCAONIEGKTFVSTVNSLVE 120  
QY 121 QOIDAMNIIQCMWLGDKLFIQYVESLFKNLFERNYKVALLYLPEVLEDSPLVPQGS 180  
Db 121 QOIDAMNIIQCMWLGDKLFIQYVESLFKNLFERNYKVALLYLPEVLEDSPLVPQGS 180  
QY 181 FOMVHCNCSVHECCCECLVPEPTAKLNDTLMLCKITSGVIFOSPMSVOPINMYKBDPP 240  
Db 181 FOMVHCNCSVHECCCECLVPEPTAKLNDTLMLCKITSGVIFOSPMSVOPINMYKBDPP 240  
QY 241 LGLHMEITDDGNLKSISWSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMEITDDGNLKSISWSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPGLSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREKNI 360  
Db 301 GSSYEVOVRGKRLDGPGLSDMSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREKNI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEPLNLTGPKGKITYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEPLNLTGPKGKITYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVININISCEFDGYLTMTCRWSTSTIQSLAESTLQKRYHRSSLYCSDIPSIIH 480  
Db 421 RYAEIYVIDVININISCEFDGYLTMTCRWSTSTIQSLAESTLQKRYHRSSLYCSDIPSIIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINSLGSLDPTCYLPDSYVVKPLPP 540  
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMIRINSLGSLDPTCYLPDSYVVKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPFENNLOFOIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYVMDIKVPMRGPEFWRIINGDTMKREKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATVYVMDIKVPMRGPEFWRIINGDTMKREKNV 660  
QY 661 TLMLKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLTEQAHTVTVLAINSI 720  
Db 661 TLMLKPLMKNDLSQVQRYVINHHTSCNGTWSDEVGNHTKFTFLTEQAHTVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMFYIIEWKNLNED 780  
Db 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMFYIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKRYIHDFPIEKYQFSLYPIFMEGVGPKIINSFTQODIEKHQSDA 840  
Db 781 GEIKWLRISSSVKRYIHDFPIEKYQFSLYPIFMEGVGPKIINSFTQODIEKHQSDA 840  
QY 841 GLYVIVPVITISSIILLGTLILSHQRMKLFMEDVPPNPNCSWAQGLNFQKPEFTEHLFI 900  
Db 841 GLYVIVPVITISSIILLGTLILSHQRMKLFMEDVPPNPNCSWAQGLNFQKPEFTEHLFI 900  
QY 901 KHTASVTCGPLLPEPTISEDIVDSWKNKDEMPTTVVSLSTTDLEKGSVCISQDFN 960  
Db 901 KHTASVTCGPLLPEPTISEDIVDSWKNKDEMPTTVVSLSTTDLEKGSVCISQDFN 960  
QY 961 SVNFSEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTCKCFSSKNSPL 1020  
Db 961 SVNFSEAGTEVTYEDESOROPFVKYATLISNSKPSSETGEEQGLINSSVTCKCFSSKNSPL 1020  
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
Db 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLITDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1140

Db 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLT 1164  
Db 1141 YMPQFOTCSTQTHKIMENKMDLT 1164

## RESULT 31

US-08-570-142C-4

; Sequence 4, Application US/08570142C

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS

; TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

; TITLE OF INVENTION: INCLUDING OBESITY

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: Windows95

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/570,142C

; FILING DATE: 11-DEC-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/562,663

; FILING DATE: 27-NOV-1995

; APPLICATION NUMBER: 08/566,622

; FILING DATE: 04-DEC-1995

; APPLICATION NUMBER: 08/569,485

; FILING DATE: 08-DEC-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Melkiohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/014001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1165 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-570-142C-4

Query Match 82.6%; Score 962; DB 9; Length 1165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1162; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60

QY 61 NGHYETAVERPNSGTHFSNLSKTFHCGRSEQDRNCSICADNIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAVERPNSGTHFSNLSKTFHCGRSEQDRNCSICADNIEGKTFVSTVNSLVE 120

QY 121 QOIDANWNIOGWLKGDCLKFICVYESLFKNLFRNRYNKVHLLVLPVELEDSPLVPQKGS 180

Db 121 QOIDANWNIOGWLKGDCLKFICVYESLFKNLFRNRYNKVHLLVLPVELEDSPLVPQKGS 180

QY 181 FQMVHCNSVHECECLVPVPFAKNDTLMCLKITSGCVIFQSPLMSTVOPINMKPDP 240  
Db 181 FQMVHCNSVHECECLVPVPFAKNDTLMCLKITSGCVIFQSPLMSTVOPINMKPDP 240

QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVSATSLYDSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVYSENSTTVIREADKIVSATSLYDSILP 300

QY 301 GSSYEYQVRGKRLDGPQIWSMDSTPRVFTTQDVITYEPKILTSVGSNVSFHCYKKENKI 360  
Db 301 GSSYEYQVRGKRLDGPQIWSMDSTPRVFTTQDVITYEPKILTSVGSNVSFHCYKKENKI 360

QY 361 VPSKEIWMNLAEKIPQSOYDVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHCHH 420  
Db 361 VPSKEIWMNLAEKIPQSOYDVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHCHH 420

QY 421 RYAEIYVIDVINISCEITDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIH 480  
Db 421 RYAEIYVIDVINISCEITDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIH 480

QY 481 PISEPKDCYLOSDGFECIFQPIFLSGYTWIRINHSIGSLDSPPTCVLPDSYVKKPLPP 540  
Db 481 PISEPKDCYLOSDGFECIFQPIFLSGYTWIRINHSIGSLDSPPTCVLPDSYVKKPLPP 540

QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSYSLPV 600  
Db 541 SSVKAEITINIGLKLISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSYSLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKYPMRGPEIWRINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKYPMRGPEIWRINGDTMKKEKNV 660

QY 661 TLLMKPLKNDSLCSYQRYVINHTSCNGTSEYDGNHTKFTFLMTQAHYVYLAINSI 720  
Db 661 TLLMKPLKNDSLCSYQRYVINHTSCNGTSEYDGNHTKFTFLMTQAHYVYLAINSI 720

QY 721 GASVANFLTFSWPMKRYNIVQSLAYPLNSCVIYSWILSPDYKLMFYIEMKNLNE 780  
Db 721 GASVANFLTFSWPMKRYNIVQSLAYPLNSCVIYSWILSPDYKLMFYIEMKNLNE 780

QY 781 GEIKWLRISSVKKYVYHDFPIPIEKOYQSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSVKKYVYHDFPIPIEKOYQSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKCLFWEDEVNPNKNSWAQGLNFOKPEFPEHLFI 900  
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKCLFWEDEVNPNKNSWAQGLNFOKPEFPEHLFI 900

QY 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVVSLSLTDLEKGSVCISDQFN 960  
Db 901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTVVSLSLTDLEKGSVCISDQFN 960

QY 961 SVNFESEAGTEVYEDSQRQOPFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020  
Db 961 SVNFESEAGTEVYEDSQRQOPFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020

QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKRSIYYL 1080  
Db 1021 KDSFNSNSWEIEAQAFILSDQHPNIIISPHLTFSEGLDELKLEGNFPEENNDKRSIYYL 1080

QY 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140  
Db 1081 GVTSIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLT 1164  
Db 1141 YMPQFOTCSTQTHKIMENKMDLT 1164

RESULT 32

US-08-582-825-1  
; Sequence 1, Application US/08582825  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,825  
; FILING DATE: 04-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-582-825-1

Query Match 76.5%; Score 891; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSVNSLVF 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSVNSLVF 120  
QY 121 QOIDANWNIQCWLKGDKLFCYVESLFKNLFRNYKVVHLLVLPVEVLEDSPLVPQKGS 180  
DB 121 QOIDANWNIQCWLKGDKLFCYVESLFKNLFRNYKVVHLLVLPVEVLEDSPLVPQKGS 180  
QY 181 FQMVHNCVSHECCCLVVPPTAKLNDTLMLCKITSGGVIFQSPLMVSQPINNVKPPDP 240  
DB 181 FQMVHNCVSHECCCLVVPPTAKLNDTLMLCKITSGGVIFQSPLMVSQPINNVKPPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVYKSENSTTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSGSVNSFHCITYKKENKI 360  
DB 301 GSSYEVOVRGKRDLGPGIWSDMSTPRVFTTQDVITYFPFKILTSGSVNSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMMLAEKIPQSOYDVSDHVSQVTFEENLNETKPRGKFTYDAYVCCNEHECHH 420  
DB 361 VPSKEIYVMMMLAEKIPQSOYDVSDHVSQVTFEENLNETKPRGKFTYDAYVCCNEHECHH 420  
QY 421 RYAEIYVIDVNNINISCTDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLVCSDDIPSIIH 480  
DB 421 RYAEIYVIDVNNINISCTDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLVCSDDIPSIIH 480  
QY 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540

DB 481 PISEPKDCYLOSDFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540  
QY 541 SSYKAEITINIGLKISWEKVPENNLOFQIRYGLSGKEVQWKHYEVYDAKSYSVSLPV 600  
DB 541 SSYKAEITINIGLKISWEKVPENNLOFQIRYGLSGKEVQWKHYEVYDAKSYSVSLPV 600  
QY 601 PDLCAVYAVQVRKRLDGLGWSNWSNPATYVMDIKVPMKGFEFWRIINGDTMKKENY 660  
DB 601 PDLCAVYAVQVRKRLDGLGWSNWSNPATYVMDIKVPMKGFEFWRIINGDTMKKENY 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLTEQAHTVTVLAINSI 720  
DB 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLTEQAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIWSLSPSDYKLMYFIEWKLNED 780  
DB 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIWSLSPSDYKLMYFIEWKLNED 780  
QY 781 GEIKWLRISSSVKKYVIHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYVIHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVIISSILLGTLISHQRMKLFMEDVPNPKNCSSWAQGLNFQK 891  
DB 841 GLYIVPVIISSILLGTLISHQRMKLFMEDVPNPKNCSSWAQGLNFQK 891

RESULT 33  
US-08-582-825A-1  
; Sequence 1, Application US/08582825A  
; GENERAL INFORMATION:

; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,825A  
; FILING DATE: 04-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-582-825A-1

Query Match 76.5%; Score 891; DB 9; Length 896;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSYPTPWRFKLSGMPNSTYDYFLLPAGLSKNTSNS 60



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QY 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
    |||||||
Db 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
QY 121 QOIDANMNIOQWLKGDCLKFICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180
    |||||||
Db 121 QOIDANMNIOQWLKGDCLKFICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCECLVPVPFAKNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 181 FQMVHCNCSVHECCCECLVPVPFAKNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
    |||||||
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRDLDPGIMSDMSPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
    |||||||
Db 301 GSSYEVQVRGKRDLDPGIMSDMSPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
    |||||||
Db 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSLYCSDIPSIIH 480
    |||||||
Db 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSLYCSDIPSIIH 480
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKIISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKIISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720
    |||||||
Db 661 TLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLASAPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
    |||||||
Db 721 GASVANFNLTFSWPMKVNIVQSLASAPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
    |||||||
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVYVLISSSILLGLTLLISHQMKKLFWEDEVNPKNCSWAQGLNFQK 891
    |||||||
Db 841 GLYVIVYVLISSSILLGLTLLISHQMKKLFWEDEVNPKNCSWAQGLNFQK 891
```

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; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,005
; FILING DATE: 08-Jan-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-585-005-3
```

Query Match 76.5%; Score 891; DB 9; Length 896;  
Best local similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRKLSQMPNSTYDYFLPAGISKNTSNS 60
    |||||||
Db 1 MICQKFCVLLHMEFIYVITAFNLSPITPWRKLSQMPNSTYDYFLPAGISKNTSNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
    |||||||
Db 61 NGHYETAVEPKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120
QY 121 QOIDANMNIOQWLKGDCLKFICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180
    |||||||
Db 121 QOIDANMNIOQWLKGDCLKFICYVESLFKNLFRNRYKVVHLLYVLEVLDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCECLVPVPFAKNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 181 FQMVHCNCSVHECCCECLVPVPFAKNDTLLMCLKITSGGVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
    |||||||
Db 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRDLDPGIMSDMSPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
    |||||||
Db 301 GSSYEVQVRGKRDLDPGIMSDMSPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
    |||||||
Db 361 VPSKEIVMMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSLYCSDIPSIIH 480
    |||||||
Db 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQLRHRSLSLYCSDIPSIIH 480
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKIISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKIISWEKVPFPENNLOQIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPATYVMDIKVPMRGPEFWRLINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSSEDEVGNHTKFTFLWTEQAHTVTVLAINSI 720
    |||||||
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|||||  
Db 661 TLMLKPLMKNDLSCSVQRYVINHHTSCNGTWEEDVGNHTKFTFLMTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPWPSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFLIEWKLNED 780  
Db 721 GASVANENLTFSPWPSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFLIEWKLNED 780  
QY 781 GEIKWLRISSSVKRYIHDHFPIEKEYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKRYIHDHFPIEKEYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAOGLNFOK 891  
Db 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAOGLNFOK 891

## RESULT 35

US-08-667-197-3  
; Sequence 3, Application US/08667197  
; GENERAL INFORMATION:  
; APPLICANT: Mathews, William  
; TITLE OF INVENTION: USES FOR WSX LIGANDS  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,197  
; FILING DATE: 20-Jun-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585005  
; FILING DATE: 01/08/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: P-40,378  
; REFERENCE/DOCKET NUMBER: P0986P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-667-197-3

Query Match 76.5%; Score 891; DB 10; Length 896;  
Best Local Similarity. 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMEFIYVITAFNLSPYTPMRKFLSCMPNSTYDYFLPAGLSKNTSNS 60  
Db 1 MICQKFCVVLHMEFIYVITAFNLSPYTPMRKFLSCMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVERKFNSSGTHFSNLSKTFHCGRSEQDRNCISLACADNIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAVERKFNSSGTHFSNLSKTFHCGRSEQDRNCISLACADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANWNIOGWLKGDKLFIQYVESLFEKNLFERNYNYKVHLLYVLPVELEDSPLVPQKGS 180  
Db 121 QOIDANWNIOGWLKGDKLFIQYVESLFEKNLFERNYNYKVHLLYVLPVELEDSPLVPQKGS 180

QY 181 EQMVHNCNVHECCCELVPEPTAKLNDTLMLCKLITSGCVIFQSPPLMSVQPINMVKRDP 240  
Db 181 EQMVHNCNVHECCCELVPEPTAKLNDTLMLCKLITSGCVIFQSPPLMSVQPINMVKRDP 240  
QY 241 LGLHMEITDDGNLKISWSSPLVPEPLQYQVKYSENSTVIVREADKIVSATSLVDLSILP 300  
Db 241 LGLHMEITDDGNLKISWSSPLVPEPLQYQVKYSENSTVIVREADKIVSATSLVDLSILP 300  
QY 301 GSSYEVOVRGKRDLDPGIMSDMSTPRVFTTQDVIVFPFKILTSVGSNVSFHCYKKNKI 360  
Db 301 GSSYEVOVRGKRDLDPGIMSDMSTPRVFTTQDVIVFPFKILTSVGSNVSFHCYKKNKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420  
Db 361 VPSKEIYVMMNLAEKIPQSOYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHCCH 420  
QY 421 RYAEIYVIDVININISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSSLYCSDIPSIH 480  
Db 421 RYAEIYVIDVININISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHRSSLYCSDIPSIH 480  
QY 481 PISEPKDCYQSDGFYEICIFQPIFLSGYTMWIRINSLGSLDSPTCVLPDSVYKPLPP 540  
Db 481 PISEPKDCYQSDGFYEICIFQPIFLSGYTMWIRINSLGSLDSPTCVLPDSVYKPLPP 540  
QY 541 SSVKAEITINIGLTKISWEKVPPENNLOFOIRYGLSGKEVQWKHYEYDAKSKVSLPV 600  
Db 541 SSVKAEITINIGLTKISWEKVPPENNLOFOIRYGLSGKEVQWKHYEYDAKSKVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKYPMRGPENRIINGDTMKREKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKYPMRGPENRIINGDTMKREKNV 660  
QY 661 TLMLKPLMKNDLSCSVQRYVINHHTSCNGTWEEDVGNHTKFTFLMTEQAHVTVLAINSI 720  
Db 661 TLMLKPLMKNDLSCSVQRYVINHHTSCNGTWEEDVGNHTKFTFLMTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPWPSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFLIEWKLNED 780  
Db 721 GASVANENLTFSPWPSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFLIEWKLNED 780  
QY 781 GEIKWLRISSSVKRYIHDHFPIEKEYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKRYIHDHFPIEKEYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAOGLNFOK 891  
Db 841 GLYIVPVISSSILLGLTLLISHQRMKLFMEDVPPNPKNCWSAOGLNFOK 891

## RESULT 36

US-08-779-457-3  
; Sequence 3, Application US/08779457  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Chiang, Nancy Y.  
; APPLICANT: Kyung, Jib Kim  
; APPLICANT: Mathews, William  
; APPLICANT: Rodrigues, Maria L.  
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-3

Query Match 76.5%; Score 891; DB 11; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPITPWREKLSGMPNSTYDYELLPAGLSKNTS 60
DB 1 MICOKFCVLLHWEFIYVITAFNLSPITPWREKLSGMPNSTYDYELLPAGLSKNTS 60
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSL 120
DB 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSL 120
QY 121 QOIDANNNIQCWLKGDLLKFLICVYSLFKNLFERNYNYKVHLLYVLEVLDSPLVPQKS 180
DB 121 QOIDANNNIQCWLKGDLLKFLICVYSLFKNLFERNYNYKVHLLYVLEVLDSPLVPQKS 180
QY 181 FQVHNCNSVHECCCLVPPVPTAKNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240
DB 181 FQVHNCNSVHECCCLVPPVPTAKNDTLLMCLKITSGVIFQSPPLMSVQPINMVKPDP 240
QY 241 LGHMETDDGNLKLISWSSPPLVPPLOYQVKYSENSTVIREADKIVSATSLVDSILP 300
DB 241 LGHMETDDGNLKLISWSSPPLVPPLOYQVKYSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVGRKRLDGPGLWSWSTPRTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
DB 301 GSSYEYQVGRKRLDGPGLWSWSTPRTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNINISCEITDGLTKMTCRWSTSTIOSLAESTLQIRHRSLLYCSIDIPSIH 480
DB 421 RYAEIYVIDVNINISCEITDGLTKMTCRWSTSTIOSLAESTLQIRHRSLLYCSIDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEVYDAKSRSVSLPV 600
DB 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEVYDAKSRSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFRRIINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPATYVMDIKVPMRGPEFRRIINGDTMKKEKNV 660

QY 661 TLWKPLMKNDLSQVQRYVINIHTSCNGTWSEDEVGNHTKFTFLMTEQAHVTLAINSI 720
DB 661 TLWKPLMKNDLSQVQRYVINIHTSCNGTWSEDEVGNHTKFTFLMTEQAHVTLAINSI 720
QY 721 GASVANFNLTFSWPMMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
DB 721 GASVANFNLTFSWPMMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
QY 781 GEIKWLRISSSVKKYIYHDFPIEKKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKKYIYHDFPIEKKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCSTNAOGLNFQK 891
DB 841 GLYIVPVISSSILLGLTLLISHQRMKLLFWEDEVNPNKNCSTNAOGLNFQK 891

RESULT 37

US-08-780-562-3
Sequence 3, Application US/08780562
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: MSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-562-3

Query Match 76.5%; Score 891; DB 11; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPITPWREKLSGMPNSTYDYELLPAGLSKNTS 60
DB 1 MICOKFCVLLHWEFIYVITAFNLSPITPWREKLSGMPNSTYDYELLPAGLSKNTS 60
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSL 120

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Db      61 NGHYETAVERFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
OY      121 QOIDANWNIOCWLGDKLFLICYVESLFKNLFERNYKVVHLLVLEVEDSPVLPQKS 180
Db      121 QOIDANWNIOCWLGDKLFLICYVESLFKNLFERNYKVVHLLVLEVEDSPVLPQKS 180
OY      181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
Db      181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
OY      241 LGLHMETIDGDLKISWSSPPLVPFLQYQVYKSENSTVIREADKIVSATSLVDSILP 300
Db      241 LGLHMETIDGDLKISWSSPPLVPFLQYQVYKSENSTVIREADKIVSATSLVDSILP 300
OY      301 GSSYEVOVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEFHCITYKKENKI 360
Db      301 GSSYEVOVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEFHCITYKKENKI 360
OY      361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db      361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
OY      421 RYAEIYVIDVNNINISCETDGYLTFTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSII 480
Db      421 RYAEIYVIDVNNINISCETDGYLTFTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSII 480
OY      481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db      481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
OY      541 SSVKAETITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db      541 SSVKAETITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
OY      601 PDLCAVYAVOVRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db      601 PDLCAVYAVOVRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
OY      661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720
Db      661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720
OY      721 GASVANFNLFSPWPMKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
Db      721 GASVANFNLFSPWPMKVNIVQSLAAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780
OY      781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db      781 GEIKWLRISSSVKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
OY      841 GLYVIVPVITISSILLGLTLLISHQRMKLFMEDVVPNPKNCMAQGLNFQK 891
Db      841 GLYVIVPVITISSILLGLTLLISHQRMKLFMEDVVPNPKNCMAQGLNFQK 891

```

RESULT 38

US-08-585-005-4

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: Sequence 4, Application US/08585005
: GENERAL INFORMATION:
: APPLICANT: Matthews, William
: APPLICANT: Bennett, Brian
: TITLE OF INVENTION: WSX RECEPTOR
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

```

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/585,005
: FILING DATE: 08-Jan-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0986
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 923 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-585-005-4

```

Query Match 76.5%; Score 891; DB 9; Length 923;

Best Local Similarity: 100.0%; Pred. No. 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 MICQKFCVYLLHMEFIYVITAFNLSTPTTPWRFKLSGMPNSTDYFLLPAGLSKNTSNS 60
Db      1 MICQKFCVYLLHMEFIYVITAFNLSTPTTPWRFKLSGMPNSTDYFLLPAGLSKNTSNS 60
OY      61 NGHYETAVERFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db      61 NGHYETAVERFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
OY      121 QOIDANWNIOCWLGDKLFLICYVESLFKNLFERNYKVVHLLVLEVEDSPVLPQKS 180
Db      121 QOIDANWNIOCWLGDKLFLICYVESLFKNLFERNYKVVHLLVLEVEDSPVLPQKS 180
OY      181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
Db      181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240
OY      241 LGLHMETIDGDLKISWSSPPLVPFLQYQVYKSENSTVIREADKIVSATSLVDSILP 300
Db      241 LGLHMETIDGDLKISWSSPPLVPFLQYQVYKSENSTVIREADKIVSATSLVDSILP 300
OY      301 GSSYEVOVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEFHCITYKKENKI 360
Db      301 GSSYEVOVGRKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSEFHCITYKKENKI 360
OY      361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db      361 VPSKEIYVMMNLAEKIPQSQYDVVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
OY      421 RYAEIYVIDVNNINISCETDGYLTFTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSII 480
Db      421 RYAEIYVIDVNNINISCETDGYLTFTKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSII 480
OY      481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db      481 PISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
OY      541 SSVKAETITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
Db      541 SSVKAETITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV 600
OY      601 PDLCAVYAVOVRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db      601 PDLCAVYAVOVRCKRLDGLGYSWNSNPAITVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
OY      661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720

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Db 661 TLLMKPLMKNDLSVORVYINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVALINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTODDIEKHOSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTODDIEKHOSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWSAOGLNFOK 891  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWSAOGLNFOK 891

## RESULT 39

US-08-667-197-4  
: Sequence 4, Application US/08667197  
: GENERAL INFORMATION:  
: APPLICANT: Matthews, William  
: TITLE OF INVENTION: USES FOR WSX LIGANDS  
: NUMBER OF SEQUENCES: 47  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Winpatin (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/667,197  
: FILING DATE: 20-Jun-1996  
: CLASSIFICATION: 424  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/585005  
: FILING DATE: 01/08/96  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Lee, Wendy M.  
: REGISTRATION NUMBER: P-40,378  
: REFERENCE/DOCKET NUMBER: P0986P1  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415/225-1994  
: TELEFAX: 415/952-9881  
: TELEX: 910/371-7168  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 923 amino acids  
: TYPE: Amino Acid  
: TOPOLOGY: Linear  
: US-08-667-197-4

Query Match 76.5%; Score 891; DB 10; Length 923;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVTAFNLSYPTPWRFKLSGMPNSTDYDYLFPAGLSKNTSNS 60  
Db 1 MICOKFCVLLHWEFIYVTAFNLSYPTPWRFKLSGMPNSTDYDYLFPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLYF 120  
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLYF 120  
QY 121 QOIDANMNIOQWLKGLKFLICYVESLFKNLFRNRYNYKYLHLLVLPVLEDSPLVPQKGS 180  
Db 121 QOIDANMNIOQWLKGLKFLICYVESLFKNLFRNRYNYKYLHLLVLPVLEDSPLVPQKGS 180

QY 181 FQVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVLFQSPILMSVQPINMKRDPDP 240  
Db 181 FQVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSQGVLFQSPILMSVQPINMKRDPDP 240  
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOYQVKSSENSTYVIREADKIVSATSLVDSILP 300  
Db 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOYQVKSSENSTYVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPGLMSWSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKNKI 360  
Db 301 GSSYEVOVRGKRLDGPGLMSWSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKKNKI 360  
QY 361 VPSKEIYWMNLAEKIPQSOYDVYSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYWMNLAEKIPQSOYDVYSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
Db 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540  
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVYKPLRP 540  
QY 541 SSVKAEITINIGLKISWEKPYPPENNLOFOIRYGLSGKEVQMKHYEYDAKSKSVSLPY 600  
Db 541 SSVKAEITINIGLKISWEKPYPPENNLOFOIRYGLSGKEVQMKHYEYDAKSKSVSLPY 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYSNWSNPAYTVMDIKVPMGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYSNWSNPAYTVMDIKVPMGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSVORVYINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVALINSI 720  
Db 661 TLLMKPLMKNDLSVORVYINHHTSCNGTWSDEVGNHTKFTFLMTEQAHVTVALINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNED 780  
Db 721 GASVANFNLTFSWPMKSVNIQSLAYPLNSSCVIYSWILSPSDYKLMYFIIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTODDIEKHOSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFTODDIEKHOSDA 840  
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWSAOGLNFOK 891  
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWSAOGLNFOK 891

## RESULT 40

US-08-779-457-4  
: Sequence 4, Application US/08779457  
: GENERAL INFORMATION:  
: APPLICANT: Carter, Paul J.  
: APPLICANT: Chiang, Nancy Y.  
: APPLICANT: Kyung, Jin Kim  
: APPLICANT: Matthews, William  
: APPLICANT: Rodrigues, Maria L.  
: TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES  
: NUMBER OF SEQUENCES: 51  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Winpatin (Genentech)  
: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,457  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667197  
FILING DATE: 06/20/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 923 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-779-457-4

Query Match 76.5%; Score 891; DB 11; Length 923;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMEFIYVITAFNLSYPTPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVVLHMEFIYVITAFNLSYPTPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLV 120  
DB 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLV 120  
QY 121 QOIDANNNIQCWLKGDCLKFICVESLFRNLYKVVHLLVLPVEYLEDSPVLPQKS 180  
DB 121 QOIDANNNIQCWLKGDCLKFICVESLFRNLYKVVHLLVLPVEYLEDSPVLPQKS 180  
QY 181 FQMVHCNCSVHECCCLVPTAKLNDTLMLCKITSGVIFQSPMSVQPINMVKPDP 240  
DB 181 FQMVHCNCSVHECCCLVPTAKLNDTLMLCKITSGVIFQSPMSVQPINMVKPDP 240  
QY 241 LGLHMEITDGNLKITSSSPPLVPFLOQVYKSENSTTVIREADKIYATSLLVDSILP 300  
DB 241 LGLHMEITDGNLKITSSSPPLVPFLOQVYKSENSTTVIREADKIYATSLLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPISWDSMTPRVFTQDVITYFPKILTSVGSNVFHCITYKKENKI 360  
DB 301 GSSYEVOVRGKRLDGPISWDSMTPRVFTQDVITYFPKILTSVGSNVFHCITYKKENKI 360  
QY 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIVMMNLAEKIPQSOYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYIDVNNINISCETDGYLTMTKCRNSTSTIOSLAESTLQLRHSSSLYCSIPSII 480  
DB 421 RYAEIYIDVNNINISCETDGYLTMTKCRNSTSTIOSLAESTLQLRHSSSLYCSIPSII 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 540  
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 540  
QY 541 SSVKAEITINIGLKISWEKVPFPENNIOQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKISWEKVPFPENNIOQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYWSNNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVYAVOVRCKRLDGLGYWSNNSNPATYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLMKPLMKNDISLVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDISLVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANENLTFSPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSILLGLTLLISHQRMKLFMEDVPPNPKNSWAQGLNFQK 891  
DB 841 GLYVIVPVISSILLGLTLLISHQRMKLFMEDVPPNPKNSWAQGLNFQK 891

RESULT 41  
US-08-780-562-4

Sequence 4, Application us/08780562  
GENERAL INFORMATION:  
APPLICANT: Mathews, William  
APPLICANT: Bennett, Brian  
TITLE OF INVENTION: WSX RECEPTOR  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: us/08/780,562  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/  
FILING DATE: 01/08/97  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 923 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-780-562-4

Query Match 76.5%; Score 891; DB 11; Length 923;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVVLHMEFIYVITAFNLSYPTPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVVLHMEFIYVITAFNLSYPTPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHETAVEPKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLV 120



```

Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQKS 180
    |||||||
Db 121 QQIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQKS 180
QY 181 FQVHNCNSVHECCCLVPVPTAKINDTLLMCLKITSQVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 181 FQVHNCNSVHECCCLVPVPTAKINDTLLMCLKITSQVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKISWSSPLVPPLQYQVKYSENSTVIREADKIVSATSLVDSILP 300
    |||||||
Db 241 LGLHMEITDDGNLKISWSSPLVPPLQYQVKYSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTTODVYIFPKILTSVGSNVSFHCYKKENKI 360
    |||||||
Db 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTTODVYIFPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVCCNEHECH 420
    |||||||
Db 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVCCNEHECH 420
QY 421 RYAEIYIDVNNINISCEITDGYLTMTKCRWSTSTIOSLAESTILOLRYHRSSLYCSDIPSIH 480
    |||||||
Db 421 RYAEIYIDVNNINISCEITDGYLTMTKCRWSTSTIOSLAESTILOLRYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEYVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPFWRIINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720
    |||||||
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNE 780
    |||||||
Db 721 GASVANFNLTFSWPMKVNIVQSLASAYPLNSSCVIVSWILSPDYKLMYFIIEWKNLNE 780
QY 781 GEIKMLRISSSVKYYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
    |||||||
Db 781 GEIKMLRISSSVKYYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLVYIVPVITISSIILLGTLISHQRMKLFMEDVPPNPKNCMAOGLNFQK 891
    |||||||
Db 841 GLVYIVPVITISSIILLGTLISHQRMKLFMEDVPPNPKNCMAOGLNFQK 891

```

## RESULT 42

US-08-774-414-1

Sequence 1, Application US/08774414

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI

APPLICANT: WELCHER, ANDREW A.

APPLICANT: FLETCHER, FREDERICK A.

TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehaviiland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

```

: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/774,414
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Pessin, Karol M.
: REFERENCE/DOCKET NUMBER: A-382-A
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 965 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-774-414-1

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Query Match 76.5%; Score 891; DB 11; length 965;

Best local Similarity 100.0%; Pred. No. 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICQRCVLLHMEFIYVITAFNLSYPTIPWRKLSKMPNNTYVYFLLPAGLSKNTSNS 60
    |||||||
Db 1 MICQRCVLLHMEFIYVITAFNLSYPTIPWRKLSKMPNNTYVYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
    |||||||
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQKS 180
    |||||||
Db 121 QQIDANMNIOQWLKGLDKLFICYVESLFKNLFRNRYNKVHLLVLPVLEDSPLVPQKS 180
QY 181 FQVHNCNSVHECCCLVPVPTAKINDTLLMCLKITSQVIFQSPILMSVQPINMVKPDP 240
    |||||||
Db 181 FQVHNCNSVHECCCLVPVPTAKINDTLLMCLKITSQVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKISWSSPLVPPLQYQVKYSENSTVIREADKIVSATSLVDSILP 300
    |||||||
Db 241 LGLHMEITDDGNLKISWSSPLVPPLQYQVKYSENSTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTTODVYIFPKILTSVGSNVSFHCYKKENKI 360
    |||||||
Db 301 GSSYEYQVRGKRLDGPGLSDWSTPRVFTTODVYIFPKILTSVGSNVSFHCYKKENKI 360
QY 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVCCNEHECH 420
    |||||||
Db 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAVCCNEHECH 420
QY 421 RYAEIYIDVNNINISCEITDGYLTMTKCRWSTSTIOSLAESTILOLRYHRSSLYCSDIPSIH 480
    |||||||
Db 421 RYAEIYIDVNNINISCEITDGYLTMTKCRWSTSTIOSLAESTILOLRYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
    |||||||
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEYVYDAKSKSVSLPV 600
    |||||||
Db 541 SSVKAEITINIGLKLISWEKVPFENNLOFOIRYGLSGKEVQWMEYVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPFWRIINGDTMKKEKNV 660
    |||||||
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720
    |||||||
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTLAINSI 720

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QY 721 GASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYIIEKKNLND 780  
DB 721 GASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYIIEKKNLND 780  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQK 891  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQK 891

RESULT 43  
US-09-671-049-1  
; Sequence 1, Application US/09671049  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; WELCHER, ANDREW A.  
; FLETCHER, FREDERICK A.  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/671,049  
; FILING DATE: 27-Sep-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,414  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pesslin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382-A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 965 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-671-049-1

Query Match 76.5%; Score 891; DB 20; Length 965;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTFWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
DB 1 MICQKFCVLLHWEFIYVITAFNLSTYPTFWRFKLSCMPNSTYDYFLPAGLSKNTSNS 60  
QY 61 NGHYETAVEPKNSSGTHFSNLSKTTFHCCRSSEQDRNCSLCAADNIEGTFVSTVNSLVE 120  
DB 61 NGHYETAVEPKNSSGTHFSNLSKTTFHCCRSSEQDRNCSLCAADNIEGTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQMLKGDCLKFICVESLEFKNLFRNRYNKVHLVLPVEVLDSPLVPQKGS 180  
DB 121 QOIDANMNIOQMLKGDCLKFICVESLEFKNLFRNRYNKVHLVLPVEVLDSPLVPQKGS 180  
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
DB 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240

DB 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPILMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYKYSNSTVIREADKIVSATSLVDLSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFPLOQYKYSNSTVIREADKIVSATSLVDLSILP 300  
QY 301 GSSYEVOVRGKRDLGPGIWSMDSTPRVFTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360  
DB 301 GSSYEVOVRGKRDLGPGIWSMDSTPRVFTQDVIYFPPKILTSVGSNVSFHCYKKNKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVNIINISCEITDGYLTMTKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480  
DB 421 RYAEIYVIDVNIINISCEITDGYLTMTKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIDPSIH 480  
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMIRINHSLSGLSDSPPCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKISWEKVPFENNLOQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKISWEKVPFENNLOQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
QY 601 PDLCAVAVOYQKRLDGLGYSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
DB 601 PDLCAVAVOYQKRLDGLGYSNWSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSEDEVGNHTKFTLWTEQAHVTVALINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINHHTSCNGTWSEDEVGNHTKFTLWTEQAHVTVALINSI 720  
QY 721 GASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYIIEKKNLND 780  
DB 721 GASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMYIIEKKNLND 780  
QY 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQK 891  
DB 841 GLYVIVPVISSSILLGLTLLISHQRMKLEWEDVNPKNCSWAQGLNFQK 891

RESULT 44  
US-08-582-825-5  
; Sequence 5, Application US/08582825  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,825  
; FILING DATE: 04-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pesslin, Karol M.

REFERENCE/DOCKET NUMBER: A-382  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 969 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-582-825-5

Query Match 76.5%; Score 891; DB 9; Length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANWNIQCWLKGDCLKFICVESLFEKNLFRNYNYKVHLLYLPEVLEDSPLVPQKGS 180  
Db 121 QQIDANWNIQCWLKGDCLKFICVESLFEKNLFRNYNYKVHLLYLPEVLEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMKPDPP 240  
Db 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMKPDPP 240  
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYQVKSSENSTVIREADKIVATSLLVDSILP 300  
Db 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYQVKSSENSTVIREADKIVATSLLVDSILP 300  
QY 301 GSSYEYQVRGKRDLGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEYQVRGKRDLGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCYLBDSPVKPLPP 540  
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCYLBDSPVKPLPP 540  
QY 541 SSYKAEITINIGLLKISWEKPYFPENNLOFOIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
Db 541 SSYKAEITINIGLLKISWEKPYFPENNLOFOIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYMSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYMSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDLSLGSVQRYVINHHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720  
Db 661 TLLMKPLMKNDLSLGSVQRYVINHHTSCNGTWSSEVDGNHTKFTFLWTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIVSWILSPSDYKIMYFIIEKNLNE 780  
Db 721 GASVANFNLTFSWPMKSVNIYQSLAYPLNSSCVIVSWILSPSDYKIMYFIIEKNLNE 780  
QY 781 GEIKMLRISSSVKKYIYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKKYIYIHDHFIPLEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVPNPKNCSSWAQGLNFQK 891  
Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVPNPKNCSSWAQGLNFQK 891

Db 841 GLYVIVPVIISSSILLGLTLISHQRMKLLFWEDVPNPKNCSSWAQGLNFQK 891  
RESULT 45  
US-08-582-825A-5  
; Sequence 5, Application US/08582825A  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,825A  
; FILING DATE: 04-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessinn, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 969 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-582-825A-5

Query Match 76.5%; Score 891; DB 9; Length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTYPTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60  
QY 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
Db 61 NGHYETAVERPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120  
QY 121 QQIDANWNIQCWLKGDCLKFICVESLFEKNLFRNYNYKVHLLYLPEVLEDSPLVPQKGS 180  
Db 121 QQIDANWNIQCWLKGDCLKFICVESLFEKNLFRNYNYKVHLLYLPEVLEDSPLVPQKGS 180  
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMKPDPP 240  
Db 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMKPDPP 240  
QY 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYQVKSSENSTVIREADKIVATSLLVDSILP 300  
Db 241 LGLHMEITDDGNLKSISWSSPPLVPFPLOQYQVKSSENSTVIREADKIVATSLLVDSILP 300  
QY 301 GSSYEYQVRGKRDLGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEYQVRGKRDLGPGIWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIYVMMNLAEKIPQSQDYDVSDHYSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480  
Db 421 RYAEIYVIDVININISCEITDGYLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCSIDIPSIH 480

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|||||
Db 421 RYAEIYVIDVNIINISCEITDGYLTMTCRMSTSTIQSLAESTLQLRHYRHSLSYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGEFECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
Db 481 PISEPKDCYLOSDGEFECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVVDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVVDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSGVNHTKFTFLWTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSGVNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNE 780
Db 721 GASVANFNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNE 780
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVYPNPKNCMAOGLNFQK 891
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVYPNPKNCMAOGLNFQK 891
```

```
RESULT 46
US-08-774-414-5
; Sequence 5, Application US/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,414
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-774-414-5
```

```
Query Match 76.5%; Score 891; Db 11; Length 969;
Best Local Similarity 100.0%; Pred. No. 0;
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Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHMEFIYITAFNLSTPTPWREKLSCMPNSTYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHMEFIYITAFNLSTPTPWREKLSCMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEPKFNSSGTHFSNLSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIQCWLGDKLFIQYVESLFKNLFRNRYKVHLVLPVELDPSLPVQKS 180
Db 121 QOIDANWNIQCWLGDKLFIQYVESLFKNLFRNRYKVHLVLPVELDPSLPVQKS 180
QY 181 FQMVHNCNVHECCGLVPVPTAKLNDTLMLCKITSGGVIFQSPLMVOPINMKPDP 240
Db 181 FQMVHNCNVHECCGLVPVPTAKLNDTLMLCKITSGGVIFQSPLMVOPINMKPDP 240
QY 241 LGLHMEITDGNLTKISWSSPPLVPFLOYQVKSSENSTTVIREADKIVSATSLVDISILP 300
Db 241 LGLHMEITDGNLTKISWSSPPLVPFLOYQVKSSENSTTVIREADKIVSATSLVDISILP 300
QY 301 GSSYEVOVRGKRLDGPISWDSWSTPRVFTTQDVLYFPFKILTSVGSNVSHCIYKKENKI 360
Db 301 GSSYEVOVRGKRLDGPISWDSWSTPRVFTTQDVLYFPFKILTSVGSNVSHCIYKKENKI 360
QY 361 VPSKEIWWWNLAEKIPQSOYDVSDHVSQVTFENLNETKPRGKIYDAYCCNEHECH 420
Db 361 VPSKEIWWWNLAEKIPQSOYDVSDHVSQVTFENLNETKPRGKIYDAYCCNEHECH 420
QY 421 RYAEIYVIDVNIINISCEITDGYLTMTCRMSTSTIQSLAESTLQLRHYRHSLSYCSDIPSIH 480
Db 421 RYAEIYVIDVNIINISCEITDGYLTMTCRMSTSTIQSLAESTLQLRHYRHSLSYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGEFECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
Db 481 PISEPKDCYLOSDGEFECIFQPIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLRP 540
QY 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVVDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVVDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSGVNHTKFTFLWTEQAHVTVLAINSI 720
Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSGVNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNE 780
Db 721 GASVANFNLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNE 780
QY 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVYPNPKNCMAOGLNFQK 891
Db 841 GLYIVPVIISSSILLGLTLLISHQRMKLFMEDVYPNPKNCMAOGLNFQK 891
```

```
RESULT 47
US-08-774-414-6
; Sequence 6, Application US/08774414
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: WELCHER, ANDREW A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; NUMBER OF SEQUENCES: 33
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,414  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Pessin, Karol M.  
REFERENCE/DOCKET NUMBER: A-382-A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 969 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-774-414-6

Query Match 76.5%; Score 891; DB 11; length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVYLLHWEFIYVITAFNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVYLLHWEFIYVITAFNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 120  
QY 121 QOIDANNNIQCWLKGLKLFICYVESLFRNRYNYKVHLLVPEVLEDSPLVPQKS 180  
DB 121 QOIDANNNIQCWLKGLKLFICYVESLFRNRYNYKVHLLVPEVLEDSPLVPQKS 180  
QY 181 FQWVHCNCSVHECCCECLVPTAKLNDTLLMCLKITSQVIFQSPIMSVQPINMVKPDP 240  
DB 181 FQWVHCNCSVHECCCECLVPTAKLNDTLLMCLKITSQVIFQSPIMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKISWSSPLVPFLOYQVYKSENSTVIREADKIYATSLLVDSILP 300  
DB 241 LGLHMETDDGNLKISWSSPLVPFLOYQVYKSENSTVIREADKIYATSLLVDSILP 300  
QY 301 GSSYEVOYRGKRLDGPGLMSDWSSTPRYFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVOYRGKRLDGPGLMSDWSSTPRYFTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYVMMNLAEKIPQSQDYVVSVDHVKVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYVMMNLAEKIPQSQDYVVSVDHVKVTFENLNETKPRGFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVDVININISCEYDGLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
DB 421 RYAEIYVDVININISCEYDGLTKMTCRMSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLISGYTMIRINHSLSGLSDSPPTCYLDPDSVVKPLPP 540  
DB 481 PISEPKDCYLOSDFEYECIFQPIFLISGYTMIRINHSLSGLSDSPPTCYLDPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQMKMEVYDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRCKRLDGLGYSNMSNPATYVMDIKVPMRGPERWRIINGDTMKKEKNY 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYSNMSNPATYVMDIKVPMRGPERWRIINGDTMKKEKNY 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHSCNGTWSDEVGNHTKFTFLTEQAHVTVLAINSI 720  
DB 661 TLLMKPLMKNDSLCSVQRYVINHHSCNGTWSDEVGNHTKFTFLTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780  
DB 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKKYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYVIYVYIISSTILLGTLISHQRMKLFWEDVNPKNCSNAQGLNFOK 891  
DB 841 GLYVIYVYIISSTILLGTLISHQRMKLFWEDVNPKNCSNAQGLNFOK 891

RESULT 48  
US-09-671-049-5  
Sequence 5, Application US/09671049

GENERAL INFORMATION:  
APPLICANT: CHANG, MING-SHI  
FLETCHER, ANDREW A.  
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/671,049  
FILING DATE: 27-Sep-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/774,414  
FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pessin, Karol M.

REFERENCE/DOCKET NUMBER: A-382-A  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 969 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-671-049-5

Query Match 76.5%; Score 891; DB 20; length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVYLLHWEFIYVITAFNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVYLLHWEFIYVITAFNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVEPKFNSSGTHFSNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 120  
DB 61 NGHYETAVEPKFNSSGTHFSNLSTPTWRFKLSGMPNSTYDYFLLPAGLSKNTS 120

Db 61 NGHYETAVEPKENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNYKVVHLLVLPVLEDSPLVPQKS 180  
Db 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNYKVVHLLVLPVLEDSPLVPQKS 180  
QY 181 FOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVKPDP 240  
Db 181 FOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKSISWSSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300  
Db 241 LGLHMETDDGNLKSISWSSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIWMNMNLAERIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMNMNLAERIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480  
Db 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWESEVGNHTKFTFLMTQEAHTVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWESEVGNHTKFTFLMTQEAHTVTVLAINSI 720  
QY 721 GASVANFNLTFSWPMKRYNIVQSLASAYPLNSCVIYSWILSPSDYKLMYFIEMKNLNE 780  
Db 721 GASVANFNLTFSWPMKRYNIVQSLASAYPLNSCVIYSWILSPSDYKLMYFIEMKNLNE 780  
QY 781 GEIKMLRISSSVKYYIHDHFIPRIEYQFSLPIFMEGVGKPKIINSFTQDIEKHQSDA 840  
Db 781 GEIKMLRISSSVKYYIHDHFIPRIEYQFSLPIFMEGVGKPKIINSFTQDIEKHQSDA 840  
QY 841 GLYIVTVPIISSISLLGLTLLISHQRMKLLFMEVDVNPKNCSWAQGLNFQK 891  
Db 841 GLYIVTVPIISSISLLGLTLLISHQRMKLLFMEVDVNPKNCSWAQGLNFQK 891

RESULT 49  
US-09-671-049-6  
; Sequence 6, Application US/09671049  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, MING-SHI  
; WELCHER, ANDREW A.  
; FLETCHER, FREDERICK A.  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/671,049  
FILING DATE: 27-Sep-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,414  
FILING DATE: 31-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pessin, Karol M.  
REFERENCE/DOCKET NUMBER: A-382-A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 969 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-671-049-6

Query Match 76.5%; Score 891; DB 20; Length 969;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MICQKFCVLLHWEIYVITAENLSYPTIPWRKLSMPNNTYDFLLPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEIYVITAENLSYPTIPWRKLSMPNNTYDFLLPAGLSKNTS 60  
QY 61 NGHYETAVEPKENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
Db 61 NGHYETAVEPKENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNYKVVHLLVLPVLEDSPLVPQKS 180  
Db 121 QOIDANMNIOQWLKGLKLFICYVESLFKNLFRNYKVVHLLVLPVLEDSPLVPQKS 180  
QY 181 FOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVKPDP 240  
Db 181 FOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINMVKPDP 240  
QY 241 LGLHMETDDGNLKSISWSSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300  
Db 241 LGLHMETDDGNLKSISWSSPPLVPEPLQYQVKSSENSTTVIREADKIVSATSLLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
Db 301 GSSYEVOVRGKRLDGPIMSDWSTPRVFTTQDVITYPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIWMNMNLAERIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
Db 361 VPSKEIWMNMNLAERIPQSOQYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480  
Db 421 RYAEIYVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480  
QY 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLKISWEKVPFENNLOFOIRYGLSGKEVQWKMEYVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVYAVOVRCKRLDGLGYSNWSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWESEVGNHTKFTFLMTQEAHTVTVLAINSI 720



|||||  
Db 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWEDEVGNHTKFTPLMTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIIEWKNLNE 780  
Db 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIIEWKNLNE 780  
QY 781 GEIKWLRISSSVKKYIHDHFPIEIKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFPIEIKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQK 891  
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQK 891

RESULT 50  
US-08-582-825-3  
; Sequence 3, Application US/08582825  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavenland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,825  
; FILING DATE: 04-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol M.  
; REFERENCE/DOCKET NUMBER: A-382  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 995 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-582-825-3

Query Match 76.5%; Score 891; DB 9; Length 995;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSGMPNSTYDYFILPAGLSKNTS 60  
Db 1 MICQKFCVLLHWEFIYVITAFNLSTPTPWRFKLSGMPNSTYDYFILPAGLSKNTS 60  
QY 61 NGHETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLACADNIEGKTFVSTVNSLYF 120  
Db 61 NGHETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLACADNIEGKTFVSTVNSLYF 120  
QY 121 QOTDANMNIOQWLKGLDLFCYVESLFLKLFNRYNYKVHLLVLPVLEDSPLVPQKGS 180  
Db 121 QOTDANMNIOQWLKGLDLFCYVESLFLKLFNRYNYKVHLLVLPVLEDSPLVPQKGS 180  
QY 181 FOMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGVLFQSPPLMSVQPINMVKPDP 240  
Db 181 FOMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGVLFQSPPLMSVQPINMVKPDP 240

QY 241 LGLHMEITDDGNLKSISWSSPLVPEFPLQYQVKYSENSTFVIREADKIVSATSLVDSLIP 300  
Db 241 LGLHMEITDDGNLKSISWSSPLVPEFPLQYQVKYSENSTFVIREADKIVSATSLVDSLIP 300  
QY 301 GSSYEVOVRGKRLLDGPGLMSDSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREK 360  
Db 301 GSSYEVOVRGKRLLDGPGLMSDSTPRVFTTQDVITYFPFKILTSVGSNVSFHCITYKREK 360  
QY 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTFEFLNENKPRGKFTYDAVYCCNEHECH 420  
Db 361 VPSKEIYVMMNLAEKIPQSOQYDVVSDHVSQVTFEFLNENKPRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIVIDVININISCEITDGYLTMTCTRWSTSTQSLAESTLQLRHRSLSLYCSDIPSIH 480  
Db 421 RYAEIVIDVININISCEITDGYLTMTCTRWSTSTQSLAESTLQLRHRSLSLYCSDIPSIH 480  
QY 481 PISEBKDCYLQSDGFYECIFOPFIPLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPP 540  
Db 481 PISEBKDCYLQSDGFYECIFOPFIPLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLLKISWEKPEPPENNLQOIRYGLSGREVQWKMEVYDAKSKSVSLPV 600  
Db 541 SSVKAEITINIGLLKISWEKPEPPENNLQOIRYGLSGREVQWKMEVYDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYNSMNSNPATVMDIKVPMRGPETWRIINGDTMKREKNV 660  
Db 601 PDLCAVYAVQVRCKRLDGLGYNSMNSNPATVMDIKVPMRGPETWRIINGDTMKREKNV 660  
QY 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWEDEVGNHTKFTPLMTEQAHVTVLAINSI 720  
Db 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWEDEVGNHTKFTPLMTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIIEWKNLNE 780  
Db 721 GASVANENLTFSPMSKVNIVQSLAYPLNSSCVIWSILSPSDYKLMYFIIEWKNLNE 780  
QY 781 GEIKWLRISSSVKKYIHDHFPIEIKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFPIEIKYQFSLYPIFMEGVGPKIINSFTODDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQK 891  
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFQK 891

Search completed: May 18, 2002, 07:07:51  
Job time: 350 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 07:02:51 ; Search time 13.83 Seconds  
(without alignments)  
2226.469 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVLLHMEFIYIT.....QTCSTQTHKIMENKCDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 107366 segs, 26430961 residues

Word size : 0

Total number of hits satisfying chosen parameters: 107366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : Pending\_Patents\_AA\_New:\*  
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3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	2.0	23	5	US-09-991-548-6
2	8	0.7	102	5	US-09-540-209B-8563
3	8	0.7	1887	5	US-09-853-180-3
4	7	0.6	20	6	US-10-027-400-13
5	7	0.6	50	1	PCT-US02-09188-770
6	7	0.6	50	1	PCT-US02-09257-507
7	7	0.6	50	1	PCT-US02-09370-800
8	7	0.6	50	6	US-10-103-295-169
9	7	0.6	50	6	US-10-105-299-3604
10	7	0.6	64	5	US-09-540-209B-6882
11	7	0.6	66	5	US-09-540-209B-6912
12	7	0.6	81	6	US-10-103-295-265
13	7	0.6	86	1	PCT-US02-09921-616
14	7	0.6	122	5	US-09-620-393B-6470
15	7	0.6	127	6	US-10-106-698-6272
16	7	0.6	134	6	US-10-106-698-7726
17	7	0.6	176	1	PCT-US02-07826-282
18	7	0.6	176	6	US-10-097-340-282
19	7	0.6	197	6	US-10-125-540-456
20	7	0.6	206	6	US-10-106-698-6320
21	7	0.6	229	1	PCT-US01-46651-2
22	7	0.6	239	5	US-09-540-209B-8108
23	7	0.6	290	6	US-10-138-632-2
24	7	0.6	293	6	US-10-115-123-233
25	7	0.6	307	6	US-10-115-123-331
26	7	0.6	358	6	US-10-125-540-294

27	7	0.6	461	5	US-09-994-404-225	Sequence 225, App
28	7	0.6	470	5	US-09-994-404-28	Sequence 28, Appl
29	7	0.6	470	5	US-09-994-404-158	Sequence 158, App
30	7	0.6	473	1	PCT-US02-09944-442	Sequence 442, App
31	7	0.6	473	6	US-10-002-304-8	Sequence 8, Appli
32	7	0.6	473	6	US-10-002-050-8	Sequence 8, Appli
33	7	0.6	473	6	US-10-003-152-8	Sequence 8, Appli
34	7	0.6	490	6	US-10-115-123-158	Sequence 158, App
35	7	0.6	504	6	US-10-115-123-332	Sequence 332, App
36	7	0.6	578	5	US-09-573-655B-1433	Sequence 1433, Ap
37	7	0.6	642	5	US-09-540-209B-10008	Sequence 10008, A
38	7	0.6	663	1	PCT-US02-01339-2	Sequence 2, Appli
39	7	0.6	788	6	US-10-002-304-6	Sequence 6, Appli
40	7	0.6	788	6	US-10-002-050-6	Sequence 6, Appli
41	7	0.6	788	6	US-10-003-152-6	Sequence 6, Appli
42	7	0.6	885	5	US-09-540-209B-5548	Sequence 5548, Ap
43	7	0.6	951	5	US-09-573-655B-2349	Sequence 2349, Ap
44	7	0.6	1018	6	US-10-128-714-3585	Sequence 3585, Ap
45	7	0.6	1018	6	US-10-128-714-8585	Sequence 8585, Ap
46	7	0.6	1185	5	US-09-895-913A-246	Sequence 246, App
47	7	0.6	1523	1	PCT-US02-09809-5	Sequence 5, Appli
48	6	0.5	8	5	US-09-423-037A-17	Sequence 17, Appl
49	6	0.5	27	6	US-10-106-698-7746	Sequence 7746, Ap
50	6	0.5	30	5	US-09-623-791A-134	Sequence 134, App
51	6	0.5	30	5	US-09-991-548-23	Sequence 23, Appl
52	6	0.5	33	5	US-09-620-393B-4795	Sequence 4795, Ap
53	6	0.5	35	6	US-10-105-299-5897	Sequence 5897, Ap
54	6	0.5	40	5	US-09-312-283B-129	Sequence 129, App
55	6	0.5	43	5	US-09-620-393B-5092	Sequence 5092, Ap
56	6	0.5	44	5	US-09-554-354A-71	Sequence 71, Appl
57	6	0.5	45	6	US-10-105-299-4556	Sequence 4556, Ap
58	6	0.5	45	6	US-10-004-860-1018	Sequence 1018, Ap
59	6	0.5	46	6	US-10-004-860-938	Sequence 938, App
60	6	0.5	47	6	US-10-105-299-5700	Sequence 5700, Ap
61	6	0.5	51	5	US-09-989-903-45	Sequence 45, Appl
62	6	0.5	51	6	US-10-105-299-4837	Sequence 4837, Ap
63	6	0.5	55	5	US-09-564-951A-5	Sequence 5, Appli
64	6	0.5	55	5	US-10-105-299-4835	Sequence 4835, Ap
65	6	0.5	62	5	US-09-620-393B-8923	Sequence 8923, Ap
66	6	0.5	70	7	US-60-365-384-533	Sequence 533, App
67	6	0.5	71	6	US-10-105-299-5826	Sequence 5826, Ap
68	6	0.5	72	5	US-09-620-393B-1035	Sequence 1035, Ap
69	6	0.5	73	5	US-09-312-283B-415	Sequence 415, App
70	6	0.5	73	6	US-10-106-698-5468	Sequence 5468, Ap
71	6	0.5	78	6	US-10-106-698-5147	Sequence 5147, Ap
72	6	0.5	79	5	US-09-620-393B-3679	Sequence 3679, Ap
73	6	0.5	79	6	US-10-114-893-207	Sequence 207, App
74	6	0.5	80	1	PCT-US02-09135-233	Sequence 233, App
75	6	0.5	80	1	PCT-US02-09105-338	Sequence 338, App

## ALIGNMENTS

RESULT 1  
US-09-991-548-6  
; Sequence 6, Application US/09991548  
; GENERAL INFORMATION:  
; APPLICANT: OLSSON, Lennart  
; APPLICANT: NARANDA, Tatjana  
; TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS  
; FILE REFERENCE: 213542000101  
; CURRENT APPLICATION NUMBER: US/09/991, 548  
; PRIOR FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 09/028, 937  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 08/788, 820  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: 08/701, 382  
; PRIOR FILING DATE: 1996-08-22  
; PRIOR APPLICATION NUMBER: 08/612, 999  
; PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human leptin receptor  
US-09-991-548-6

Query Match 2.0%; Score 23; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e-15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 KKENKIVPSKEIYWMNLAEKIP 377  
Db 1 KKENKIVPSKEIYWMNLAEKIP 23

## RESULT 2

US-09-540-209B-8563  
; Sequence 8563, Application US/09540209B  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
; FILE REFERENCE: 2709,1001-001  
; CURRENT APPLICATION NUMBER: US/09/540,209B  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 8563  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-09-540-209B-8563

Query Match 0.7%; Score 8; DB 5; Length 102;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 655 KKEKNVTL 662  
Db 27 KKEKNVTL 34

## RESULT 3

US-09-853-180-3  
; Sequence 3, Application US/09853180  
; GENERAL INFORMATION:  
; APPLICANT: Chirica, Madaline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; FILE REFERENCE: DX01074  
; CURRENT APPLICATION NUMBER: US/09/853,180  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/203,426  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1887  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-180-3

Query Match 0.7%; Score 8; DB 5; Length 1887;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 620 GYWSNWSN 627  
Db 1673 GYWSNWSN 1680

## RESULT 4

US-10-027-400-13  
; Sequence 13, Application US/10027400  
; GENERAL INFORMATION:  
; APPLICANT: WILDIAMS, Lewis T.  
; TITLE OF INVENTION: ESCOBEDO, Jaime A.  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market, Steuart Street Tower, 20th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/027,400  
FILING DATE: 19-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,917  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 07/151,414  
FILING DATE: 02-FEB-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-267-2-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/326-2400  
TELEFAX: 415/326-2422

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "Peptide Y719p scrambled.  
Contains a phosphate group at position 15."  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-027-400-13

Query Match 0.6%; Score 7; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 634 MDIKVPM 640  
Db 2 MDIKVPM 8

## RESULT 5

PCT-US02-09188-770  
; Sequence 770, Application PC/TUS0209188  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Secreted Proteins

```
; FILE REFERENCE: PS952PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09188
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1732
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 770
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09188-770
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Query Match          0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 521 SLDSPT 527

Db 27 SLDSPT 33

```
RESULT 6
PCT-US02-09257-507
; Sequence 507, Application PC/TUS0209257
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS957PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09257
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 994
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 507
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09257-507
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Query Match          0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 521 SLDSPT 527

Db 27 SLDSPT 33

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RESULT 7
PCT-US02-09370-800
; Sequence 800, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS954PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09370
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
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; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1834
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 800
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09370-800
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Query Match          0.6%; Score 7; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 521 SLDSPT 527

Db 27 SLDSPT 33

```
RESULT 8
US-10-103-295-169
; Sequence 169, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-295-169
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Query Match          0.6%; Score 7; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 521 SLDSPT 527

Db 27 SLDSPT 33

```
RESULT 9
US-10-105-299-3604
; Sequence 3604, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
```



;; Prior Application removed - See File Wrapper or Palm  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 3604  
;; LENGTH: 50  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-105-299-3604

Query Match 0.6%; Score 7; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 SLDSPT 527  
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Db 27 SLDSPT 33

RESULT 10  
US-09-540-209B-6882  
; Sequence 6882, Application US/09540209B  
; GENERAL INFORMATION:

;; APPLICANT: Gary L. Breton  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
;; FILE REFERENCE: 2709.1001-001  
;; CURRENT APPLICATION NUMBER: US/09/540,209B  
;; CURRENT FILING DATE: 2000-04-04  
;; NUMBER OF SEQ ID NOS: 10444  
;; SEQ ID NO 6882  
;; LENGTH: 64  
;; TYPE: PRT  
;; ORGANISM: B.fragilis  
US-09-540-209B-6882

Query Match 0.6%; Score 7; DB 5; Length 64;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 PVISSS 853  
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Db 32 PVISSS 38

RESULT 11  
US-09-540-209B-6912  
; Sequence 6912, Application US/09540209B  
; GENERAL INFORMATION:

;; APPLICANT: Gary L. Breton  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
;; FILE REFERENCE: 2709.1001-001  
;; CURRENT APPLICATION NUMBER: US/09/540,209B  
;; CURRENT FILING DATE: 2000-04-04  
;; NUMBER OF SEQ ID NOS: 10444  
;; SEQ ID NO 6912  
;; LENGTH: 66  
;; TYPE: PRT  
;; ORGANISM: B.fragilis  
US-09-540-209B-6912

Query Match 0.6%; Score 7; DB 5; Length 66;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 READKIV 288  
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Db 60 READKIV 66

RESULT 12

US-10-103-295-265

;; Sequence 265, Application US/10103295  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: 71 Human Secreted Proteins  
;; FILE REFERENCE: P2030P2  
;; CURRENT APPLICATION NUMBER: US/10/103,295  
;; CURRENT FILING DATE: 2002-03-22  
;; PRIOR APPLICATION NUMBER: PCT/US01/29871  
;; PRIOR FILING DATE: 2001-09-24  
;; PRIOR APPLICATION NUMBER: PCT/US01/00911  
;; PRIOR FILING DATE: 2001-01-12  
;; PRIOR APPLICATION NUMBER: 60/234,925  
;; PRIOR FILING DATE: 2000-09-25  
;; PRIOR APPLICATION NUMBER: 09/482,273  
;; PRIOR FILING DATE: 2000-01-13  
;; PRIOR APPLICATION NUMBER: PCT/US99/15849  
;; PRIOR FILING DATE: 1999-07-14  
;; PRIOR APPLICATION NUMBER: 60/092,921  
;; PRIOR FILING DATE: 1998-07-15  
;; PRIOR APPLICATION NUMBER: 60/092,922  
;; PRIOR FILING DATE: 1998-07-15  
;; PRIOR APPLICATION NUMBER: 60/092,956  
;; PRIOR FILING DATE: 1998-07-15  
;; NUMBER OF SEQ ID NOS: 417  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 265  
;; LENGTH: 81  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (20)  
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-103-295-265

Query Match 0.6%; Score 7; DB 6; Length 81;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 SLDSPT 527  
|||||  
Db 58 SLDSPT 64

RESULT 13  
PCT-US02-09921-616  
; Sequence 616, Application PC/TUS0209921  
; GENERAL INFORMATION:

;; APPLICANT: INCYTE GENOMICS, INC.  
;; APPLICANT: DAFEO, Abel  
;; APPLICANT: JONES, Anissa L.  
;; APPLICANT: TRAN, Alanna-Phung B.  
;; APPLICANT: DAHL, Christopher R.  
;; APPLICANT: GIETZEN, Darryl  
;; APPLICANT: CHINN, Joyce  
;; APPLICANT: DUFOUR, Gerard E.  
;; APPLICANT: HILMAN, Jennifer L.  
;; APPLICANT: YU, Jimmy Y.  
;; APPLICANT: TUASON, Olivia  
;; APPLICANT: YAP, Pierre E.  
;; APPLICANT: AMSHEY, Stefan R.  
;; APPLICANT: DAUGHERTY, Sean C.  
;; APPLICANT: DAM, Tam C.  
;; APPLICANT: LITV, Tommy F.  
;; APPLICANT: NGUYEN, Duy-Viet An  
;; APPLICANT: KLEEFELD, Yael  
;; APPLICANT: GERSTIN JR., Edward H.  
;; APPLICANT: PERALTA, Careyna H.  
;; APPLICANT: DAVID, Marie H.  
;; APPLICANT: LEWIS, Samantha A.  
;; APPLICANT: CHEN, Alice J.

```
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1232 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09921
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 1146
; SOFTWARE: PERL Program
; SEQ ID NO 616
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:001923.1.orf3a:2001MAR30
PCT-US02-09921-616
```

```
Query Match          0.6%; Score 7; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 530 LPDSVVK 536
|||||
Db 29 LPDSVVK 35
```

```
RESULT 14
US-09-620-393B-6470
; Sequence 6470, Application US/09620393B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6470
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..122
; OTHER INFORMATION: Xaa is any amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..122
; OTHER INFORMATION: Ceres Seq. ID 1392769
US-09-620-393B-6470
```

```
Query Match          0.6%; Score 7; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1080 LGVTSIK 1086
|||||
Db 32 LGVTSIK 38
```

```
RESULT 15
```

```
US-10-106-698-6272
; Sequence 6272, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6272
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6272
```

```
Query Match          0.6%; Score 7; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 860 LLISHQR 866
|||||
Db 116 LLISHQR 122
```

```
RESULT 16
US-10-106-698-7726
; Sequence 7726, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7726
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7726
```

Query Match 0.6%; Score 7; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 597 SLPVDDL 603  
Db 70 SLPVDDL 76

RESULT 17

PCT-US02-07826-282  
; Sequence 282, Application PC/TUS0207826  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer  
; FILE REFERENCE: MRI-030PC  
; CURRENT APPLICATION NUMBER: PCT/US02/07826  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 282  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-07826-282

Query Match 0.6%; Score 7; DB 1; Length 176;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 QIDANWN 128  
Db 93 QIDANWN 99

RESULT 18

US-10-097-340-282  
; Sequence 282, Application US/10097340  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNAVAPU  
; APPLICANT: Sebastian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISSEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. BAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumel ZHAO  
; APPLICANT: Karen GLATT

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer  
; FILE REFERENCE: MRI-030  
; CURRENT APPLICATION NUMBER: US/10/097,340  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 282  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-097-340-282

Query Match 0.6%; Score 7; DB 6; Length 176;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 QIDANWN 128  
Db 93 QIDANWN 99

RESULT 19

US-10-125-540-456  
; Sequence 456, Application US/10125540  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT214C1  
; CURRENT APPLICATION NUMBER: US/10/125,540  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 646  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 456  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (183)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-125-540-456

Query Match 0.6%; Score 7; DB 6; Length 197;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 LLPAGLS 54  
Db 174 LLPAGLS 180

RESULT 20

US-10-106-698-6320  
; Sequence 6320, Application US/10106698  
; GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
FILE REFERENCE: PA005P1  
CURRENT APPLICATION NUMBER: US/10/106,698  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: PCT/US00/26524  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/157,137  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: US 60/163,280  
PRIOR FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 8564  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 6320  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (178)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-6320

Query Match 0.6%; Score 7; DB 6; Length 206;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 QIDAMWN 128  
Db 119 QIDAMWN 125

RESULT 21  
PCT-US01-46651-2  
Sequence 2, Application PC/TUS0146651  
GENERAL INFORMATION:  
APPLICANT: Washington State University Research Foundation  
APPLICANT: Druka, Arnis  
APPLICANT: Von Weltstein, Dieter  
TITLE OF INVENTION: Plant Promoters, and Methods of Use  
FILE REFERENCE: WSUR18192  
CURRENT APPLICATION NUMBER: PCT/US01/46651  
CURRENT FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/247,161  
PRIOR FILING DATE: 2000-11-09  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 229  
TYPE: PRT  
ORGANISM: Hordeum Vulgare  
PCT-US01-46651-2

Query Match 0.6%; Score 7; DB 1; Length 229;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 851 SSSILL 857  
Db 4 SSSILL 10

RESULT 22  
US-09-540-209B-8108  
Sequence 8108, Application US/09540209B  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
FILE REFERENCE: 2709.1001-001  
CURRENT APPLICATION NUMBER: US/09/540,209B

CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 10444  
SEQ ID NO 8108  
LENGTH: 259  
TYPE: PRT  
ORGANISM: B.fragilis  
US-09-540-209B-8108

Query Match 0.6%; Score 7; DB 5; Length 259;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LPAGLSK 55  
Db 25 LPAGLSK 31

RESULT 23  
US-10-138-632-2  
Sequence 2, Application US/10138632  
GENERAL INFORMATION:  
APPLICANT: Ozaki, Akio  
Mori, Hideo  
Shibasaki, Takeshi  
Ando, Katsuhiko  
Ochiai, Keiko  
Chiba, Shigeru  
Uosaki, Youichi

TITLE OF INVENTION: Process for Producing  
Cis-3-Hydroxy-L-Proline

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS  
STREET: 1300 NORTH SEVENTEENTH STREET  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22209

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release: #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,632  
FILING DATE: 06-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/455,406  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/708,856  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/301,654  
FILING DATE: 07-SEP-1994  
APPLICATION NUMBER: 08/474,135  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Terry, David T.  
REGISTRATION NUMBER: 20178  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-312-6600  
TELEFAX: 703-312-6666  
TELEX: 248545

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Streptomyces sp.  
STRAIN: TH1

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-138-632-2

Query Match 0.6%; Score 7; DB 6; Length 290;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 VLEDSPL 174  
|||||  
DB 126 VLEDSPL 132

RESULT 24  
US-10-115-123-233  
Sequence 233, Application US/10115123

GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P2029G30APID2  
CURRENT APPLICATION NUMBER: US/10/115,123  
PRIOR FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: PCT/US99/13418  
PRIOR FILING DATE: 1999-06-15  
PRIOR APPLICATION NUMBER: 60/089,507  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,508  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,509  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,510  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/090,112  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090,113  
PRIOR FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 233  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (134)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-115-123-233

Query Match 0.6%; Score 7; DB 6; Length 293;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NTSNSNG 62  
|||||  
DB 182 NTSNSNG 188

RESULT 25  
US-10-115-123-331

Sequence 331, Application US/10115123  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P2029G30APID2  
CURRENT APPLICATION NUMBER: US/10/115,123  
PRIOR FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: PCT/US99/13418  
PRIOR FILING DATE: 1999-06-15  
PRIOR APPLICATION NUMBER: 60/089,507  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,508  
PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,509  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,510  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/090,112  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090,113  
PRIOR FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 331  
LENGTH: 307  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (148)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-115-123-331

Query Match 0.6%; Score 7; DB 6; Length 307;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 NTSNSNG 62  
|||||  
DB 196 NTSNSNG 202

RESULT 26  
US-10-125-540-294

Sequence 294, Application US/10125540  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PTZ14C1  
CURRENT APPLICATION NUMBER: US/10/125,540  
PRIOR FILING DATE: 2002-04-19  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 646  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 294  
LENGTH: 358  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-125-540-294

Query Match 0.6%; Score 7; DB 6; Length 358;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54  
|||||  
DB 174 LLPAGLS 180

RESULT 27  
US-09-994-404-225

Sequence 225, Application US/09994404  
GENERAL INFORMATION:  
APPLICANT: ESSER, KLAUS M.  
APPLICANT: CHAN, JOHN Y.  
APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN  
APPLICANT: DELVECCHIO, ALFRED MICHAEL  
APPLICANT: DILLON, SUSAN B.  
APPLICANT: LEARY, JEFFREY JOSEPH  
APPLICANT: SUTTON, DAVID  
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES  
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2  
FILE REFERENCE: P50583  
CURRENT APPLICATION NUMBER: US/09/994,404



```
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-225
```

```
Query Match          0.6%; Score 7; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 855 LLLGTL 861
    |||||
DB 222 LLLGTL 228
```

```
RESULT 28
US-09-994-404-28
; Sequence 28, Application US/09994404
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: CHAN, JOHN Y.
; APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN
; APPLICANT: DELVECCHIO, ALFRED MICHAEL
; APPLICANT: DILLON, SUSAN B.
; APPLICANT: LEARY, JEFFREY JOSEPH
; APPLICANT: SUTTON, DAVID
; TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
; FILE REFERENCE: P50583
; CURRENT APPLICATION NUMBER: US/09/994,404
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-28
```

```
Query Match          0.6%; Score 7; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 855 LLLGTL 861
    |||||
DB 231 LLLGTL 237
```

```
RESULT 29
US-09-994-404-158
; Sequence 158, Application US/09994404
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: CHAN, JOHN Y.
; APPLICANT: DABROWSKI-AMARAL, CHRISTINE ELLEN
; APPLICANT: DELVECCHIO, ALFRED MICHAEL
```

```
; APPLICANT: DILLON, SUSAN B.
; APPLICANT: LEARY, JEFFREY JOSEPH
; APPLICANT: SUTTON, DAVID
; TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
; FILE REFERENCE: P50583
; CURRENT APPLICATION NUMBER: US/09/994,404
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/297,477
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/030,279
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/049,018
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 303
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-158
```

```
Query Match          0.6%; Score 7; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 855 LLLGTL 861
    |||||
DB 231 LLLGTL 237
```

```
RESULT 30
PCT-US02-09944-442
; Sequence 442, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFEO, ABEL
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHEY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN, JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
```

```
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 442
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:208190.2.orf1:2001MAR30
PCT-US02-09944-442
```

```
Query Match          0.6%; Score 7; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 861 LISHQM 867
      |||||
Db 345 LISHQM 351
```

```
RESULT 31
US-10-002-304-8
; Sequence 8, Application US/10002304
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-54 CON-S8
; CURRENT APPLICATION NUMBER: US/10/002,304
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-304-8
```

```
Query Match          0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 48 LLPAGLS 54
      |||||
Db 289 LLPAGLS 295
```

```
RESULT 32
US-10-002-050-8
; Sequence 8, Application US/10002050
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Polyp
; FILE REFERENCE: 15966-554 Cura-54 CON-S14
; CURRENT APPLICATION NUMBER: US/10/002,050
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
```

```
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-050-8
```

```
Query Match          0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 48 LLPAGLS 54
      |||||
Db 289 LLPAGLS 295
```

```
RESULT 33
US-10-003-152-8
; Sequence 8, Application US/10003152
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldog, Ferenc
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: Novel Amino Acid Sequences for Human Semaphorin-Like Polypepti
; FILE REFERENCE: 15966-554 Cura-54 CON-S12
; CURRENT APPLICATION NUMBER: US/10/003,152
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-152-8
```

```
Query Match          0.6%; Score 7; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 48 LLPAGLS 54
      |||||
Db 289 LLPAGLS 295
```

```
RESULT 34
US-10-115-123-158
; Sequence 158, Application US/10115123
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
```

PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,510  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/090,112  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090,113  
PRIOR FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 158  
LENGTH: 490  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (134)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (389)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-115-123-158

Query Match 0.6%; Score 7; DB 6; Length 490;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 NTSNSNG 62  
Db 182 NTSNSNG 188

RESULT 35  
US-10-115-123-332  
Sequence 332, Application US/10115123  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P2029G30APID2  
CURRENT APPLICATION NUMBER: US/10/115,123  
CURRENT FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: PCT/US99/13418  
PRIOR FILING DATE: 1999-06-15  
PRIOR APPLICATION NUMBER: 60/089,507  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,508  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,509  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089,510  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/090,112  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090,113  
PRIOR FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 332  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (148)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (403)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-115-123-332

Query Match 0.6%; Score 7; DB 6; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 NTSNSNG 62  
Db 196 NTSNSNG 202

RESULT 36  
US-09-573-655B-1433  
Sequence 1433, Application US/09573655B  
GENERAL INFORMATION:  
APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid  
FILE REFERENCE: 2750-0876P  
CURRENT APPLICATION NUMBER: US/09/573,655B  
CURRENT FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 3281  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1433  
LENGTH: 578  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-573-655B-1433

Query Match 0.6%; Score 7; DB 5; Length 578;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CADNIEG 108  
Db 71 CADNIEG 77

RESULT 37  
US-09-540-209B-10008  
Sequence 10008, Application US/09540209B  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES  
FILE REFERENCE: 2709.1001-001  
CURRENT APPLICATION NUMBER: US/09/540,209B  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 10444  
SEQ ID NO 10008  
LENGTH: 642  
TYPE: PRT  
ORGANISM: B. fragilis  
US-09-540-209B-10008

Query Match 0.6%; Score 7; DB 5; Length 642;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 LGTLIS 863  
Db 138 LGTLIS 144

RESULT 38  
PCT-US02-01339-2  
Sequence 2, Application PC/TUS0201339  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.  
APPLICANT: LEE, Ernestine A.  
APPLICANT: WALIA, Narinder K.  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: TANG, Y. Tom  
APPLICANT: YUE, Henry

APPLICANT: THANGAVELU, Kavitha  
APPLICANT: XU, Yuning  
APPLICANT: ARVIZU, Chandra  
APPLICANT: WARREN, Bridget A.  
APPLICANT: YAO, Monique G.  
APPLICANT: AU-YOUNG, Janice  
APPLICANT: HAFALIA, April J.A.  
APPLICANT: ELLIOTT, Vicki S.  
APPLICANT: KALLICK, Deborah A.  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: RICHARDSON, Thomas W.  
APPLICANT: KHAN, Farrah A.  
APPLICANT: LU, Yan  
APPLICANT: SWARNAKAR, Anita  
APPLICANT: RAMKUMAR, Jayalaxmi  
APPLICANT: NGUYEN, Daniel B.  
APPLICANT: GRAUL, Richard  
APPLICANT: LU, Dzung Aina M.  
TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS  
FILE REFERENCE: PI-0346 PCT  
CURRENT APPLICATION NUMBER: PCT/US02/01339  
PRIOR APPLICATION NUMBER: 60/262,838; 60/265,927; 60/271,196; 60/274,549; 60/334,179  
PRIOR FILING DATE: 2001-01-19; 2001-02-02; 2001-02-23; 2001-03-09; 2001-11-28  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PERL Program  
SEQ ID NO 2  
LENGTH: 663  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: 2319430CD1  
PCT-US02-01339-2

Query Match 0.6%; Score 7; DB 1; Length 663;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 849 IISSTL 855  
|||||  
DB 413 IISSTL 419

RESULT 39  
US-10-002-304-6  
Sequence 6, Application US/10002304  
GENERAL INFORMATION:  
APPLICANT: Shinkets, Richard  
APPLICANT: Fernandes, Elma  
APPLICANT: Vernet, Corine  
APPLICANT: Yang, Meijia  
APPLICANT: Boldog, Ferenc  
APPLICANT: Herrmann, John  
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby  
FILE REFERENCE: 15966-554 Cura-54 CON-S8  
CURRENT APPLICATION NUMBER: US/10/002,304  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/604,286  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/140,584  
PRIOR FILING DATE: 1999-06-23  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 788  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-304-6

Query Match 0.6%; Score 7; DB 6; Length 788;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 48 LLPAGLS 54  
|||||  
DB 604 LLPAGLS 610

RESULT 40  
US-10-002-050-6  
Sequence 6, Application US/10002050  
GENERAL INFORMATION:  
APPLICANT: Shinkets, Richard  
APPLICANT: Fernandes, Elma  
APPLICANT: Vernet, Corine  
APPLICANT: Yang, Meijia  
APPLICANT: Boldog, Ferenc  
APPLICANT: Herrmann, John  
TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Po  
FILE REFERENCE: 15966-554 Cura-54 CON-S14  
CURRENT APPLICATION NUMBER: US/10/002,050  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/604,286  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/140,584  
PRIOR FILING DATE: 1999-06-23  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 788  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-002-050-6

Query Match 0.6%; Score 7; DB 6; Length 788;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 LLPAGLS 54  
|||||  
DB 604 LLPAGLS 610

RESULT 41  
US-10-003-152-6  
Sequence 6, Application US/10003152  
GENERAL INFORMATION:  
APPLICANT: Shinkets, Richard  
APPLICANT: Fernandes, Elma  
APPLICANT: Vernet, Corine  
APPLICANT: Yang, Meijia  
APPLICANT: Boldog, Ferenc  
APPLICANT: Herrmann, John  
TITLE OF INVENTION: Novel Amino Acid Sequences for Human Semaphorin-Like Polypepti  
FILE REFERENCE: 15966-554 Cura-54 CON-S12  
CURRENT APPLICATION NUMBER: US/10/003,152  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/604,286  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/140,584  
PRIOR FILING DATE: 1999-06-23  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 788  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-003-152-6

Query Match 0.6%; Score 7; DB 6; Length 788;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 LLPAGLS 54  
|||||||

Db 604 LLPAGLS 610

RESULT 42  
US-09-540-209B-5548  
; Sequence 5548, Application US/09540209B  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1001-001  
; CURRENT APPLICATION NUMBER: US/09/540,209B  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 10444  
; SEQ ID NO 5548  
; LENGTH: 885  
; TYPE: PRT  
; ORGANISM: B.fragilis  
US-09-540-209B-5548

Query Match 0.6%; Score 7; DB 5; Length 885;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1127 NINLGTS 1133  
|||||||

Db 205 NINLGTS 211

RESULT 43  
US-09-573-655B-2349  
; Sequence 2349, Application US/09573655B  
; GENERAL INFORMATION:  
; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Thereby  
; FILE REFERENCE: 2750-0876P  
; CURRENT APPLICATION NUMBER: US/09/573,655B  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 3281  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2349  
; LENGTH: 951  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-573-655B-2349

Query Match 0.6%; Score 7; DB 5; Length 951;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 529 VLPDSVV 535  
|||||||

Db 530 VLPDSVV 536

RESULT 44  
US-10-128-714-3585  
; Sequence 3585, Application US/10128714  
; GENERAL INFORMATION:  
; APPLICANT: JIANG, Bo  
; APPLICANT: HU, WENQI  
; APPLICANT: TISHKOFF, DANIEL  
; APPLICANT: ZAMUDIO, CARLOS  
; APPLICANT: EROSHKIN, ALEXEY M  
; APPLICANT: LEMIEUX, SEBASTIEN M  
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: 10182-018-999  
; CURRENT APPLICATION NUMBER: US/10/128,714  
; CURRENT FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: US 60/285,697  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: US 60/287,066  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/295,890  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/303,899  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 60/316,362  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8603  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3585  
; LENGTH: 1018  
; TYPE: PRT  
; ORGANISM: Aspergillus fumigatus  
US-10-128-714-3585

Query Match 0.6%; Score 7; DB 6; Length 1018;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VVSLST 945  
|||||||

Db 771 VVSLST 777

RESULT 45  
US-10-128-714-8585  
; Sequence 8585, Application US/10128714  
; GENERAL INFORMATION:  
; APPLICANT: JIANG, Bo  
; APPLICANT: HU, WENQI  
; APPLICANT: TISHKOFF, DANIEL  
; APPLICANT: ZAMUDIO, CARLOS  
; APPLICANT: EROSHKIN, ALEXEY M  
; APPLICANT: LEMIEUX, SEBASTIEN M  
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
; FILE REFERENCE: 10182-018-999  
; CURRENT APPLICATION NUMBER: US/10/128,714  
; CURRENT FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: US 60/285,697  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: US 60/287,066  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/295,890  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/303,899  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 60/316,362  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8603  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8585  
; LENGTH: 1018  
; TYPE: PRT  
; ORGANISM: Aspergillus fumigatus  
US-10-128-714-8585

Query Match 0.6%; Score 7; DB 6; Length 1018;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 VVSLST 945  
|||||||

Db 771 VVSLST 777



```
RESULT 46
US-09-895-913A-246
; Sequence 246, Application US/09895913A
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 1185
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-246

Query Match
Best Local Similarity 0.6%; Score 7; DB 5; Length 1185;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SATSLV 295
Db 775 SATSLV 781

RESULT 47
PCT-US02-09809-5
; Sequence 5, Application PC/TUS0209809
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LU, DYUNG AINA M.
; APPLICANT: ARVIZU, CHANDRA S.
; APPLICANT: GANDHI, AMEENA R.
; APPLICANT: HAFALIA, APRIL J.A.
; APPLICANT: DING, LI
; APPLICANT: LU, YAN
; APPLICANT: RAMKUMAR, JAYALAXMI
; APPLICANT: SWARNAKER, ANITA
; APPLICANT: TANG, Y. TOM
; APPLICANT: YUE, HENRY
; APPLICANT: TRAN, BAO
; APPLICANT: LEE, SOO Y.
; APPLICANT: WARREN, BRIDGET A.
; APPLICANT: NGUYEN, DANNIEL B.
; APPLICANT: THANGAVELU, KAVITHA
; APPLICANT: YAO, MONIQUE G.
; APPLICANT: ELLIOTT, VICKI S.
; APPLICANT: BAUGHN, MARIAH R.
; APPLICANT: EMERLING, BROOKE M.
; APPLICANT: LAL, PREETI
; APPLICANT: GIETZEN, KIMBERLY J.
; APPLICANT: BECHA, SHANYA D.
; APPLICANT: MARQUIS, JOSEPH P.
; APPLICANT: KABLE, AMY E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PF-0921 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09809
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,387; 60/282,335; 60/286,663; 60/285,484; 60/350,702;
; PRIOR FILING DATE: 2001-03-30; 2001-04-05; 2001-04-13; 2001-04-19; 2002-01-18; 2002-0
; NUMBER OF SEQ ID NOS: 46
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; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 1510943CD1
PCT-US02-09809-5

Query Match
Best Local Similarity 0.6%; Score 7; DB 1; Length 1523;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 965 SEAGTE 971
Db 714 SEAGTE 720

RESULT 48
US-09-423-037A-17
; Sequence 17, Application US/09423037A
; GENERAL INFORMATION:
; APPLICANT: HEERY, DAVID MICHAEL
; APPLICANT: PARKER, MALCOLM GEORGE
; TITLE OF INVENTION: INHIBITORS OF NUCLEAR PROTEIN/NUCLEAR RECEPTOR
; FILE REFERENCE: 009901/0264015
; CURRENT APPLICATION NUMBER: US/09/423,037A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/GB98/01238
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: GB 9708676.3
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: DNA binding domain
US-09-423-037A-17

Query Match
Best Local Similarity 0.5%; Score 6; DB 5; Length 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 GPLLLE 914
Db 3 GPLLLE 8

RESULT 49
US-10-106-698-7746
; Sequence 7746, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 7746
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7746
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Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 712 VTVLAI 717
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Db 4 VTVLAI 9
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RESULT 50
US-09-623-791A-134
; Sequence 134, Application US/09623791A
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TUMOR TISSUE
; FILE REFERENCE: ALBRE 11
; CURRENT APPLICATION NUMBER: US/09/623,791A
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/DE99/00721
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-791A-134
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Query Match          0.5%; Score 6; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 576 LSGREY 581
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Db 23 LSGREY 28
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Search completed: May 18, 2002, 07:07:09  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 18, 2002, 06:59:21 ; Search time 18.41 Seconds  
(without alignments)  
1545.672 Million cell updates/sec

Title: US-08-779-457-2  
Perfect score: 1165  
Sequence: 1 MICQKFCVVLHMEFIYIT.....QTCSTQTHKIMENKMDLTV 1165

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1165	100.0	1165 2 US-08-599-455B-4	Sequence 4, Appli
2	1165	100.0	1165 4 US-09-069-781B-4	Sequence 4, Appli
3	1064	91.3	1165 4 US-09-093-814-1	Sequence 1, Appli
4	1064	91.3	1165 4 US-08-618-957A-11	Sequence 11, Appli
5	681	58.5	896 4 US-08-618-957A-10	Sequence 10, Appli
6	681	58.5	898 2 US-08-618-957A-9	Sequence 36, Appli
7	681	58.5	906 4 US-08-618-957A-9	Sequence 9, Appli
8	681	58.5	908 2 US-08-693-697-33	Sequence 33, Appli
9	681	58.5	958 4 US-08-618-957A-8	Sequence 8, Appli
10	681	58.5	960 1 US-08-355-888A-8	Sequence 8, Appli
11	681	58.5	960 2 US-08-693-697-8	Sequence 8, Appli
12	681	58.5	960 2 US-08-640-389A-3	Sequence 3, Appli
13	681	58.5	960 3 US-08-693-696-8	Sequence 8, Appli
14	580	49.8	960 2 US-08-588-190-3	Sequence 3, Appli
15	580	49.8	960 4 US-08-618-957A-3	Sequence 3, Appli
16	474	40.7	908 2 US-08-588-526-3	Sequence 3, Appli
17	470	40.3	1165 2 US-08-640-389A-11	Sequence 11, Appli
18	459	39.4	569 1 US-08-306-231-3	Sequence 3, Appli
19	307	26.4	896 2 US-08-640-389A-10	Sequence 10, Appli
20	307	26.4	906 2 US-08-640-389A-9	Sequence 9, Appli
21	307	26.4	958 2 US-08-640-389A-8	Sequence 8, Appli
22	77	6.6	77 4 US-08-803-346-64	Sequence 64, Appli
23	76	6.5	76 4 US-08-803-346-61	Sequence 61, Appli
24	42	3.6	894 2 US-08-599-455B-2	Sequence 2, Appli
25	42	3.6	894 4 US-09-069-781B-2	Sequence 2, Appli
26	42	3.6	894 4 US-08-618-957A-12	Sequence 12, Appli
27	42	3.6	895 4 US-08-827-962-19	Sequence 19, Appli

28	42	3.6	895 4 US-08-827-962-21	Sequence 21, Appli
29	42	3.6	896 2 US-08-640-389A-12	Sequence 12, Appli
30	42	3.6	1162 2 US-08-599-455B-43	Sequence 43, Appli
31	42	3.6	1162 4 US-08-827-962-15	Sequence 15, Appli
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33	42	3.6	1162 4 US-08-803-346-1	Sequence 1, Appli
34	42	3.6	1162 4 US-09-069-781B-43	Sequence 43, Appli
35	24	2.1	77 4 US-08-803-346-63	Sequence 63, Appli
36	23	2.0	23 3 US-08-701-382-6	Sequence 6, Appli
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57	10	0.9	13 2 US-08-693-696-24	Sequence 24, Appli
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61	9	0.8	9 4 US-09-069-781B-31	Sequence 31, Appli
62	8	0.7	8 2 US-08-599-455B-29	Sequence 29, Appli
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69	7	0.6	15 1 US-08-355-888A-26	Sequence 26, Appli
70	7	0.6	15 2 US-08-693-697-26	Sequence 26, Appli
71	7	0.6	15 3 US-08-693-696-26	Sequence 26, Appli
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73	7	0.6	101 4 US-09-199-637A-289	Sequence 289, Appli
74	7	0.6	224 1 US-08-707-793A-6	Sequence 6, Appli
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## ALIGNMENTS

RESULT 1  
US-08-599-455B-4  
Sequence 4, Application US/08599455B  
Patent No. 5972621  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT  
MODULATE BODY WEIGHT USING THE OB RECEPTOR  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,455B  
FILING DATE: 22-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-599-455B-4

Query Match 100.0%; Score 1165; DB 2; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MICQKFCVLLHMEFIYITAFNLSYPTIPWRFKLSGMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFSVNSLVE 120  
DB 61 NGHYETAVERPKFNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFSVNSLVE 120  
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DB 121 QOIDANWNIQCWLKGLKFLICYVESLFFKNLFRNYKVHLLYVLPEVLDESLVPQKGS 180  
QY 181 FQWVHCNCSVHECEGLVPVPTAKLNDTLMLCLKITSQVIFQSPIMSVQPIINWVKPDP 240  
DB 181 FQWVHCNCSVHECEGLVPVPTAKLNDTLMLCLKITSQVIFQSPIMSVQPIINWVKPDP 240  
QY 241 LGLHMEITDDGNLKISMSPPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKISMSPPPLVPPLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
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DB 301 GSSYEYQVRGKRLDGPGLWSDWSTPRVFTTQDYITFPKILTSVGSNVSFHCILYKKNKI 360  
QY 361 VPSKEIWMWNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIWMWNLAEKIPQSQYDVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECH 420  
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DB 421 RYAEIYVIDVNIINISCEITDGYLTMTKCRWSTSTIOSLAESTLQLRHYRSSLGSDIPS 480  
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DB 481 PISEPKDCYLOSDFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCYLPDSVVKPLPP 540  
QY 541 SSVKAEITINIGLKLISWEKPVPENNLOFOIRYGLSGKEVQNMKYVYDAKSVSPLV 600  
DB 541 SSVKAEITINIGLKLISWEKPVPENNLOFOIRYGLSGKEVQNMKYVYDAKSVSPLV 600  
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DB 661 TLLMKPLMKNDSLCSQVRVYINHTSCNGTWSDEYGNHTKFTFLMTFOAHTVTLAINSI 720  
QY 721 GASVANFNLTFSPMSKYNIVQSLAYSAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
DB 721 GASVANFNLTFSPMSKYNIVQSLAYSAYPLNSSCVIWSILSPSDYKLMYFIEMKNLNE 780  
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DB 781 GEIKWLRISSSVKRYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840  
QY 841 GLYIVPVITISSILGLTLLISHQRMKLFMEDVYVNPKNCSWAQGLNFOKPETFEHLFI 900  
DB 841 GLYIVPVITISSILGLTLLISHQRMKLFMEDVYVNPKNCSWAQGLNFOKPETFEHLFI 900  
QY 901 KHTASVTCGPLLPEITISEDISVDTSWKNKDEMPFTVVSLLSTTDLKGSVCISDQFN 960  
DB 901 KHTASVTCGPLLPEITISEDISVDTSWKNKDEMPFTVVSLLSTTDLKGSVCISDQFN 960  
QY 961 SVNFESEAGTEVTEYEDESQROPEVKYATLISNKRSETGEEGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFESEAGTEVTEYEDESQROPEVKYATLISNKRSETGEEGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNFPEENDKKSIIYL 1080  
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNIISPHLTFSEGLDELKLEGNFPEENDKKSIIYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPAPCLFTDIRVLODSCSHFVENNINIGTSSKKTFFAS 1140  
DB 1141 GVTSIKKRESGVLLTDKSRVSCPAPCLFTDIRVLODSCSHFVENNINIGTSSKKTFFAS 1140  
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165  
RESULT 2  
US-09-069-781B-4  
Sequence 4, Application US/09069781B  
Patent No. 6287782  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/09/069,781B  
FILING DATE: 29-APRIL-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: US 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: US 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: US 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: US 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: US 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: US 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: US 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: US 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-069-781B-4

Query Match 100.0%; Score 1165; DB 4; Length 1165;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MICOKFCVLLHMEFIYVITAFNLSTYPTWRFKLSGMPNSTYDYFLPAGLSKNTS 60  
QY 61 NGHYETAVERPKNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSNLVE 120  
DB 61 NGHYETAVERPKNSGTHFSNLSKTFHCCFRSEODRNCSLCADNIEGKTFVSNLVE 120  
QY 121 QOIDANWNIQCWLKGDILFICYVESLEFKNLFRNRYKVVHLLVLPVLEDSPLVPQGS 180  
DB 121 QOIDANWNIQCWLKGDILFICYVESLEFKNLFRNRYKVVHLLVLPVLEDSPLVPQGS 180  
QY 181 FQMVHCNCSVHECCGLVFPVTAKLNDTLMLCLKITSGGVTFQSPIMSVQPTINMYKPD 240  
DB 181 FQMVHCNCSVHECCGLVFPVTAKLNDTLMLCLKITSGGVTFQSPIMSVQPTINMYKPD 240  
QY 241 LGLHMEITDDGNLKSISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
DB 241 LGLHMEITDDGNLKSISWSSPLVPFLQYQVKSSENSTVIREADKIVSATSLVDSILP 300  
QY 301 GSSYEYQVRGKRLDGPIMSDMSTPRVFTTQDVYIYFPFKILTSVGSNVSEHCYKKE 360  
DB 301 GSSYEYQVRGKRLDGPIMSDMSTPRVFTTQDVYIYFPFKILTSVGSNVSEHCYKKE 360  
QY 361 VPSKEIYVMMNLAEKIFQSOYDVVDVSKVYFFNLNETKPRGKFTYDAVYCCNEHECH 420  
DB 361 VPSKEIYVMMNLAEKIFQSOYDVVDVSKVYFFNLNETKPRGKFTYDAVYCCNEHECH 420  
QY 421 RYAEIYVIDVNIINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHYRSSLVCS 480  
DB 421 RYAEIYVIDVNIINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHYRSSLVCS 480

DB 421 RYAEIYVIDVNIINISCEITDGYLTMTCRWSTSTIQSLAESTLQLRHYRSSLVCS 480  
QY 481 PISEPKDCYLOSDFYECIFQPIELLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLP 540  
DB 481 PISEPKDCYLOSDFYECIFQPIELLSGYTMWIRINHSLGSLDSPPTCVLPDSVYKPLP 540  
QY 541 SSVKAEITINIGLKSWEKVPPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
DB 541 SSVKAEITINIGLKSWEKVPPENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDMKKEKNV 660  
DB 601 PDLCAVYAVQVRCKRLDGLGYWSNWSNPATYVMDIKVPMRGPEFWRIINGDMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVYLAINSI 720  
DB 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVYLAINSI 720  
QY 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNSSCVIYSWILSPSDYKIMYFIEMKNLNE 780  
DB 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNSSCVIYSWILSPSDYKIMYFIEMKNLNE 780  
QY 781 GEIKWLRISSVKKYITHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSVKKYITHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPKNCWSAOGNLNOKPETFEHLFI 900  
DB 841 GLYVIVPVISSSILLGLTLLISHORMKLLFWEDEVNPKNCWSAOGNLNOKPETFEHLFI 900  
QY 901 KHTASVTCGPLLEPFIISEDIVDTSWKNKDEMPITVVSLLSTDLKESVYCISDOFN 960  
DB 901 KHTASVTCGPLLEPFIISEDIVDTSWKNKDEMPITVVSLLSTDLKESVYCISDOFN 960  
QY 961 SVNSEAEGTEVYTEDSQRPVKKYATLISNSKPSGTGEEGLINSVTKCFSSKNSPL 1020  
DB 961 SVNSEAEGTEVYTEDSQRPVKKYATLISNSKPSGTGEEGLINSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSSSWEIEAOFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNCKSIYYL 1080  
DB 1021 KDSFNSSSWEIEAOFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNCKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLDQSCSHVENNINLGTSKTFAS 1140  
DB 1141 YMPQFQTCSTQTHKIMENKCDLTV 1165

RESULT 3  
US-09-093-814-1  
; Sequence 1, Application US/09093814  
; Patent No. 6270981  
; GENERAL INFORMATION:  
; APPLICANT: Carpenter et al.  
; TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS  
; FILE REFERENCE: REG 580-A  
; CURRENT APPLICATION NUMBER: US/09/093,814  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: 60/049,108  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1165  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-093-814-1  
Query Match 91.3%; Score 1064; DB 4; Length 1165;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSTPTPRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
QY 121 QOIDANMNIOQWLKGDCLKFICYVESLEFKNLFRNYKVHLLYLPLEVLEDSPLVPQKS 180  
DB 121 QOIDANMNIOQWLKGDCLKFICYVESLEFKNLFRNYKVHLLYLPLEVLEDSPLVPQKS 180  
QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPIMSVQPINMVKPDP 240  
DB 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPIMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTTVIREADKIVSATSLLVDSILP 300  
DB 241 LGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTTVIREADKIVSATSLLVDSILP 300  
QY 301 GSSYEVOVRGKRLDGPVIMSDWSTPRVFTQDVITYEPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVOVRGKRLDGPVIMSDWSTPRVFTQDVITYEPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYMMNLAEKIPQSOYDVSDHVSKEYFENLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYMMNLAEKIPQSOYDVSDHVSKEYFENLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVNNINISCEITDGYLTMTKCRNSTIQLSLAESTLQLRHSSLYCSDIPSIH 480  
DB 421 RYAEIYVIDVNNINISCEITDGYLTMTKCRNSTIQLSLAESTLQLRHSSLYCSDIPSIH 480  
QY 481 PISEPKDCYLOSDFYECIFQPIFLSGITMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540  
DB 481 PISEPKDCYLOSDFYECIFQPIFLSGITMIRINHSLSGLSDSPPTCVLPDSVVKPLP 540  
QY 541 SSVKAETITINIGLLKISWEKVPFENNLOFQIRYGLSGEVOWKMEYVDAKSKSVSLPV 600  
DB 541 SSVKAETITINIGLLKISWEKVPFENNLOFQIRYGLSGEVOWKMEYVDAKSKSVSLPV 600  
QY 601 PDLCAVYAVOYRCKRLDGLGWSNWSNPATVVMIDIKVPMRGPEFWRLNGDTMKKENV 660  
DB 601 PDLCAVYAVOYRCKRLDGLGWSNWSNPATVVMIDIKVPMRGPEFWRLNGDTMKKENV 660  
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTLAINSI 720  
DB 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTFLMTEQAHTVTLAINSI 720  
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMFTIEWKNLNE 780  
DB 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMFTIEWKNLNE 780  
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQESLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFELFI 900  
DB 841 GLYVIVPVIISSSILLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFQKPEFELFI 900  
QY 901 KHTASVTCGPLLEPETISEDIVDSMKNKDEMPPTVVSLSLTDLEKGSVCISDQFN 960  
DB 901 KHTASVTCGPLLEPETISEDIVDSMKNKDEMPPTVVSLSLTDLEKGSVCISDQFN 960  
QY 961 SVNFSEAEGETVTEDESQROPFVKYATLLISNKPSETGEQGLINSSVTKCFSSKNSPL 1020  
DB 961 SVNFSEAEGETVTEDESQROPFVKYATLLISNKPSETGEQGLINSSVTKCFSSKNSPL 1020  
QY 1021 KDSFNSNSWEIEAQAFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDDKSIYYL 1080  
DB 1021 KDSFNSNSWEIEAQAFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDDKSIYYL 1080

DB 1021 KDSFNSNSWEIEAQAFILSDQHPNITISPHLTFSEGLDELKLEGNFPEENNDDKSIYYL 1080  
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
DB 1081 GVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKTFAS 1140  
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165  
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 4

US-08-618-957A-11  
; Sequence 11, Application US/08618957A  
; Patent No. 6355237  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. Ralph  
; APPLICANT: Clotf, Joseph  
; APPLICANT: Zupancic, Thomas Joel  
; APPLICANT: Shafer, Alan Wayne  
; TITLE OF INVENTION: METHODS FOR USING THE OBSE  
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
; TITLE OF INVENTION: DEVELOPMENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penline & Edmonds LLP  
; STREET: 1155 Avenue of The Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/618,957A  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 008907-0033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-618-957A-11

Query Match 91.3%; Score 1064; DB 4; Length 1165;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHMEFIYVITAFNLSTPTPRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
DB 1 MICQKFCVLLHMEFIYVITAFNLSTPTPRFKLSCMPNSTYDYFLLPAGLSKNTS 60  
QY 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120  
DB 61 NGHYETAVERKFNSSGTHFSNLSTKTFHCCEFRSEQDRNCSLCADNIEGKTFVSTVNSLVE 120

QY	121	QOIDANMNIOCWLGDKLFI	CVESL	FKNLFRN	NYKVHLLYL	PEVL	EDSP	LV	PQKS	180
Db	121	QOIDANMNIOCWLGDKLFI	CVESL	FKNLFRN	NYKVHLLYL	PEVL	EDSP	LV	PQKS	180
QY	181	FQMVHNC	SVHECC	ELVP	PVPTAK	NDTL	MLCK	IT	SGVIF	QSP
Db	181	FQMVHNC	SVHECC	ELVP	PVPTAK	NDTL	MLCK	IT	SGVIF	QSP
QY	241	LGLHMEIT	DDGN	LKIS	WSSP	PLVP	PLP	LO	YQV	K
Db	241	LGLHMEIT	DDGN	LKIS	WSSP	PLVP	PLP	LO	YQV	K
QY	301	GSSYEV	QVRG	KRLD	PGI	WSD	WST	PR	FT	Q
Db	301	GSSYEV	QVRG	KRLD	PGI	WSD	WST	PR	FT	Q
QY	361	VPSKEI	WMMNL	AEKIP	QSO	YDV	SD	HV	SKV	T
Db	361	VPSKEI	WMMNL	AEKIP	QSO	YDV	SD	HV	SKV	T
QY	421	RYAEL	YIDV	NINIS	CE	TD	GY	LT	K	M
Db	421	RYAEL	YIDV	NINIS	CE	TD	GY	LT	K	M
QY	481	PISEPK	DCYL	QSDG	FYE	CI	FQ	P	I	F
Db	481	PISEPK	DCYL	QSDG	FYE	CI	FQ	P	I	F
QY	541	SSVKA	EIT	IN	IG	LK	IS	WE	K	P
Db	541	SSVKA	EIT	IN	IG	LK	IS	WE	K	P
QY	601	PDLCA	VYAV	QVR	CK	R	L	D	G	I
Db	601	PDLCA	VYAV	QVR	CK	R	L	D	G	I
QY	661	TLLMK	PLM	K	N	D	S	L	C	S
Db	661	TLLMK	PLM	K	N	D	S	L	C	S
QY	721	GASV	AN	FN	L	T	F	S	W	P
Db	721	GASV	AN	FN	L	T	F	S	W	P
QY	781	GEIK	W	L	R	I	S	S	V	K
Db	781	GEIK	W	L	R	I	S	S	V	K
QY	841	GLYV	I	V	P	V	I	S	S	I
Db	841	GLYV	I	V	P	V	I	S	S	I
QY	901	KHTA	S	V	T	C	G	P	L	L
Db	901	KHTA	S	V	T	C	G	P	L	L
QY	961	SVNF	SE	A	E	G	T	E	V	T
Db	961	SVNF	SE	A	E	G	T	E	V	T
QY	1021	KDSF	S	N	S	S	W	E	I	A
Db	1021	KDSF	S	N	S	S	W	E	I	A
QY	1081	GVTS	I	K	R	E	S	G	V	L
Db	1081	GVTS	I	K	R	E	S	G	V	L
QY	1141	YMPQ	F	O	T	C	S	T	O	T
Db	1141	YMPQ	F	O	T	C	S	T	O	T

RESULT 5  
US-08-618-957A-10  
; Sequence 10, Application US/08618957A  
; Patent No. 6355237  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. Ralph  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas Joel  
; APPLICANT: Shafer, Alan Wayne  
; TITLE OF INVENTION: METHODS FOR USING THE OBSE  
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
; NUMBER OF INVENTIONS: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 008907-0033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 896 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-618-957A-10

QY	110	TFVSTVNSLVE	QO	IDANMN	IOCW	LK	DKLFI	CVESL	FKNLFRN	NYKVHLLYL	PEVL	169
Db	110	TFVSTVNSLVE	QO	IDANMN	IOCW	LK	DKLFI	CVESL	FKNLFRN	NYKVHLLYL	PEVL	169
QY	170	EDSP	LV	PQKS	FQ	MVHNC	SVHECC	ELVP	PVPTAK	NDTL	MLCK	IT
Db	170	EDSP	LV	PQKS	FQ	MVHNC	SVHECC	ELVP	PVPTAK	NDTL	MLCK	IT
QY	230	QPIN	NV	KP	DP	PL	GLHMEIT	DDGN	LKIS	WSSP	PLVP	PLP
Db	230	QPIN	NV	KP	DP	PL	GLHMEIT	DDGN	LKIS	WSSP	PLVP	PLP
QY	290	ATSL	LV	DSIL	PGSS	YEV	QVRG	KRLD	PGI	WSD	WST	PR
Db	290	ATSL	LV	DSIL	PGSS	YEV	QVRG	KRLD	PGI	WSD	WST	PR
QY	350	FHC	IYK	KEN	K	IV	P	SKEI	WMMNL	AEKIP	QSO	YDV
Db	350	FHC	IYK	KEN	K	IV	P	SKEI	WMMNL	AEKIP	QSO	YDV

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QY 410 VYCCNEHECHHRYAELVIDVININISCETDGYLTMTCRMSTSTIOSLAESTLQLRHRS 469
    |||
Db 410 VYCCNEHECHHRYAELVIDVININISCETDGYLTMTCRMSTSTIOSLAESTLQLRHRS 469
QY 470 SLYCS DIPSIHPIS EPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCV 529
    |||
Db 470 SLYCS DIPSIHPIS EPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCV 529
QY 530 LPDSVVKPLPPSSVKA EITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYV 589
    |||
Db 530 LPDSVVKPLPPSSVKA EITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYV 589
QY 590 DAKSKSVSLPVPDLCAYVAVOVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 649
    |||
Db 590 DAKSKSVSLPVPDLCAYVAVOVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 649
QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWEDEVGNHTKFTFLWTEOA 709
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Db 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWEDEVGNHTKFTFLWTEOA 709
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIQSLASAYPLNSSCVIWSWILSPSDYKLMY 769
    |||
Db 710 HTVTVLAINSIGASVANENLTFSPMSKVNIQSLASAYPLNSSCVIWSWILSPSDYKLMY 769
QY 770 FIIEWKNLNEDEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
    |||
Db 770 FIIEWKNLNEDEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
QY 830 ODDIEKHQSDAGLYIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCMAOGLNF 889
    |||
Db 830 ODDIEKHQSDAGLYIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCMAOGLNF 889
QY 890 QK 891
    ||
Db 890 QK 891

RESULT 6
US-08-693-697-36
; Sequence 36, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556

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; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-36

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Query Match          58.5%; Score 681; DB 2; Length 898;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFSVNSLVFQOIDANWNIQCLKGLDKLFICYVESLFLKRLFRIYNYKHLVLP EVL 169
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Db 112 TFSVNSLVFQOIDANWNIQCLKGLDKLFICYVESLFLKRLFRIYNYKHLVLP EVL 171
QY 170 EDSPLVPQKGFQWVHNCNSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFQSP LMSV 229
    |||
Db 172 EDSPLVPQKGFQWVHNCNSVHECCCECLVPVPTAKLNDTLLMCLKITSGVIFRSP LMSV 231
QY 230 QPIMVKKPDPPLGLHMEITDDGNLKLISWSSPPLVPFPLOQVKYSENSTTVI READKIVS 289
    |||
Db 232 QPIMVKKPDPPLGLHMEITDDGNLKLISWSSPPLVPFPLOQVKYSENSTTVI READKIVS 291
QY 290 ATSLVDSILPGSSYEVOVRGKRRLDGPGLSDWSTPRVFTTQDVYIYEPKILTSVGS NVS 349
    |||
Db 292 ATSLVDSILPGSSYEVOVRGKRRLDGPGLSDWSTPRVFTTQDVYIYEPKILTSVGS NVS 351
QY 350 FHCYKKKENKIYPSKEIYVMMNLAEKIPQSOYDVVSDHVSKVTFNLTNETKPRGKFTYDA 409
    |||
Db 352 FHCYKKKENKIYPSKEIYVMMNLAEKIPQSOYDVVSDHVSKVTFNLTNETKPRGKFTYDA 411
QY 410 VYCCNEHECHHRYAELVIDVININISCETDGYLTMTCRMSTSTIOSLAESTLQLRHRS 469
    |||
Db 412 VYCCNEHECHHRYAELVIDVININISCETDGYLTMTCRMSTSTIOSLAESTLQLRHRS 471
QY 470 SLYCS DIPSIHPIS EPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCV 529
    |||
Db 472 SLYCS DIPSIHPIS EPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSPPTCV 531
QY 530 LPDSVVKPLPPSSVKA EITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYV 589
    |||
Db 532 LPDSVVKPLPPSSVKA EITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVQWKMEYV 591
QY 590 DAKSKSVSLPVPDLCAYVAVOVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 649
    |||
Db 592 DAKSKSVSLPVPDLCAYVAVOVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 651
QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWEDEVGNHTKFTFLWTEOA 709
    |||
Db 652 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWEDEVGNHTKFTFLWTEOA 711
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIQSLASAYPLNSSCVIWSWILSPSDYKLMY 769
    |||
Db 712 HTVTVLAINSIGASVANENLTFSPMSKVNIQSLASAYPLNSSCVIWSWILSPSDYKLMY 771
QY 770 FIIEWKNLNEDEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
    |||
Db 772 FIIEWKNLNEDEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 831
QY 830 ODDIEKHQSDAGLYIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCMAOGLNF 889
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Db 832 ODDIEKHQSDAGLYIVPVISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCMAOGLNF 891
QY 890 QK 891
    ||
Db 892 QK 893

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RESULT 7  
US-08-618-957A-9  
; Sequence 9, Application US/08618957A  
; Patent No. 6355237  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. Ralph  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas Joel  
; APPLICANT: Shafer, Alan Wayne  
; TITLE OF INVENTION: METHODS FOR USING THE OBSE  
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
; TITLE OF INVENTION: DEVELOPMENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of The Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/618,957A  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 008907-0033-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 906 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-618-957A-9

Query Match 58.5%; Score 681; DB 4; Length 906;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFOQIDANMNIQCLKGLKLFICYVESLEFKNLERNYNYKVHLLVLPVYL 169  
DB 110 TFEVSTVNSLVFOQIDANMNIQCLKGLKLFICYVESLEFKNLERNYNYKVHLLVLPVYL 169  
QY 170 EDSPLVPQKGSFQWVHCNCSVHECCCECLVPVPTAKLNDPILLMCLKITSGVIFQSPMSV 229  
DB 170 EDSPLVPQKGSFQWVHCNCSVHECCCECLVPVPTAKLNDPILLMCLKITSGVIFQSPMSV 229  
QY 230 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPPLOVQVKYSENSTVIREADKIVS 289  
DB 230 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPPLOVQVKYSENSTVIREADKIVS 289  
QY 290 ATSLAVDSILPGSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVIFPPKILTSVGSNVS 349  
DB 290 ATSLAVDSILPGSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVIFPPKILTSVGSNVS 349  
QY 350 FHCITYKKENKIVPSKEIYWMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDA 409  
DB 350 FHCITYKKENKIVPSKEIYWMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDA 409

QY 410 VCCNEHECHHRYAELVYIDVININISCESTDGYLTKMTCRWSTSTIQSLAESTIQLRHRS 469  
DB 410 VCCNEHECHHRYAELVYIDVININISCESTDGYLTKMTCRWSTSTIQSLAESTIQLRHRS 469  
QY 470 SLVCSIDPSIHPISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSIGSLDSPPTCV 529  
DB 470 SLVCSIDPSIHPISEPKDCYLQSDGFYECIFQPIFLISGYTMWIRINHSIGSLDSPPTCV 529  
QY 530 LPDSVVKPLPPSSVKAETITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQMKMEYV 589  
DB 530 LPDSVVKPLPPSSVKAETITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQMKMEYV 589  
QY 590 DAKSKSVSLPVPDLCAYVAVOVRCKRLDGLGYWSNNSNPATVVMIDIKVPMRGPETWRII 649  
DB 590 DAKSKSVSLPVPDLCAYVAVOVRCKRLDGLGYWSNNSNPATVVMIDIKVPMRGPETWRII 649  
QY 650 NGDTMKKEKNVTLWKPLMKNDSLCSVQRYVINHHTSCNGTWEDEVGNHTKFTFLWTEQA 709  
DB 650 NGDTMKKEKNVTLWKPLMKNDSLCSVQRYVINHHTSCNGTWEDEVGNHTKFTFLWTEQA 709  
QY 710 HTVTVLAINSIGASVANFNLFSPMPSKVINVOQLSAYPLNSSCVIVSWILSPSDKIMY 769  
DB 710 HTVTVLAINSIGASVANFNLFSPMPSKVINVOQLSAYPLNSSCVIVSWILSPSDKIMY 769  
QY 770 FIEWKNLNEDGEIKWLRISSSVKYYITHDFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829  
DB 770 FIEWKNLNEDGEIKWLRISSSVKYYITHDFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829  
QY 830 QDDIEKHQSDAGLVIVPVITISSILLGLTLLISHQRMKLFWEDEVPNPKNCMAQGLNF 889  
DB 830 QDDIEKHQSDAGLVIVPVITISSILLGLTLLISHQRMKLFWEDEVPNPKNCMAQGLNF 889  
QY 890 QK 891  
DB 890 QK 891

RESULT 8  
US-08-693-697-33  
; Sequence 33, Application US/08693697  
; Patent No. 5869610  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/693,697  
; FILING DATE: 05-AUG-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0037-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556



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; ; TELEX: 66141 PENNIE
; ; INFORMATION FOR SEQ ID NO:
; ; SEQUENCE CHARACTERISTICS
; ; LENGTH: 908 amino acid
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; FRAGMENT TYPE: internal
US-08-693-697-33

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Query Match	58.5%	Score 681;	DB 2;	Length 908;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 781; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	110	TFVSTVNSLVFQOQIDANMNIOQCWLKGDGKLFICYVESLEFKNLEFRNRYNYKVHLLYLPEVL	169
Db	112	TFVSTVNSLVFQOQIDANMNIOQCWLKGDGKLFICYVESLEFKNLEFRNRYNYKVHLLYLPEVL	171
QY	170	EDSPLVPQKGSFQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPILMSV	229
Db	172	EDSPLVPQKGSFQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFRSPILMSV	231
QY	230	QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTTVIREADKTVS	289
Db	232	QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVXSENSTTVIREADKTVS	291
QY	290	ATSLLVDSILPBGSSYEVQVRGKRLDGPGIWSDMSTPRVFTQDVIYFPKILTSVGSNVS	349
Db	292	ATSLLVDSILPBGSSYEVQVRGKRLDGPGIWSDMSTPRVFTQDVIYFPKILTSVGSNVS	351
QY	350	FHCITYKKENKIVPSKEIVMMMNLAETIPQOQYDVVSDHVSKEYTFNLNETKPRGKFTYDA	409
Db	352	FHCITYKKENKIVPSKEIVMMMNLAETIPQOQYDVVSDHVSKEYTFNLNETKPRGKFTYDA	411
QY	410	VYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLOLRHRS	469
Db	412	VYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIOSLAESTLOLRHRS	471
QY	470	SLYCSDDIPSIHPISEPKDCYLOSDGYECIFQPIFLLSGYMWIRINHSLSGLDSPPTCV	529
Db	472	SLYCSDDIPSIHPISEPKDCYLOSDGYECIFQPIFLLSGYMWIRINHSLSGLDSPPTCV	531
QY	530	LPDSVVKPLPBPSSVKAETINIGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKMYEY	589
Db	532	LPDSVVKPLPBPSSVKAETINIGLKLISWEKPVFPENNLOQIRYGLSGKEVQWKMYEY	591
QY	590	DAKSKSVSLVPDLCAYVAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEFWRII	649
Db	592	DAKSKSVSLVPDLCAYVAVQVRCKRLDGLGYWSNMSNPATVYMDIKVPMRGPEFWRII	651
QY	650	NGDTMKKEKNVTLLMKPLMKNDSLCSQORYVINHTSCNGTWSSEVDGNHTKFTFLWTEQA	709
Db	652	NGDTMKKEKNVTLLMKPLMKNDSLCSQORYVINHTSCNGTWSSEVDGNHTKFTFLWTEQA	711
QY	710	HTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMY	769
Db	712	HTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMY	771
QY	770	FIIEWKNLNEDEGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT	829
Db	772	FIIEWKNLNEDEGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT	831
QY	830	QDDIEKHOSDAGLYIVPVIISSSILLGLTLLISHQRMKLFMEDVVPNPKNCSMAQGLNF	889
Db	832	QDDIEKHOSDAGLYIVPVIISSSILLGLTLLISHQRMKLFMEDVVPNPKNCSMAQGLNF	891
QY	890	QK 891	
Db	892	QK 893	

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1      RESULT      9
2      US-08-618-957A-8
3      : Sequence 8, Application US/08618957A
4      : Patent No. 6355237
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Snodgrass, H. Ralph
9      :
10     : APPLICANT: Cioffi, Joseph
11     :
12     : APPLICANT: Zupancic, Thomas Joel
13     :
14     : APPLICANT: Shafer, Alan Wayne
15     :
16     : TITLE OF INVENTION: METHODS FOR USING THE OBES
17     :
18     : TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
19     :
20     : TITLE OF INVENTION: DEVELOPMENT
21     :
22     : NUMBER OF SEQUENCES: 28
23     :
24     : CORRESPONDENCE ADDRESS:
25     :
26     : ADDRESSEE: Pennie & Edmonds LLP
27     :
28     : STREET: 1155 Avenue of The Americas
29     :
30     : CITY: New York
31     :
32     : STATE: NY
33     :
34     : COUNTRY: USA
35     :
36     : ZIP: 10036-2811
37     :
38     : COMPUTER READABLE FORM:
39     :
40     : MEDIUM TYPE: Diskette
41     :
42     : COMPUTER: IBM Compatible
43     :
44     : OPERATING SYSTEM: DOS
45     :
46     : SOFTWARE: FastSeq Version 2.0
47     :
48     : CURRENT APPLICATION DATA:
49     :
50     : APPLICATION NUMBER: US/08/618,957A
51     :
52     : FILING DATE: 20-MAR-1996
53     :
54     : CLASSIFICATION: 435
55     :
56     : PRIOR APPLICATION DATA:
57     :
58     : APPLICATION NUMBER:
59     :
60     : FILING DATE:
61     :
62     : ATTORNEY/AGENT INFORMATION:
63     :
64     : NAME: Poissant, Brian M.
65     :
66     : REGISTRATION NUMBER: 28,462
67     :
68     : REFERENCE/DOCKET NUMBER: 008907-0033-999
69     :
70     : TELECOMMUNICATION INFORMATION:
71     :
72     : TELEPHONE: 650-493-4935
73     :
74     : TELEFAX: 650-493-5556
75     :
76     : TELEX: 66141 PENNIE
77     :
78     : INFORMATION FOR SEQ ID NO: 8:
79     :
80     : SEQUENCE CHARACTERISTICS:
81     :
82     : LENGTH: 958 amino acids
83     :
84     : TYPE: amino acid
85     :
86     : STRANDEDNESS: single
87     :
88     : TOPOLOGY: linear
89     :
90     : MOLECULE TYPE: protein
91     :
92     : US-08-618-957A-8

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Query Match	58.5%	Score 681;	DB 4;	Length 958;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 781; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

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QY 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHRS 469
      |||
Db 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHRS 469
QY 470 SLVCSDDPSIHPISEPKDCYLOSDFEYECIFQPIFLSGYTMTRINHSLSGLSDSPPTCV 529
      |||
Db 470 SLVCSDDPSIHPISEPKDCYLOSDFEYECIFQPIFLSGYTMTRINHSLSGLSDSPPTCV 529
QY 530 LPDSVVKPLPPSSVKAETITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589
      |||
Db 530 LPDSVVKPLPPSSVKAETITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589
QY 590 DAKSKSVSLPVPDLCAYAVQVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 649
      |||
Db 590 DAKSKSVSLPVPDLCAYAVQVRCRRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRII 649
QY 650 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQA 709
      |||
Db 650 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQA 709
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMY 769
      |||
Db 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMY 769
QY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFT 829
      |||
Db 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFT 829
QY 830 QDDIEKHQSDAGLYIVPVISSSILLGLTLLSHQRMKLFWEDEVNPNKNCSWAOGILNF 889
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Db 830 QDDIEKHQSDAGLYIVPVISSSILLGLTLLSHQRMKLFWEDEVNPNKNCSWAOGILNF 889
QY 890 OK 891
      ||
Db 890 OK 891

RESULT 10
US-08-355-888A-8
; Sequence 8, Application US/08355888A
; Patent No. 5763211
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
```

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      ; TELEX: 66141 PENNIE
      ; INFORMATION FOR SEQ ID NO: 8:
      ; SEQUENCE CHARACTERISTICS:
      ; LENGTH: 960 amino acids
      ; TYPE: amino acid
      ; TOPOLOGY: linear
      ; MOLECULE TYPE: protein
      ; US-08-355-888A-8

Query Match      58.5%; Score 681; DB 1; Length 960;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFQOIIDANWNIOGWLKGLKLFICYVESLEFKNLEFRNRYNKVHLLYLPEYL 169
      |||
Db 112 TFEVSTVNSLVFQOIIDANWNIOGWLKGLKLFICYVESLEFKNLEFRNRYNKVHLLYLPEYL 171
QY 170 EDSPLVPQKGSFQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPILMSV 229
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Db 172 EDSPLVPQKGSFQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFRSPILMSV 231
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      |||
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      |||
Db 652 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINNHTSCNGTWSDEVGNHTKFTFLWTEQA 711
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMY 769
      |||
Db 712 HTVTVLAINSIGASVANENLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSDYKLMY 771
QY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFT 829
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Db 772 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKKIINSFT 831
QY 830 QDDIEKHQSDAGLYIVPVISSSILLGLTLLSHQRMKLFWEDEVNPNKNCSWAOGILNF 889
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Db 832 QDDIEKHQSDAGLYIVPVISSSILLGLTLLSHQRMKLFWEDEVNPNKNCSWAOGILNF 891
QY 890 OK 891
      ||
Db 892 OK 893

RESULT 11
US-08-693-697-8
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; Sequence 8, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-697-8

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Query Match 58.5%; Score 681; DB 2; Length 960;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 110 TFEVSTVNSLVFOQIDANWNIQWLKGLKLFICVESLEFKNFRNYKYVLLVLEVL 169
DB 112 TFEVSTVNSLVFOQIDANWNIQWLKGLKLFICVESLEFKNFRNYKYVLLVLEVL 171
QY 170 EDSPLVPQKGSFQVWHNCNSVHECCCELVPPVPTAKLNDTLLMCLKITSQVIFQSPMSV 229
DB 172 EDSPLVPQKGSFQVWHNCNSVHECCCELVPPVPTAKLNDTLLMCLKITSQVIFQSPMSV 231
QY 230 QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTIVIREADKIYS 289
DB 232 QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFLQYQVKYSENSTIVIREADKIYS 291
QY 290 ATSLVDSILPGSSEYQVGRKRLDGPGLSDWSTPRVFTTQDVITYFPFKILTSVGSNVS 349
DB 292 ATSLVDSILPGSSEYQVGRKRLDGPGLSDWSTPRVFTTQDVITYFPFKILTSVGSNVS 351
QY 350 FHCYKKKENKIYPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFNLTNETKPRGFTYDA 409
DB 352 FHCYKKKENKIYPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFNLTNETKPRGFTYDA 411
QY 410 VYCCNEHECHHRYAEIYDVNININISCETDGLTKMTCRWSTSTIQSLAESTLQRLYHRS 469
DB 412 VYCCNEHECHHRYAEIYDVNININISCETDGLTKMTCRWSTSTIQSLAESTLQRLYHRS 471
QY 470 SLYCSDIPSIHPISPEPKDCYLQSDGFYEICIFQPIFLLSGYTWMIRINHSLSLSDSPPTCV 529

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DB 472 SLYCSDIPSIHPISPEPKDCYLQSDGFYEICIFQPIFLLSGYTWMIRINHSLSLSDSPPTCV 531
QY 530 LPDSVVKPLPPSSVKAETITINIGLKLISWEKVPYPPENNLQFOIRYGLSGKEVQWKMEYV 589
DB 532 LPDSVVKPLPPSSVKAETITINIGLKLISWEKVPYPPENNLQFOIRYGLSGKEVQWKMEYV 591
QY 590 DAKSKSVSLPVPDCAVYAVQVRCRRLDGLGYSMNSNPAYTVVMDLKVPMPGPEFWRII 649
DB 592 DAKSKSVSLPVPDCAVYAVQVRCRRLDGLGYSMNSNPAYTVVMDLKVPMPGPEFWRII 651
QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSQVGNHTKFTLWTEQA 709
DB 652 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSQVGNHTKFTLWTEQA 711
QY 710 HTVTVLAINSIGASVANFNLTFSMPMSKVNIQSLASAYPLNSSCVIYSWILSPSDYKLMY 769
DB 712 HTVTVLAINSIGASVANFNLTFSMPMSKVNIQSLASAYPLNSSCVIYSWILSPSDYKLMY 771
QY 770 FIEWKNLNEDGEIKMLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
DB 772 FIEWKNLNEDGEIKMLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 831
QY 830 QDDIEKHQSDAGLYIVPVIISSSILLGLTLISHQRMKKLFWEQVPPNPKNSWAQGLNF 889
DB 832 QDDIEKHQSDAGLYIVPVIISSSILLGLTLISHQRMKKLFWEQVPPNPKNSWAQGLNF 891
QY 890 QK 891
DB 892 QK 893

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RESULT 12
US-08-640-389A-3
; Sequence 3, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE: protein  
US-08-640-389A-3

Query Match 58.5%; Score 681; DB 2; Length 960;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFOQIDANWNIQCWLKGDCLKFICVESLEFKNLFRNRYNKVHLLYLPEVL 169  
DB 112 TFEVSTVNSLVFOQIDANWNIQCWLKGDCLKFICVESLEFKNLFRNRYNKVHLLYLPEVL 171  
QY 170 EDSPLVPQKGFQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPIMSV 229  
DB 172 EDSPLVPQKGFQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGVIFRSPIMSV 231  
QY 230 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPLOYQVKSSENSTTVIREADKIYS 289  
DB 232 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPLOYQVKSSENSTTVIREADKIYS 291  
QY 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDVYIYPPKILTSVGSNVS 349  
DB 292 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDVYIYPPKILTSVGSNVS 351  
QY 350 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFENLNETKPRGKFTYDA 409  
DB 352 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFENLNETKPRGKFTYDA 411  
QY 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHYRS 469  
DB 412 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHYRS 471  
QY 470 SLVCSDDIPSIHIPSEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDSPPTCV 529  
DB 472 SLVCSDDIPSIHIPSEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDSPPTCV 531  
QY 530 LPDSVVKPLPSSSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589  
DB 532 LPDSVVKPLPSSSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 591  
QY 590 DAKSKSVSLPVPDLCAVYAVOYRCKRLDGLGYWSNMSNPATVYVMDIKVPMRGPEFWRII 649  
DB 592 DAKSKSVSLPVPDLCAVYAVOYRCKRLDGLGYWSNMSNPATVYVMDIKVPMRGPEFWRII 651  
QY 650 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQA 709  
DB 652 NGDTMKKEKNVTLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQA 711  
QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSVNIQSLASAPLNSSCVIVSWILSPSDYKLMY 769  
DB 712 HTVTVLAINSIGASVANFNLTFSWPMKSVNIQSLASAPLNSSCVIVSWILSPSDYKLMY 771  
QY 770 FLEWKNLNEDGEIKWLRISSSVKYYIHDHFIPTEKYQFSLYPIFMEGVGKPKIINSFT 829  
DB 772 FLEWKNLNEDGEIKWLRISSSVKYYIHDHFIPTEKYQFSLYPIFMEGVGKPKIINSFT 831  
QY 830 QDDIEKHQSDAGLYVIVPVISSSILLGLTLLISHQRMKLEWEDVPNPKNCWSAQGLNF 889  
DB 832 QDDIEKHQSDAGLYVIVPVISSSILLGLTLLISHQRMKLEWEDVPNPKNCWSAQGLNF 891  
QY 890 OK 891  
DB 892 OK 893

RESULT 13  
US-08-693-696-8  
Sequence 8, Application US/08693696  
Patent No. 6005080  
GENERAL INFORMATION:  
APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas J.

APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/693,696  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/355,888  
FILING DATE: 14-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 7225-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-693-696-8

Query Match 58.5%; Score 681; DB 3; Length 960;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 781; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVFOQIDANWNIQCWLKGDCLKFICVESLEFKNLFRNRYNKVHLLYLPEVL 169  
DB 112 TFEVSTVNSLVFOQIDANWNIQCWLKGDCLKFICVESLEFKNLFRNRYNKVHLLYLPEVL 171  
QY 170 EDSPLVPQKGFQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPIMSV 229  
DB 172 EDSPLVPQKGFQMVHNCNSVHECCCLVPVPTAKLNDTLMLCKITSGVIFRSPIMSV 231  
QY 230 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPLOYQVKSSENSTTVIREADKIYS 289  
DB 232 QPINMVKPDPPLGLHMETDDGNLKISWSSPPLVPLOYQVKSSENSTTVIREADKIYS 291  
QY 290 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDVYIYPPKILTSVGSNVS 349  
DB 292 ATSLVDSILPGSSYEVOVGRKRLDGPIMSDMSTPRVFTTQDVYIYPPKILTSVGSNVS 351  
QY 350 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFENLNETKPRGKFTYDA 409  
DB 352 FHCITYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSKVTFENLNETKPRGKFTYDA 411  
QY 410 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHYRS 469  
DB 412 VYCCNEHECHHRYAELVIDVININISCEITDGYLTMTGCRWSTSTIOSLAESTLQLRHYRS 471  
QY 470 SLVCSDDIPSIHIPSEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDSPPTCV 529  
DB 472 SLVCSDDIPSIHIPSEPKDCYLQSDGFYECIFQPIFLLSGYTMTIRINHSLSGLSDSPPTCV 531  
QY 530 LPDSVVKPLPSSSVKAEITINIGLLKISWEKPVFPENNLOFOIRYGLSGKEVQWKMEYV 589

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|||||
Db 532 LPDSVVKPLPSSVKAETITINIGLTKISWEKVPENNLOFOIRYGLSGREVQWKMEYEV 591
QY 590 DAKSKSVSLPVPDLCAYAVAVQVRCKRLDGLGWSNMSNPAYTVVMDIKVPMRGPEFWRII 649
Db 592 DAKSKSVSLPVPDLCAYAVAVQVRCKRLDGLGWSNMSNPAYTVVMDIKVPMRGPEFWRII 651
QY 650 NGDTMKKEKNVTLLMKPLMKNDLSLSVQRYVINHTSCNGTWSSEDEVGNHTKFTFLWTEQA 709
Db 652 NGDTMKKEKNVTLLMKPLMKNDLSLSVQRYVINHTSCNGTWSSEDEVGNHTKFTFLWTEQA 711
QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSNLTSPSDYKLMY 769
Db 712 HTVTVLAINSIGASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSNLTSPSDYKLMY 771
QY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFT 829
Db 772 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFT 831
QY 830 QDDIEKHQSDAGLYIVPVISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNF 889
Db 832 QDDIEKHQSDAGLYIVPVISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNF 891
QY 890 OK 891
Db 892 OK 893
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## RESULT 14

US-08-588-190-3

Sequence 3, Application US/08588190

Patent No. 5856098

## GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas Joel  
APPLICANT: Shafer, Alan Wayne  
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR  
TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of The Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,190  
FILING DATE: 18-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 008907-0029-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-588-190-3

Query Match 49.8%; Score 580; DB 2; Length 960;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 110 TFSVTNSLVFQIDANWNIQCMWLGDKLFICIVESLEKLFERNYKVALLYLPEVL 169
Db 112 TFSVTNSLVFQIDANWNIQCMWLGDKLFICIVESLEKLFERNYKVALLYLPEVL 171
QY 170 EDSPLVPQKGFQWVHCNCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPPLMSV 229
Db 172 EDSPLVPQKGFQWVHCNCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFRSPLMSV 231
QY 230 OPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPEPLQOVKYSNSTVVIREADKIVS 289
Db 232 OPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPEPLQOVKYSNSTVVIREADKIVS 291
QY 290 ATSLVDSILPGSSYEVOVRGKRLDGPGLNSDWSSTPRVFTTQDVYIFPPKILTSVGSNVS 349
Db 292 ATSLVDSILPGSSYEVOVRGKRLDGPGLNSDWSSTPRVFTTQDVYIFPPKILTSVGSNVS 351
QY 350 FHCIIYKKENKIYPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFINLNETKPRGKFTYDA 409
Db 352 FHCIIYKKENKIYPSKEIYVMMNLAEKIPQSQDYVSDHVSQVTFINLNETKPRGKFTYDA 411
QY 410 VYCCNEHECHHRYAELVIDVININISCEITDGLTKMTCRWSTSTYQSLAESTLQRLRYHRS 469
Db 412 VYCCNEHECHHRYAELVIDVININISCEITDGLTKMTCRWSTSTYQSLAESTLQRLRYHRS 471
QY 470 SLYCSDIPSIHPISSEPKDCYLOSDFEYECIQQPIFLLSGYTMWIRINHSGLSDSPPTCV 529
Db 472 SLYCSDIPSIHPISSEPKDCYLOSDFEYECIQQPIFLLSGYTMWIRINHSGLSDSPPTCV 531
QY 530 LPDSVVKPLPSSVKAETITINIGLTKISWEKVPENNLOFOIRYGLSGREVQWKMEYEV 589
Db 532 LPDSVVKPLPSSVKAETITINIGLTKISWEKVPENNLOFOIRYGLSGREVQWKMEYEV 591
QY 590 DAKSKSVSLPVPDLCAYAVAVQVRCKRLDGLGWSNMSNPAYTVVMDIKVPMRGPEFWRII 649
Db 592 DAKSKSVSLPVPDLCAYAVAVQVRCKRLDGLGWSNMSNPAYTVVMDIKVPMRGPEFWRII 651
QY 650 NGDTMKKEKNVTLLMKPLMKNDLSLSVQRYVINHTSCNGTWSSEDEVGNHTKFTFLWTEQA 709
Db 652 NGDTMKKEKNVTLLMKPLMKNDLSLSVQRYVINHTSCNGTWSSEDEVGNHTKFTFLWTEQA 711
QY 710 HTVTVLAINSIGASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSNLTSPSDYKLMY 769
Db 712 HTVTVLAINSIGASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIYSNLTSPSDYKLMY 771
QY 770 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFT 829
Db 772 FIEWKNLNEDGEIKWLRISSSVKKYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFT 831
QY 830 QDDIEKHQSDAGLYIVPVISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNF 889
Db 832 QDDIEKHQSDAGLYIVPVISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNF 891
QY 890 OK 891
Db 892 OK 893
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## RESULT 15

US-08-618-957A-3

Sequence 3, Application US/08618957A

Patent No. 6355237

## GENERAL INFORMATION:

APPLICANT: Snodgrass, H. Ralph  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas Joel



APPLICANT: Shafer, Alan Wayne  
TITLE OF INVENTION: METHODS FOR USING THE OBSE  
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC  
TITLE OF INVENTION: DEVELOPMENT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of The Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,957A  
FILING DATE: 20-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 008907-0033-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 960 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-618-957A-3

Query Match 49.8%; Score 580; DB 4; Length 960;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 110 TFSVTNSLVFQOQIDANWNIQWLKGLKLFICYVESLFKNLFRNYKVHLYLPEVL 169  
Db 112 TFSVTNSLVFQOQIDANWNIQWLKGLKLFICYVESLFKNLFRNYKVHLYLPEVL 171  
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Db 172 EDSPLVPQKGSFQWVHCNCSVHCECECLVPVPTAKINDTLMLCKITSGVIFQSPMSV 231  
QY 230 QPINMVKPDPPLGLHMETDDCNLKISWSSPPLVPFLQYQVKSSENSTVIREADKIVS 289  
Db 232 QPINMVKPDPPLGLHMETDDCNLKISWSSPPLVPFLQYQVKSSENSTVIREADKIVS 291  
QY 290 ATSLLVDSILPGSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVYIFPKILTSVGSNVS 349  
Db 292 ATSLLVDSILPGSSYEVQVGRKRLDGPGLWSDWSTPRVFTTQDVYIFPKILTSVGSNVS 351  
QY 350 FHCIIYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDA 409  
Db 352 FHCIIYKKENKIVPSKEIYVMMNLAEKIPQSQDYDVSDHVSQVTFENLNETKPRGKFTYDA 411  
QY 410 VYCCNEHECHHRYAELVYDVNININISCETDGYLTMTQWSTSTIOSLAESTIQRLYHRS 469  
Db 412 VYCCNEHECHHRYAELVYDVNININISCETDGYLTMTQWSTSTIOSLAESTIQRLYHRS 471  
QY 470 SLVCSDIPIPSIHPISEPKCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLSDSPPTCV 529  
Db 472 SLVCSDIPIPSIHPISEPKCYLQSDGFYECIFQPIFLISGYTMWIRINHSLSGLSDSPPTCV 531

QY 530 LPDSVVKPLPPSSVKAELTINIGLLKISWEKPVFPENNIOFOIRYGLSGKEVQWMEYV 589  
Db 532 LPDSVVKPLPPSSVKAELTINIGLLKISWEKPVFPENNIOFOIRYGLSGKEVQWMEYV 591  
QY 590 DAKRSVSLPVPDLCAYYAVQVRCRLDGLGYSWNSNPNAYTVVMDIKVPMRGPFEWRIL 649  
Db 592 DAKRSVSLPVPDLCAYYAVQVRCRLDGLGYSWNSNPNAYTVVMDIKVPMRGPFEWRIL 651  
QY 650 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSQEDVGNHTKFTFLWTEQA 709  
Db 652 NGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVINHTSCNGTWSQEDVGNHTKFTFLWTEQA 711  
QY 710 HTVTVLAINSIGASVANENLTFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKILMY 769  
Db 712 HTVTVLAINSIGASVANENLTFSPMSKVNIVQSLSAVPLNSSCVIVSWILSPSDYKILMY 771  
QY 770 FIEWKNLNEDGEIKWLRISSSVKYYIHDHFIPIEKYQESLYP.FMEGVGKPKIINSFT 829  
Db 772 FIEWKNLNEDGEIKWLRISSSVKYYIHDHFIPIEKYQESLYP.FMEGVGKPKIINSFT 831  
QY 830 QDDIEKHQSDAGLYVIVPVISSILLGLTLLISHQRMKFLWEDVPPNPKNCMAQGLNF 889  
Db 832 QDDIEKHQSDAGLYVIVPVISSILLGLTLLISHQRMKFLWEDVPPNPKNCMAQGLNF 891  
QY 890 QK 891  
Db 892 QK 893  
RESULT 16  
US-08-588-526-3  
Sequence 3, Application US/08588526  
Patent No. 5882860  
GENERAL INFORMATION:  
APPLICANT: Snodgrass, H.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas  
APPLICANT: Shafer, Alan  
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR  
TITLE OF INVENTION: VARIANT  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,526  
FILING DATE: 18-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein



US-08-588-526-3

Query Match 40.7%; Score 474; DB 2; Length 908;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 774; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 110 TFEVSTVNSLVEFOIDANMNIOGWLKGLKLFICYVESLFRNRYKVLHLLVLEVL 169  
DB 112 TFEVSTVNSLVEFOIDANMNIOGWLKGLKLFICYVESLFRNRYKVLHLLVLEVL 171  
QY 170 EDSPLVPQKSGFQWVHCNCSVHECCCLVPPVPTAKLNDTLLMCKITSGGVI FQSP LMSV 229  
DB 172 EDSPLVPQKSGFQWVHCNCSVHECCCLVPPVPTAKLNDTLLMCKITSGGVI FQSP LMSV 231  
QY 230 QPINMVKPDPPLGLHMEITDDGNLKSMSPPPLVPLOQYQVYKSENSTTVI READKI VS 289  
DB 232 QPINMVKPDPPLGLHMEITDDGNLKSMSPPPLVPLOQYQVYKSENSTTVI READKI VS 291  
QY 290 ATSLVDSILPQSSYEVQVRGKRDLGPGINSDMSTPRVFTTQDVYIFPPKILTSVGSNVS 349  
DB 292 ATSLVDSILPQSSYEVQVRGKRDLGPGINSDMSTPRVFTTQDVYIFPPKILTSVGSNVS 351  
QY 350 FHCITYKKENKIYPSKEIWMNMNLAEKIPQSOYDVVSDHVS KVTFFNLNETKPRGKFTYDA 409  
DB 352 FHCITYKKENKIYPSKEIWMNMNLAEKIPQSOYDVVSDHVS KVTFFNLNETKPRGKFTYDA 411  
QY 410 VYCCNEHECHHRYAELVTDVNINISCEPDGYLTMTCRWSTSTIQSLAESTLQLRHRS 469  
DB 412 VYCCNEHECHHRYAELVTDVNINISCEPDGYLTMTCRWSTSTIQSLAESTLQLRHRS 471  
QY 470 SLVCSDFPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCV 529  
DB 472 SLVCSDFPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCV 531  
QY 530 LPDSVVKPLPSSSVKAEITINIGLKISMEKVPFPENNLOFOIRYGLSGKEVQWKMEYV 589  
DB 532 LPDSVVKPLPSSSVKAEITINIGLKISMEKVPFPENNLOFOIRYGLSGKEVQWKMEYV 591  
QY 590 DAKSKSVSLPVDLCAYAVQVRCKRLDGLGYWSMNSPAYTVMDIKVPMRGPEFWRII 649  
DB 592 DAKSKSVSLPVDLCAYAVQVRCKRLDGLGYWSMNSPAYTVMDIKVPMRGPEFWRII 651  
QY 650 NGDTMKKEKNVTLWKPLMKNDSLCSVORYVINHTSCNGTSEDEVGNHTKFTFLMTEQA 709  
DB 652 NGDTMKKEKNVTLWKPLMKNDSLCSVORYVINHTSCNGTSEDEVGNHTKFTFLMTEQA 711  
QY 710 HTVTYLAINSIGASVANFNLTFSWPMKVNIVQSLAYPLNSCVIYSWILSPSDYKLMY 769  
DB 712 HTVTYLAINSIGASVANFNLTFSWPMKVNIVQSLAYPLNSCVIYSWILSPSDYKLMY 771  
QY 770 FIEWKNLNEDGEIKWLRISSSVKYYITHDFIPIEKYQFSLYPIFMGVGKPKIINSFT 829  
DB 772 FIEWKNLNEDGEIKWLRISSSVKYYITHDFIPIEKYQFSLYPIFMGVGKPKIINSFT 831  
QY 830 QDDIEKHQSDAGLYIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQG 886  
DB 832 QDDIEKHQSDAGLYIVPVIISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQG 888

RESULT 17

US-08-640-389A-11

; Sequence 11, Application US/08640389A  
; Patent No. 5912123  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: DETECTION OF THE LEPTIN  
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR  
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY  
; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penzie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/640,389A  
; FILING DATE: 29-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-640-389A-11

Query Match 40.3%; Score 470; DB 2; Length 1165;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 970; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MICQKFCVALLHMEFIYVITAFNLSYPITPWRKRLSCMPNSTYDYELLBAGLSKNTSNS 60  
DB 1 MICQKFCVALLHMEFIYVITAFNLSYPITPWRKRLSCMPNSTYDYELLBAGLSKNTSNS 60  
QY 61 NGHETAVEPKRNSSGTHFSNLSKTFPHCCRSSEODRNCSLCADNTEGKTFVSTVNSLVF 120  
DB 61 NGHETAVEPKRNSSGTHFSNLSKTFPHCCRSSEODRNCSLCADNTEGKTFVSTVNSLVF 120  
QY 121 QOIDANMNIOGWLKGLKLFICYVESLFRNRYKVLHLLVLEVLDSPLVPQKGS 180  
DB 121 QOIDANMNIOGWLKGLKLFICYVESLFRNRYKVLHLLVLEVLDSPLVPQKGS 180  
QY 181 FOMVHCNCSVHECCCLVPPVPTAKLNDTLLMCKITSGGVI FQSP LMSVQPINMVKPDP 240  
DB 181 FOMVHCNCSVHECCCLVPPVPTAKLNDTLLMCKITSGGVI FQSP LMSVQPINMVKPDP 240  
QY 241 LGLHMEITDDGNLKSMSPPPLVPLOQYQVYKSENSTTVI READKI VSATSLLVDSILP 300  
DB 241 LGLHMEITDDGNLKSMSPPPLVPLOQYQVYKSENSTTVI READKI VSATSLLVDSILP 300  
QY 301 GSSYEVQVRGKRDLGPGIWSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
DB 301 GSSYEVQVRGKRDLGPGIWSDMSTPRVFTTQDVYIFPPKILTSVGSNVSFHCITYKKENKI 360  
QY 361 VPSKEIYWMNMNLAEKIPQSOYDVVSDHVS KVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
DB 361 VPSKEIYWMNMNLAEKIPQSOYDVVSDHVS KVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420  
QY 421 RYAEIYVIDVINISCEPDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDFPSIH 480  
DB 421 RYAEIYVIDVINISCEPDGYLTMTCRWSTSTIQSLAESTLQLRHRSLSYCSDFPSIH 480  
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPCVLPDSVVKPLPP 540  
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMIRINHSLSGLDSPPCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLKISWEKVPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPY 600  
Db 541 SSVKAEITINIGLKISWEKVPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPY 600  
QY 601 PDLCAVAVAVOVRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
Db 601 PDLCAVAVAVOVRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660  
QY 661 TLLMKPLMKNDSLCSVQRYVINHTHTSCNGTWSDEVGNHRTFTFLMTEQAHVTVLAINSI 720  
Db 661 TLLMKPLMKNDSLCSVQRYVINHTHTSCNGTWSDEVGNHRTFTFLMTEQAHVTVLAINSI 720  
QY 721 GASVANENLTFSPMSKVNIQSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 780  
Db 721 GASVANENLTFSPMSKVNIQSLSAYPLNSSCVIWSILSPSDYKLMYFIEWKNLNED 780  
QY 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
Db 781 GEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840  
QY 841 GLYVIVPVISSSILLGLTLLSHQRMKLFWEDEVNPKNCWSAQGLNFOKPEFHEHLFI 900  
Db 841 GLYVIVPVISSSILLGLTLLSHQRMKLFWEDEVNPKNCWSAQGLNFOKPEFHEHLFI 900  
QY 901 KHTASVTCGPILLPEPTEISDTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960  
Db 901 KHTASVTCGPILLPEPTEISDTSWKNKDEMPPTVYSLSTDLKSGVCSISDQFN 960  
QY 961 SVNFEAEGETEVTYE 975  
Db 961 SVNFEAEGETEVTYE 975

## RESULT 18

US-08-306-231-3  
; Sequence 3, Application US/08306231  
; Patent No. 5643748

; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,231  
; FILING DATE: 14-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 569 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-306-231-3

Query Match 39.4%; Score 459; DB 1; Length 569;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 SPLMSVQPINMVKPPDPLGLHMETDGNLKSISWSSPLVPPLQYQVKSSENSTVIRE 283  
Db 111 SPLMSVQPINMVKPPDPLGLHMETDGNLKSISWSSPLVPPLQYQVKSSENSTVIRE 170  
QY 284 ADKIVSATSLLVDSILPGSSYEYQVRGKRLDGPISWDSWSTPRVITTDVITYFPKILTS 343  
Db 171 ADKIVSATSLLVDSILPGSSYEYQVRGKRLDGPISWDSWSTPRVITTDVITYFPKILTS 230  
QY 344 VGSNVSFHCITYKKENKIVPSKEIYMMNLAEKIPQSQYDVVSDHVSKVTFENLNKPRG 403  
Db 231 VGSNVSFHCITYKKENKIVPSKEIYMMNLAEKIPQSQYDVVSDHVSKVTFENLNKPRG 290  
QY 404 KETIDAVYCCNEHECHRYAELIYDVNINISCTEDGYLTMTQWSTSTIOSLAESTIQ 463  
Db 291 KETIDAVYCCNEHECHRYAELIYDVNINISCTEDGYLTMTQWSTSTIOSLAESTIQ 350  
QY 464 LRYHRSSLYCSDIPSIHPISEPKDYLQSDGEYECIFQPIFLSGYTMWIRINHSLSLD 523  
Db 351 LRYHRSSLYCSDIPSIHPISEPKDYLQSDGEYECIFQPIFLSGYTMWIRINHSLSLD 410  
QY 524 SPPTCVLPDSVVKPLPPSSVKAETINIGLKISWEKVPENNLQFQIRYGLSGKEVQW 583  
Db 411 SPPTCVLPDSVVKPLPPSSVKAETINIGLKISWEKVPENNLQFQIRYGLSGKEVQW 470  
QY 584 KMYEYVDAKSKSVSLPDLCAVAVAVOVRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGP 643  
Db 471 KMYEYVDAKSKSVSLPDLCAVAVAVOVRCKRLDGLGWSNWSNPAYTVVMDIKVPMRGP 530  
QY 644 EFWRIINGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVIN 682  
Db 531 EFWRIINGDTMKKEKNVTLLMKPLMKNDSLCSVQRYVIN 569

## RESULT 19

US-08-640-389A-10  
; Sequence 10, Application US/08640389A  
; Patent No. 5912123

; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: DETECTION OF THE LEPTIN  
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR  
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/640,389A  
; FILING DATE: 29-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 896 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-640-389A-10

Query Match 26.4%; Score 307; DB 2; Length 896;  
Best Local Similarity 99.5%; Pred. No. 3.7e-301;  
Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 282 READKIVSATSLVDSILPGSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVYIFPPKIL 341  
DB 282 READKIVSATSLVDSILPGSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVYIFPPKIL 341  
QY 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNNLAETKIPQSOYDVSDHVSKEVFFNLNETKP 401  
DB 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNNLAETKIPQSOYDVSDHVSKEVFFNLNETKP 401  
QY 402 RGKFTYDAVYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIQSLAEST 461  
DB 402 RGKFTYDAVYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIQSLAEST 461  
QY 462 LQLRVHRSSLYCSDIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGS 521  
DB 462 LQLRVHRSSLYCSDIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGS 521  
QY 522 LDSPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPVFPENNLOFOIRYGLSGKEV 581  
DB 522 LDSPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPVFPENNLOFOIRYGLSGKEV 581  
QY 582 QWKMEYVDKAKSVSLPVPDLCAVYAVOVRCKRLDGLGWSMNSNPATYVMDIKVPMR 641  
DB 582 QWKMEYVDKAKSVSLPVPDLCAVYAVOVRCKRLDGLGWSMNSNPATYVMDIKVPMR 641  
QY 642 GPEFWRIINGDTMKKEKNVTLMLKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKF 701  
DB 642 GPEFWRIINGDTMKKEKNVTLMLKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKF 701  
QY 702 TELMTEQAHTVTVLAINSIGASVANFNLTFSWPMKVNIVOSLSAYPLNSSCVIVSWILS 761  
DB 702 TELMTEQAHTVTVLAINSIGASVANFNLTFSWPMKVNIVOSLSAYPLNSSCVIVSWILS 761  
QY 762 PSDYKLMYFIIEKWNLEDGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
DB 762 PSDYKLMYFIIEKWNLEDGEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
QY 822 PKIINSFTODDIEKHQSDAGLYVIVPIISSILGLTLLISHQRMKKLFMEDVPPNPKNC 881  
DB 822 PKIINSFTODDIEKHQSDAGLYVIVPIISSILGLTLLISHQRMKKLFMEDVPPNPKNC 881  
QY 882 SWAOGILNFOR 891  
DB 882 SWAOGILNFOR 891

RESULT 20  
US-08-640-389A-9  
Sequence 9, Application US/08640389A  
Patent No. 5912123  
GENERAL INFORMATION:  
APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas J.  
APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: DETECTION OF THE LEPTIN  
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR  
TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/640,389A  
FILING DATE: 29-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 906 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-640-389A-9

Query Match 26.4%; Score 307; DB 2; Length 906;  
Best Local Similarity 99.5%; Pred. No. 3.8e-301;  
Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 282 READKIVSATSLVDSILPGSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVYIFPPKIL 341  
DB 282 READKIVSATSLVDSILPGSSYEVOVRGKRLDGPGLWSDMSTPRVFTTQDVYIFPPKIL 341  
QY 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNNLAETKIPQSOYDVSDHVSKEVFFNLNETKP 401  
DB 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNNLAETKIPQSOYDVSDHVSKEVFFNLNETKP 401  
QY 402 RGKFTYDAVYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIQSLAEST 461  
DB 402 RGKFTYDAVYCCNEHECHHRYAELVIDVNINISCEITDGYLTMTCRWSTSTIQSLAEST 461  
QY 462 LQLRVHRSSLYCSDIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGS 521  
DB 462 LQLRVHRSSLYCSDIPSIHIPSEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGS 521  
QY 522 LDSPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPVFPENNLOFOIRYGLSGKEV 581  
DB 522 LDSPTCVLPDSVVKPLPPSSVKAETITINIGLKISWEKPVFPENNLOFOIRYGLSGKEV 581  
QY 582 QWKMEYVDKAKSVSLPVPDLCAVYAVOVRCKRLDGLGWSMNSNPATYVMDIKVPMR 641  
DB 582 QWKMEYVDKAKSVSLPVPDLCAVYAVOVRCKRLDGLGWSMNSNPATYVMDIKVPMR 641  
QY 642 GPEFWRIINGDTMKKEKNVTLMLKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKF 701  
DB 642 GPEFWRIINGDTMKKEKNVTLMLKPLMKNDLSGVQRYVINHTSCNGTWSDEVGNHTKF 701  
QY 702 TELMTEQAHTVTVLAINSIGASVANFNLTFSWPMKVNIVOSLSAYPLNSSCVIVSWILS 761

|||||  
Db 702 TELMTEQAHTVTVLAINSIGASVANENLTFSPMPSKVNIVQSLAYPLNSSCVIYSWILS 761  
QY 762 PSDYKLMYFIIEWKNLNDEGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
Db 762 PSDYKLMYFIIEWKNLNDEGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
QY 822 PKINSFTODDIEKHQSDAGLYIVPVIISSSILLGTLISHQRMKLLFWEDVPNPKNC 881  
Db 822 PKINSFTODDIEKHQSDAGLYIVPVIISSSILLGTLISHQRMKLLFWEDVPNPKNC 881  
QY 882 SWAGLNFQK 891  
Db 882 SWAGLNFQK 891

RESULT 21  
US-08-640-389A-8  
; Sequence 8, Application US/08640389A  
; Patent No. 5912123

; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: DETECTION OF THE LEPTIN  
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR  
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/640,389A  
; FILING DATE: 29-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 958 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-640-389A-8

Query Match 26.4%; Score 307; DB 2: Length 958;  
Best Local Similarity 99.5%; Pred. No. 4e-301;  
Matches 607; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 282 READKIVATSLSLVDSILPGSSYEYQVRGKRLDGPGLMSDMSIPRVFTTQDVYIFPKIL 341  
Db 282 READKIVATSLSLVDSILPGSSYEYQVRGKRLDGPGLMSDMSIPRVFTTQDVYIFPKIL 341  
QY 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNLAEKIPQSQYDVVSDHVSQVTEFFNLNETKP 401  
|||||

Db 342 TSVGSNVSFHCITYKKENKIVPSKEIWMNLAEKIPQSQYDVVSDHVSQVTEFFNLNETKP 401  
QY 402 RGFETYDAVYCCNEHECHHRYAELVIDVININISCEFDGYLTMTQCRWSTSTIQSLAEST 461  
Db 402 RGFETYDAVYCCNEHECHHRYAELVIDVININISCEFDGYLTMTQCRWSTSTIQSLAEST 461  
QY 462 LQLRHRSSLYCSDIPSIHPISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSICS 521  
Db 462 LQLRHRSSLYCSDIPSIHPISEPKDCYLOSDFEYECIFQPIFLSGYTMIRINHSICS 521  
QY 522 LDSPPTCVLPDSVVKPLPPSSVKAETITNIGLLKISWEKVPENNLOFOIRYGLSGREV 581  
Db 522 LDSPPTCVLPDSVVKPLPPSSVKAETITNIGLLKISWEKVPENNLOFOIRYGLSGREV 581  
QY 582 QMKMEYVDKSKSVSLPVPDLCAVYAVOVRCKRLDGLGYMSNWSNPAYTVMDIKVPMR 641  
Db 582 QMKMEYVDKSKSVSLPVPDLCAVYAVOVRCKRLDGLGYMSNWSNPAYTVMDIKVPMR 641  
QY 642 GPEFWRIINGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHTSCNGTWSSEYVGNHTKF 701  
Db 642 GPEFWRIINGDTMKKEKNVTLMLKPLKNDSLCSVQRYVINHTSCNGTWSSEYVGNHTKF 701  
QY 702 TELMTEQAHTVTVLAINSIGASVANENLTFSPMPSKVNIVQSLAYPLNSSCVIYSWILS 761  
Db 702 TELMTEQAHTVTVLAINSIGASVANENLTFSPMPSKVNIVQSLAYPLNSSCVIYSWILS 761  
QY 762 PSDYKLMYFIIEWKNLNDEGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
Db 762 PSDYKLMYFIIEWKNLNDEGEIKWLRISSSVKKYIHDHFIPIEKYQFSLYPIFMEGVGK 821  
QY 822 PKINSFTODDIEKHQSDAGLYIVPVIISSSILLGTLISHQRMKLLFWEDVPNPKNC 881  
Db 822 PKINSFTODDIEKHQSDAGLYIVPVIISSSILLGTLISHQRMKLLFWEDVPNPKNC 881  
QY 882 SWAGLNFQK 891  
Db 882 SWAGLNFQK 891

RESULT 22  
US-08-803-346-64  
; Sequence 64, Application US/08803346  
; Patent No. 6281346  
; GENERAL INFORMATION:  
; APPLICANT: HESS, JOHN W.  
; APPLICANT: CASKEY, C. THOMAS  
; APPLICANT: LIU, QINGYUN  
; APPLICANT: PHILLIPS, MICHAEL SEAN  
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
; TITLE OF INVENTION: ENCODING THEM  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JOANNE M. GIESSEER - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,346  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GIESSEER, JOANNE M  
; REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19642Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3046  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-803-346-64

Query Match  
Best Local Similarity 100.0%; Pred. No. 6.6e-70;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 LKISWEKPVPEPNNLQFOIRYGLSGKEVQWKMVEYVDAKSKSVSLPVDLCAYVAVQVR 612  
|||||  
DB 1 LKISWEKPVPEPNNLQFOIRYGLSGKEVQWKMVEYVDAKSKSVSLPVDLCAYVAVQVR 60  
|||||

QY 613 CKRLDGLGYWSNWSNPA 629  
|||||  
DB 61 CKRLDGLGYWSNWSNPA 77  
|||||

RESULT 23  
US-08-803-346-61  
Sequence 61, Application us/08803346  
Patent No. 6281346  
GENERAL INFORMATION:  
APPLICANT: HESS, JOHN W.  
APPLICANT: CASKEY, C. THOMAS  
APPLICANT: LIU, QINGYUN  
APPLICANT: PHILLIPS, MICHAEL SEAN  
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000,  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,346  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GIESSEY, JOANNE M  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 19642Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3046  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-803-346-61

Query Match  
Best Local Similarity 100.0%; Pred. No. 6.7e-69;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 NLKISWSPPLVPEPPLQYQVKSSENSTVIREADKIVSATSLVDSLPGSSYEVOVRGK 311  
|||||  
DB 1 NLKISWSPPLVPEPPLQYQVKSSENSTVIREADKIVSATSLVDSLPGSSYEVOVRGK 60  
|||||

QY 312 RLDDPGIWSDMSTPRV 327  
|||||  
DB 61 RLDDPGIWSDMSTPRV 76  
|||||

RESULT 24  
US-08-599-455B-2  
Sequence 2, Application us/08599455B  
Patent No. 5972621  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT  
MODULATE BODY WEIGHT USING THE OB RECEPTOR  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,455B  
FILING DATE: 22-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 894 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-599-455B-2

Query Match  
3.6%; Score 42; DB 2; Length 894;





```
; APPLICANT: MERCK & CO., INC.
; TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
; FILE REFERENCE: 19693
; CURRENT APPLICATION NUMBER: US/08/827,962A
; CURRENT FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 60/016,899
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-19

Query Match      3.6%; Score 42; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

RESULT 28
US-08-827-962-21
; Sequence 21, Application US/08827962A
; Patent No. 6258944
; GENERAL INFORMATION:
; APPLICANT: MERCK & CO., INC.
; TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
; FILE REFERENCE: 19693
; CURRENT APPLICATION NUMBER: US/08/827,962A
; CURRENT FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 60/016,899
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-21

Query Match      3.6%; Score 42; DB 4; Length 895;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541
DB 498 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

RESULT 29
US-08-640-389A-12
; Sequence 12, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
```

```
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-640-389A-12

Query Match      3.6%; Score 42; DB 2; Length 896;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541
DB 500 FQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPS 541

RESULT 30
US-08-599-455B-43
; Sequence 43, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
```

APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-599-455B-43

Query Match 3.6%; Score 42; DB 2; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 539

RESULT 31  
US-08-827-962-15  
Sequence 15, Application US/08827962A  
Patent No. 6258944  
GENERAL INFORMATION:  
APPLICANT: MERCK & CO., INC.  
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS  
TITLE OF INVENTION: ENCODING THEM  
FILE REFERENCE: 19693  
CURRENT APPLICATION NUMBER: US/08/827,962A  
CURRENT FILING DATE: 1997-05-06  
PRIOR APPLICATION NUMBER: 60/016,899  
PRIOR FILING DATE: 1996-05-06  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 1162  
TYPE: PRT  
ORGANISM: Rattus No. 6258944vegicus  
US-08-827-962-15

Query Match 3.6%; Score 42; DB 4; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 539

RESULT 32  
US-08-827-962-20  
Sequence 20, Application US/08827962A  
Patent No. 6258944  
GENERAL INFORMATION:  
APPLICANT: MERCK & CO., INC.  
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS  
TITLE OF INVENTION: ENCODING THEM  
FILE REFERENCE: 19693  
CURRENT APPLICATION NUMBER: US/08/827,962A  
CURRENT FILING DATE: 1997-05-06

PRIOR APPLICATION NUMBER: 60/016,899  
PRIOR FILING DATE: 1996-05-06  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 1162  
TYPE: PRT  
ORGANISM: Rattus No. 6258944vegicus  
US-08-827-962-20

Query Match 3.6%; Score 42; DB 4; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMWIRINHSLSLDSPTCVLPDSVVKPLPPS 539

RESULT 33  
US-08-803-346-1  
Sequence 1, Application US/08803346  
Patent No. 6281346  
GENERAL INFORMATION:  
APPLICANT: HESS, JOHN W.  
APPLICANT: CASKEY, C. THOMAS  
APPLICANT: LIU, QINGYUN  
APPLICANT: PHILLIPS, MICHAEL SEAN  
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSER: JOANNE M. GIESSEER - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,346  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GIESSEER, JOANNE M  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 19642Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3046  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1162 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-803-346-1

Query Match 3.6%; Score 42; DB 4; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 34

US-09-069-781B-43

; Sequence 43, Application US/09069781B  
; Patent No. 6287782  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,781B  
; FILING DATE: 29-APRIL-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: US 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: US 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: US 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: US 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: US 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: US 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: US 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: US 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Melklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/082001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1162 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-09-069-781B-43

Query Match 3.6%; Score 42; DB 4; Length 1162;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 FQPIFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPS 541  
|||||  
Db 498 FQPIFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPPS 539

## RESULT 35

US-08-803-346-63

; Sequence 63, Application US/08803346  
; Patent No. 6281346  
; GENERAL INFORMATION:  
; APPLICANT: HESS, JOHN W.  
; APPLICANT: CASKEY, C. THOMAS  
; APPLICANT: LIU, QINGYUN  
; APPLICANT: PHILLIPS, MICHAEL SEAN  
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
; TITLE OF INVENTION: ENCODING THEM  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,346  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GIESSER, JOANNE M  
; REGISTRATION NUMBER: 32,838  
; REFERENCE/DOCKET NUMBER: 19642Y  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-3046  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 77 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-803-346-63

Query Match 2.1%; Score 24; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.2e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 SWEKPVFPENNLFQIRYGLSGKE 580  
|||||  
Db 5 SWEKPVFPENNLFQIRYGLSGKE 28

## RESULT 36

US-08-701-382-6

; Sequence 6, Application US/08701382  
; Patent No. 6004758  
; GENERAL INFORMATION:  
; APPLICANT: OLSSON, Lennart  
; APPLICANT: NAVREND, Tatajna  
; TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES INVOLVED IN  
; TITLE OF INVENTION: MODULATION OF RESPONSE TO LIGAND BINDING

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94114187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/701,382  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SHERWOOD, Pamela J.  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: A63139-1/PJS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-494-8700  
TELEFAX: 415-494-8771  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-701-382-6

Query Match 2.0%; Score 23; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.3e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIYWMNLAEKIP 377  
DB 1 KKENKIVPSKEIYWMNLAEKIP 23

RESULT 37  
US-09-028-937-6  
Sequence 6, Application US/09028937  
Patent No. 6333031  
GENERAL INFORMATION:  
APPLICANT: Olsson, Lennart  
APPLICANT: Naranda, Tatjana  
TITLE OF INVENTION: Receptor Derived Peptides As Modulators  
TITLE OF INVENTION: Of Receptor Activity  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/028,937  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/788,820  
FILING DATE: 23-JAN-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/701,382  
FILING DATE: 22-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,999  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 949-8711  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-028-937-6

Query Match 2.0%; Score 23; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.3e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIYWMNLAEKIP 377  
DB 1 KKENKIVPSKEIYWMNLAEKIP 23

RESULT 38  
US-08-788-820-6  
Sequence 6, Application US/08788820  
Patent No. 6346390  
GENERAL INFORMATION:  
APPLICANT: Olsson, Lennart  
APPLICANT: Naranda, Tatjana  
TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES INVOLVED IN  
TITLE OF INVENTION: MODULATION OF RESPONSE TO LIGAND BINDING  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/788,820  
FILING DATE: 23-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,999  
FILING DATE: 08-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/701,382  
FILING DATE: 22-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-63139-2/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 50..1030  
US-08-788-820-6

Query Match 2.0%; Score 23; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.3e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 KKENKIVPSKEIYWMNMLAEKIP 377  
|||||  
DB 1 KKENKIVPSKEIYWMNMLAEKIP 23

## RESULT 39

US-08-803-346-62  
Sequence 62, Application US/08803346  
Patent No. 6281346

## GENERAL INFORMATION:

APPLICANT: HESS, JOHN W.  
APPLICANT: CASKEY, C. THOMAS  
APPLICANT: LIU, QINGYUN  
APPLICANT: PHILLIPS, MICHAEL SEAN  
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,346  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GIESSER, JOANNE M  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 19642Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3046  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-803-346-62

Query Match 1.7%; Score 20; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.4e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 SWEKPVFPENNLOFQIRYGL 576  
|||||  
DB 5 SWEKPVFPENNLOFQIRYGL 24

## RESULT 40

US-08-306-231-14  
Sequence 14, Application US/08306231  
Patent No. 5643748

## GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas J.  
APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,231  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 7225-076  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-306-231-14

Query Match 1.3%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GSSYEVOVRGRKLDG 315  
|||||  
DB 1 GSSYEVOVRGRKLDG 15

## RESULT 41

US-08-306-231-15  
Sequence 15, Application US/08306231  
Patent No. 5643748

## GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas J.  
APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10036-2711  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/306,231  
;; FILING DATE: 14-SEP-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Poissant, Brian M.  
;; REGISTRATION NUMBER: 28,462  
;; REFERENCE/DOCKET NUMBER: 7225-076  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;;  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;;  
US-08-306-231-15

Query Match 1.3%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 CAVYAVQVRCKRLDG 618  
Db 1 CAVYAVQVRCKRLDG 15

RESULT 42  
US-08-355-888A-30  
; Sequence 30, Application US/08355888A  
; Patent No. 5763211  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/355,888A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.

;; REGISTRATION NUMBER: 28,462  
;; REFERENCE/DOCKET NUMBER: 7225-076  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;;  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;;  
US-08-355-888A-30

Query Match 1.3%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GSSYEYQVRGKRLDG 315  
Db 1 GSSYEYQVRGKRLDG 15

RESULT 43  
US-08-355-888A-31  
; Sequence 31, Application US/08355888A  
; Patent No. 5763211  
; GENERAL INFORMATION:  
; APPLICANT: Snodgrass, H. R.  
; APPLICANT: Cioffi, Joseph  
; APPLICANT: Zupancic, Thomas J.  
; APPLICANT: Shafer, Alan W.  
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/355,888A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 7225-076  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; ;  
US-08-355-888A-31

Query Match 1.3%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;





APPLICATION NUMBER: US 08/355,888  
FILING DATE: 14-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 7225-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-693-696-30

Query Match 1.3%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GSSYEVQVRGKRLDG 315  
|||||  
DB 1 GSSYEVQVRGKRLDG 15

## RESULT 47

US-08-693-696-31  
Sequence 31, Application US/08693696  
Patent No. 6005080  
GENERAL INFORMATION:  
APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas J.  
APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/693,696  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/355,888  
FILING DATE: 14-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 7225-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-693-696-31

Query Match 1.3%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 604 CAVYAVQVRCKRLDG 618  
|||||  
DB 1 CAVYAVQVRCKRLDG 15

## RESULT 48

US-08-306-231-9  
Sequence 9, Application US/08306231  
Patent No. 5643748  
GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.  
APPLICANT: Cioffi, Joseph  
APPLICANT: Zupancic, Thomas J.  
APPLICANT: Shafer, Alan W.  
TITLE OF INVENTION: Hu-B1.219, A NOVEL HEMATOPOIETIN  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,231  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 7225-076  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-306-231-9

Query Match 1.1%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 569 QFOIRYGLSGKEV 581  
|||||  
DB 1 QFOIRYGLSGKEV 13

## RESULT 49

US-08-355-888A-25  
Sequence 25, Application US/08355888A  
Patent No. 5763211

```

: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/355,888A
: FILING DATE: 14-DEC-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7225-078
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-355-888A-25

Query Match          1.1%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 QFOIRYGLSGKEV 581
DB 1 QFOIRYGLSGKEV 13

RESULT 50
US-08-693-697-25
: Sequence 25, Application US/08693697
: Patent No. 5869610
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Cioffi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
```

```

: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693,697
: FILING DATE: 05-AUG-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 8907-0037-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-493-4935
: TELEFAX: 650-493-5556
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-693-697-25
```

```

Query Match          1.1%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 QFOIRYGLSGKEV 581
DB 1 QFOIRYGLSGKEV 13
```

Search completed: May 18, 2002, 07:04:11  
Job time: 290 sec

Sun May 19 08:38:55 2002

us-08-779-457-2.01igo.ra1

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